Novel

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07-MAR-2003; 2003WO-US006962.
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Taubman MA;
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ADD93621;
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 Add31244 Streptoco
Add39659 Streptoco
Add39653 Streptoco
Add37772 Streptoco
Adx37773 Streptoco
Adx37776 Streptoco
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Add39651 Streptoco
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Adt502275 Spneumon
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                                                                                                                                                                                                                                                                                                                     2443163
              GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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                                                                                                                                                                                                                                                                                    2443163 seqs, 439378781 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                         OM protein - protein search, using sw model
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ADD93653
ADX37272
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ADX37276
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ADX37274
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ADD93631
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ADR83884
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Gapop 10.0 , Gapext 0.5
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geneseqp2000s:*
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length: 2000000000
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Maximum DB seq
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ADT50226 ADT50165

AEB91542

S agalact Streptoco Streptoco S. pyogen
M. catarr
M. catarr
L. pneumo
L. pneumo
Protein e Lactococc Usp45 pro The present sequence is that of SYI peptide comprising amino acid residues 113-132 of the glucan binding protein-B (GbpB) of Streptococcus mutans strain SK2 ADD93649. The peptide binds to a major histocompatibility complex (MHC) class II protein. It was identified as a prediction, which was used to search the primary amino acid sequence of GpbB for known MHC class II binding motifs. The peptide squence of comprise MHC class II binding motifs. The peptide caries. These comprise MHC class II binding motifs. The peptide caries. These with peptide subunits (preferably from the catalytic domain) of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Diepitopic or Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein. Protein e Streptoco Streptoco encod faeciu Glucanase Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen. MSP Abb29684 Adu69524 Adv81392 Adv81808 Adv79645 Abb55584 Abb55584 Aar14530 Aar14530 Aar1450 Abr71294 Abp71294 Abb71295 Abb71294 Abb71295 Abb71294 Abb71295 Abb71298 Abb71298 Aaw22011 (Aaw98919 (Streptococcus mutans glucan binding protein-B SYI peptide. ALIGNMENTS ADR94595
AEA58465
AEA58465
AEA58465
ADF29684
ADV859524
ADV81808
ADV79645
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ABF71295 ADD93621 standard; peptide; 20 AA. Claim 12; Page 10; 49pp; English.

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RESULT 2 ADX3724

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Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
                                                                                                                                      Streptococcus mutans glucan binding protein-B.
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/note= "HLA-binding peptide"
403. .422
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'note= "HLA-binding peptide"
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re= "HLA-binding peptide"
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/note= "HLA-binding peptide"
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note= "HLA-binding peptide"
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'note= "HLA-binding
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                                                      ADD93649 standard; protein; 431 AA.
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08-AUG-2002; 2002US-0402483P.
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/note= "HL
365. .384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
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multiepitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in passive immunisation.
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                                                                                                                                                                                                                                                                                                                                                immunogenicity; immune stimulation; glucan binding protein-B; microparticle; major histocompatibility complex; tooth disease.
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Pred. No. 1.9e-08;
; Mismatches 0; Indels
                                                                              Query Match
100.0%; Score 94; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                        Streptococcus mutant glucan binding protein B peptide #1.
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08-JAN-1999; 99US-0115142P.
12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-03632209P.
08-AUG-2002; 2002US-0402483P.
07-MAR-2003; 2003US-00383930.
                                                                                                                                                                                                                                      ADX37244 standard; peptide; 20
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Best Local Similarity 100.
Matches 20; Conservative
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(TAUB/) TAUBMAN M A.
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Gaps

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Length 431;

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caries. The compositions comprise major histocompatibility complex (MHC) class II protein-binding GDpB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Diepicopic or multiepicopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GDpB can be used in
                                                                                                                                                                                                                                                                                                                                                                                                                               Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
                                                                                                                                                      100.0%; Score 94; DB 7; 1
100.0%; Pred. No. 6.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus mutans glucan binding protein-B.
                                                                                                                                                                                    0; Mismatches
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08-AUG-2002; 2002US-0402483P
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                                                                                                                    The present sequence is the protein sequence of the glucan binding protein—B (GDpB) of Streptococcus mutans strain SK32. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions comprise major histocompatibility complex (MHC) class II protein-binding GbpB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The antibods in a mammal. Dispitopic or multiplepticip polypeptides compensated synthetically or by recombinant DNA technology. Antibodies present a staised against MHC class II binding fragments of GbpB can be used in
                          Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
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                                                                                                                                                                                                                                                                                                                                         Score 94; DB 7; ]
Pred. No. 6.8e-07;
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                                                                                             Claim 6; Page 7; 49pp; English.
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08-AUG-2002; 2002US-0402483P
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Best Local Similarity 100.00
--hes 20; Conservative
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                                                                                                                                                                                                                                                                                    passive immunisation.
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2003-845091/78.
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             GENBANK; AY046410
                                                                                                                                                                                                                                                                                                               Sequence 431 AA;
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The present sequence is the protein sequence of the glucan binding protein-B (GbpB) of Streptococcus mutans strain SSM3. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions comprise major histocompatibility complex (MHC) class II protein-binding GbpB peptides, especially HLA-binding peptides, cowpositions are used in a claimed method of eliciting production of an antibody in a mammal. Displication of mutipodicy in a mammal. Displication of mutipodic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in
Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
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Pred. No. 6.8e-07;
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Best Local Similarity
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Matches

ઠ 셤 ADX3727:

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The invention relates to a composition comprising a fragment of a glucan binding protein-B (GbpB) and a biocompatible microparticle, where the fragment binds to a major histocompatibility complex (MHC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds to a Streptococcus mutans GbpB protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
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                                                                                                    immunogenicity; immune stimulation; glucan binding protein-B; microparticle; major histocompatibility complex; tooth disease.
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                                                     Streptococcus mutant glucan binding protein B variant #2.
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100.0%; Pred. No. 6.8e-07;
ive 0; Mismatches 0;
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12-ARR-1999; 99US-015142P.
07-MAR.2002; 2002US-0363209P.
08-AUG-2002; 2002US-0402483P.
07-MAR-2003; 2003US-00383930.
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21-APR-2005 (first entry)
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                                                                                                                                                                                                   Streptococcus mutans
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(TAUB/) TAUBMAN M A.
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microparticle; major histocompatibility complex; tooth disease.
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Pred. No. 6.8e-07;
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     0; Mismatches
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08-JAN-1999; 99US-0115142P.
12-APR-1999; 99US-0020049.
07-MAR-2002; 2002US-0363209P.
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07-MAR-2003; 2003US-00383930
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Les 20; Conservative
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TAUBMAN M A.
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Matches 20
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Gaps

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10-FEB-2005

ADX37273;

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RESULT 7 ADX37273

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cach of the computed five attributes, and identifying the adheein and adhesin-like proteins having probability of being an adhesin and adhesin-like proteins having probability of being an adhesin (Pad) as equal or greater than 0.51. Also claimed is a set of 274 annotated genes encoding adhesin and adhesin-like proteins, having 274 fully defined 162-1151 base pair (SEQ ID NO: 385-658) sequences; a set of 105 hypothetical genes encoding adhesin and adhesin-like proteins, having 105 fully offined 306-15876 base pairs (SEQ ID NO: 659-763); a set of 279 annotated adhesin and adhesin-like proteins, having 105 fully defined 106-5291 base pair (SEQ ID NO: 1-279); a set of 105 hypothetical adhesin and adhesin-like proteins, having 105 fully defined 106-5291 base pair (SEQ ID NO: 1-279); a set of 105 hypothetical adhesin and adhesin-like proteins, of therapeutic potential, and identifying adhesin and adhesin-like pased on (MI). (MI) is useful for identifying adhesin and adhesin-like proteins for therapeutic potential, and identifying and short-listing proteins for further testing in development of new vaccine formulations to eliminate diseases caused by various pathogenic organisms. (MI) is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for identifying putative adhesins that are important in drug discovery and preventing therapeutics for whooping cough, pneumonia, gastric ulcer and urinary tract infections. (M1) identifies adhesins from
Computational method for identifying adhesin and adhesin like molecules, comprises computing sequence-based attributes of protein sequences using neural network software and training an artificial neural network.
                                                                                                                                 The present invention relates to a computational method (M1) for dentifying adhesin and adhesin-like proteins, by computing the sequence based attributes of protein sequences using five attribute modules of a neural network software, training an artificial neural network (ANN) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 distantly related organisms, and from bacteria belonging to a wide phylogenetic spectrum. (M1) is capable of predicting adhesive nature of unique proteins. The present sequence is a microbial pathogen adhesin
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                                                                                             Claim 16; SEQ ID NO 210; 402pp; English,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (FORS-) FORSYTH INST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 431 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a composition comprising a fragment of a glucan binding protein-B (GbpB) and a biocompatible microparticle, where the fragment binds to a major histocompatibility complex (MHC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds to a Streptococcus mutans GbpB protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gastrointestinal-gen.; urinary tract infection; antimicrobial; uropathic.
                                                                                                                                                                                                                                                                                                                                                                    New composition comprising a fragment of a glucan binding protein-B (GpB) that binds to MRC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Microbial pathogen adhesin protein sequence, SEQ ID NO:210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 431;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; SEQ ID NO 33; 73pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 KSNAATSYINAIINSKSVSD 132
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                                           98US-0081550P.
99US-0115142P.
99US-00290049.
2002US-0363209P.
2002US-0402483P.
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20-JUL-2004; 2004US-0589227P.
  09-MAR-2004; 2004US-00797821
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Best Local Similarity 100.0
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                                                                                                                                                                                                                                                                         Smith DJ, Taubman MA;
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                                                                                                                                                                                                    (SMIT/) SMITH D J.
(TAUB/) TAUBMAN M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus mutans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 431 AA;
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                                                                                                           07-MAR-2002;
08-AUG-2002;
07-MAR-2003;
                                             13-APR-1998;
08-JAN-1999;
12-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AEB91500;
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The present sequence is the protein sequence of the glucan binding protein-B (GbpB) of Streptococcus mutans strain 15JP2. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions comprise major histocompatibility complex (WHC) class II protein-binding GbpB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The artibod in a mammal. Dispitopic or multipedicip production of an antibod in a mammal. Dispitopic or multipedicip polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies
          Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
                                                                                                                   Claim 5; Page 8; 49pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Dassive immunisation
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English.

Sequence 432 AA;

Length 432; Indels 0 Score 94; DB 7; I Pred. No. 6.8e-07; 0; Mismatches 1 KSNAATSYINAIINSKSVSD 20 100.0%; Query Match 100. Best Local Similarity 100. Matches 20; Conservative 셤 8

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Gaps

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ADD93652 standard; protein; 432 AA. ADD93652; RESULT 11

29-JAN-2004 (first entry)

Streptococcus mutans glucan binding protein-B.

Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.

Streptococcus mutans.

WO2003075845-A2

18-SEP-2003

07-MAR-2003; 2003WO-US006962

07-MAR-2002; 2002US-0363209P.

(FORS-) FORSYTH INST.

Smith DJ, Taubman MA;

WPI; 2003-845091/78.

GENBANK; AY046413.

The present sequence is the protein sequence of the glucan binding protein-B (GbpB) of Streptococcus mutans strain 3SN1. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions comprise major histocompatibility complex (MHC) class II protein-binding GbpB peptides, especially HLA-binding peptides, Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein. Claim 5; Page 8; 49pp; English

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Gaps

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ch 100.0%; Score 94; DB 9; Length 432; I Similarity 100.0%; Pred. No. 6.8e-07; 20; Conservative 0; Mismatches 0; Indels

Best Local Similarity Matches 20; Conserva

Query Match

Sequence 432 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing
covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of a antibody in a mammal. Diepitopic or multiepitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunogenicity; immune stimulation; glucan binding protein-B; microparticle; major histocompatibility complex; tooth disease.
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                                                                                                                                                    100.0%; Score 94; DB 7; Length 432; 100.0%; Pred. No. 6.8e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus mutant glucan binding protein B variant #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; SEQ ID NO 31; 73pp; English.
                                                                                                                                                                                                                                                                                                                                            ADX37274 standard; protein; 432 AA
                                                                                                                                                                                                                                            KSNAATSYINAIINSKSVSD 132
                                                                                                                                                                                                                         1 KSNAATSYINAIINSKSVSD 20
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08-JAN-1999; 99US-0115142P.
12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-0363209P.
08-MUG-2002; 2002US-0402483P.
07-MAR-2003; 2003US-00383930.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mammals against dental caries.
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                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                        20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus mutans
                                                                                        passive immunisation
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(TAUB/) TAUBMAN M A.
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                                                                                                                                                                        Local Similarity
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                                                                                                                         Sequence 432 AA;
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                                                                                                                                                                                                                                                                                                                                                                             ADX37274;
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                                                                                                                                                         Query Match
                                                                                                                                                                                        Matches
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The present sequence is that of a peptide comprising amino acid residues 17-136 of the glucan binding protein-B (GbpB) of Streptococcus mutans strans SK32 ADD93649. The peptide binds to a major histocompatibility complex (MHC) class II protein. It was identified as a potential B cell epitope using a matrix-based algorithm for epitope prediction, which was used to search the primary amino acid sequence of GapB for known MHC class II binding motifs. The peptide can be used in immunogenic compositions and subunit vaccines for dental caries. These comprise MHC class II protein-binding GbpB peptides covalently linked with peptide subunits (preferably from the catalytic domain) of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Diepitopic or multiepitopic polypeptides can be raised against MHC class II binding fragments of GbpB can be used in raised against MHC class II binding fragments of GbpB can be used in
                                                                                                                                                                                                                                                                                                                                                                                                           Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
                                        Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
Streptococcus mutans glucan binding protein-B peptide fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunogenicity; immune stimulation; glucan binding protein-B;
microparticle; major histocompatibility complex; tooth disease
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Pred. No. 2.8e-05;
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                                                                                                                                                                                             07-MAR-2003; 2003WO-US006962
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08-AUG-2002; 2002US-0402483P.
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Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                 Taubman MA;
                                                                              Streptococcus mutans
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ADX37254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a composition comprising a fragment of a glucan binding protein-B (GbpB) and a biocompatible microparticle, where the fragment binds to a major histocompatibility complex (MHC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds to a Streptococcus mutans GbpB protein of the invention.
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                                                                                                                                                                                                                                                                                        immunogenicity; immune stimulation; glucan binding protein-B;
microparticle; major histocompatibility complex; tooth disease
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                                                                                                                                                                                                                                                    Streptococcus mutant glucan binding protein B variant #4.
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                      113 KSNAATSYINAIINSKSVSD 132
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KSNAATSYINAIINSKSVSD 20
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                                                                                                                               ADX37275 standard; protein; 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-APR-1998; 98US-0081550P.
08-JAN-1999; 99US-0115142P.
12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-03623099.
08-AUG-2002; 2002US-0402483P.
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                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Taubman MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SMIT/) SMITH D J.
(TAUB/) TAUBMAN M A.
                                                                                                                                                                                                                                                                                                                                                   Streptococcus mutans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2005-151644/16.
                                                                                                                                                                                                                                                                                                                                                                                       US2005031633-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JAN-2004
                                                                                                                                                                                                              21-APR-2005
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Best Local Si
Matches 20,
                                                                                                                                                                       ADX37275;
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ID ADD!
XX
AC ADD!
XX
DT 29-1
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Gaps

Search completed: January 25, 2006, 19:01:39 Job time : 70.2 secs

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0; Gaps

Query Match

79.8%; Score 75; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 16; Conservative 0; Mismatches 0; Indels

5 ATSYINAIINSKSVSD 20

<u>ራ</u> 4

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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using sw model OM protein - protein search, Run on:

January 25, 2006, 18:48:55; Search time 9.1 Seconds (without alignments) 211.465 Million cell updates/sec

US-10-797-821-1 94

1 KSNAATSYINAIINSKSVSD 20 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post_processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:* Database :

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

•	Description	secreted 45 kg pro	stres	tical pr		hypothetical Arote	uncharacterized pr	conserved hypothet	6-methylsalicilic	6-methylsalic lic	methyl-accepting c	cell wall-associat	conserved hypothet	hypothetical prote	26S proteasome reg		microbial metallop	sexual differentia	vasoactive intesti	vasoactive intesti	vasoactive intesti	vasoactive intesti	probable sugar upt	aBe,	-			cal	Ų	late expression fa
SUMMARIES	£ £	G95258	B98124	E86903	7800NC	S05542	B97273	D69978	A61197	S13178	E83838	F96937	C90216	H71453	T52488	D90387	A41335	T39379	A60038	VRHU	VRRT	A60037	B95972	F70175	C96630	\$53913	S48995	D89782	AF0462	T30429
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de	Query	67.0	67.0	62.8	62.8	51.1	48.9	47.9	47.9	47.9	47.3	46.8	46.8	46.8	46.8	46.3	45.7	45.7	44.7	44.7	44.7	44.7	44.7	44.7	44.7	44.7	44.1	43.6	43.6	43.6
	Score	63	63		29	48	46	45	45	45	44.5	44	44	44	44	43.5	43	43	42	42	42	42	42	42	42	42	41.5	41	41	41
	esult No.	1	N	m	4	S	9	7	80	Q	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

hypothetical prote	Li protein - human	T1K7.9 protein - A	transport protein	PSD2-like 26S prot	hypothetical prote	hypothetical prote	hypothetical 129.5	hypothetical prote	probable membrane	amino acid transpo	glutamate formimid	Jk-recombination s	DNA gyrase chain B	hypothetical prote
B84994	PIWL	D86392	A75018	D71619	866852	S50358	T40778	B90296	AG0201	JC7328	A48717	A47214	H71676	T21007
0 0	٦ ٦	7	7	N	N	~	N	~	N	N	~	~	N	N
376	508	695	746	959	967	995	973	1031	177	487	541	575	662	673
43.6	43.6	43.6	43.6	43.6	43.6	43.6	43.1	43.1	42.6	42.6	42.6	42.6	42.6	42.6
41	41	41	41	41	41	41	40.5	40.5	40	40	40	40	40	40
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ALIGNMENTS

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Secreted 45 kd protein [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: G9528
R;Tettelin, H; Nelson, K.E; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Hei on, J.D.; Umayam, L.A.; Holt, I.E.
Science 233, 498-506, 2001
A;Authors: Loftus, B.Y.; Pang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Reference type: DNA
A;Residus: preliminary
A;Molecule type: DNA
A;Residus: 1-322 KMRA
```

A;Cross-references: UNIPROT:Q97N55; UNIPROT:Q8DMY4; UNIPARC:UPI0000051B81; GB:AE005672; A;Experimental source: strain TIGR4 C;Genetics: A;Gene: SP2216

Gaps . 0 Length 392; 3; Indels Score 63; DB 2; Pred. No. 0.026; Query Match 67.0%; Score 63; DB Best Local Similarity 57.9%; Pred. No. 0.02 Matches 11; Conservative 5; Mismatches

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Greening stress protein GSP-781 [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: B98124
C;Accession: B98124
C;Accession: JA.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.;
E, R; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.;
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 1-392 <KUR.>
A;Conesicule type: JABA
A;Residues: 1-392 <KUR.>
C;Conesicule type: DNA
A;Conesicule type:

A;Gene: gsp-781

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A;Molecule type: DNA
A;Reaidues: 1-507 <PUB-
A;Cross-references: UNIPROT:P13692; UNIPARC:UPI000016F6FC; GB:X16421; EMBL:M26048; NID::
A;Note: the authors translated the codon CGT for residues 221 and 223 as Lys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Date: 18-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: B97273
C;Accession: B97273
C;Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
C;Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conserved hypothetical protein yrpD - Bacillus subtilis
CiSpecies: Bacillus subtilis
CiAccession: D69979 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
CiAccession: D69979
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; ChArter, D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, X.; Fuma, S.; Galizzi, A.; Galle
iech, J.; Harwood, C.R.; Henaut, A.; Hibbert, M.; Holsappel, S.; Hosonon, S.; Houloo, M.F
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Laudinois
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Pottetell
A;Authors: Schleich, S.; Schroeter, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Pottetell
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Ston
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Voshida,
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Attle: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Ance of the Gram-positive bacterium Bacillus subtilis.
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A, Residues: 1-235 <KUN>
A, Cross-references: UNIPROT:005411; UNIPARC:UPI0000607DD; GB:Z99117; GB:AL009126; NID:
A, Experimental source: strain 168
C;Genetics:
A, Gene: yrpD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     uncharacterized protein containing conserved domain, related to YABE B. subtilis C-term
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Cross-references: UNIPROT: 097ES4; UNIPARC: UPI00000CA6E8; GB: AE001437; PIDN: AAK80973.1 A, Experimental source: Clostridium acetobutylicum ATCC824
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                                                                                                                                                                  Length 507;
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                                                                                                                                                                                                                                   2; Indels
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Pred. No. 12;
4; Mismatches
                                                                                                                                                                  Score 48; DB 2;
Pred. No. 8.3;
                                                                                                                                                                                                                                       9; Mismatches
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                                                                                                                                                                     51.1%;
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                                                                                                                                      Query Match
Best Local Similarity 38...
T; Conservative
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Best Local Similarity 44.4
Matches 8; Conservative
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A;Status: preliminary
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:Q9CDJ1; UNIPARC:UP10000C6BFC; GB:AE005176; PID:g12725296; A;Experimental source: strain IL1403
C;Genetics: A;Gene: usp45
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C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
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C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Nucleat Acida Res. 17, 6724, 1989
A;Title: A protein of unusual composition from Enterococcus faecium.
A;Reference number: S05542; MUID:89385998; PMID:2780297
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   Length 392
                                                                        Indels
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   Score 63; DB 2;
Pred. No. 0.026;
5; Mismatches 3
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NSSATNYMDAVVNSKSLTD 131
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   Query Match 67.0%;
Best Local Similarity 57.9%;
Matches 11; Conservative !
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Best Local Similarity 47.2.,
9; Conservative
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les 9; Conserv
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Matches
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methyl-accepting chemotaxis protein BH1509 [imported] - Bacillus halodurans (strain C-1 C; Species: Bacillus halodurans C; Species: Bacillus halodurans C; Species: Bacillus halodurans C; Species: Date: 01-bec-2000 #sequence_revision 01-bec-2000 #text_change 09-Jul-2004 C; Accession: E83838 R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir Nucleic Acids Res. 28, 4317-4331, 2000 A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A; Accession: E83838
                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q9KCRO; UNIPARC:UPI00000C3BFC; GB:AP001512; GB:BA00004; NIO
A;Experimental source: strain C-125
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell wall-associated hydrolase [imported] - Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Species: Clostridium acetobutylicum (C; Species: Clostridium acetobutylicum (C; Species: Clostridium acetobutylicum (C; Species: Clostridium (C; Species: Clostridium (C; Spacession: F96937)
R; Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee (FNolling, J.; Bennett, G.N.; Koonin, B.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Classes (Comparative MulD:21359325)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q97M90; UNIPARC:UPI00000C9E11; GB:AE001437; PIDN:AAK78289.1 A;Experimental source: Clostridium acetobutylicum ATCC824 C;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: CAC0308
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C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Date: 24-May-2001
R;Shc, 0; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Charlong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
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Pred. No. 2
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Best Local Similarity 35.3%;
Matches 12; Conservative
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Best Local Similarity
Matches 8; Conserva
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A;Molecule type: DNA
A;Residues: 1-500 <STO>
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A; Residues: 1-392 < KUR>
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-418 < KUR>
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C;Accession: 461197
R;Wang, I.K.; Reeves, C.; Gaucher, G.M.
C;Accession: A61197
R;Wang, I.K.; Reeves, C.; Gaucher, G.M.
R;Wang, I.K.; Reeves, C.; Gaucher, G.M.
R;Wang, I.K.; Reeves, C.; Gaucher, G.M.
A;Title: Isolation and sequencing of a genomic DNA clone containing the 3' terminus of the A;Reference number: A61197; MUID:91215532; PMID:2021899
A;Accession: A61197
A;Accession: A61197
A;Accession: A61197
A;Accession: A61197
A;Accession: A61197
A;Residues: 1-622 < WAN>
A;Residues: 1-622 < WAN>
A;Cross-references: 1-622 < WAN>
A;Cross-references: AunyPROT:Q7M524; UNIPARC:UPI0000178970
C;Superfamily: Streptomyces hygroscopicus probable polyketide synthase module 4; 3-oxoachomology; [acyl-carrier-protein] S-malonyltransferase homology c;Reywords: carrier protein acyl carrier protein homology <ACP>
F;259-452/Domain: short-chain alcohol dehydrogenase homology cACP>
F;545-615/Domain: acyl carrier protein homology <ACP>
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R;Beck, J.; Ripka, S.; Siegner, A.; Schiltz, E.; Schweizer, E.
Bur. J. Blochen. 192, 487-498, 1990
A;Title: The multifunctional 6-methylaalicylic acid synthase gene of Penicillium patulum A;Reference number: S13178; MUID:91006137; PMID:2209605
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1774 cBEC>
A;Cross-references: UNIPROT:P22367; UNIPARC:UPI000012F5D3; GB:X55776; NID:g3211; PIDN:CA
C;Superfamily: Streptomyces hygroscopicus probable polyketide synthase module 4; 3-oxoac
C;Superfamily: Carrier-protein] S-malonyltransferase homology
C;Keywords: carrier protein
F;54-455/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OASI>
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C;Species: Penicillium griseofulvum
C;Date: 21-Nov-1993 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S13178
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         Length 235;
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             Score 45; DB
Pred. No. 11;
7; Mismatches
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5; Mismatches
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1608 ASTDFINAELESKGITD 1624
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455 ASTDFINAELESKGITD 471
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         Query Match
Best Local Similarity 42.1%;
Matches 8; Conservative
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les 8; Conservative
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C;Species: Schizosaccharomyces pombe
C;Date: 24-0ct-2000 #sequence_revision 24-0ct-2000 #text_change 09-Jul-2004
C;Date: 24-0ct-2000 #sequence_revision 24-0ct-2000 #text_change 09-Jul-2004
C;Date: 24-0ct-2000 #sequence_revision 24-0ct-2000 #text_change 09-Jul-2004
C;Accession: T52488
R;Wilkinson, C; Wallace, M.; Seeger, M.; Dubiel, W.; Gordon, C.
A;Berence number: 22603
A,Abecription: Characterization of Mts4 a subunit of the 26S protease demonstrates that A;Reference number: 22603
A,Accession: T52488
A;Accession: T54888
A;Accession: 
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A, Experimental source: strain OT3
A, Note: Libia accession replaces an interim accession for a sequence replaced by GenBank C, Genetics:
A, Gene: PH0287
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C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C;Accession: H71453
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                                                                                                                  DB 2; Length 418;
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llarity 35.0%; Pred. No. 64;
Conservative 7; Mismatches 6
                                                                                                              Query Match

46.8%; Score 44; DB

Best Local Similarity 60.0%; Pred. No. 30;

Matches 9; Conservative 3; Mismatches
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Matches 7; Conserva
C;Genetics:
A;Gene: SSO0686
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R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Jong, I.; Singh, R.K.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, I arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
Submitted to GenBank, April 2001
A.P. Sensen, C.W.; Van der Oost, J.
A.P. Seripion: Sulfolobus solfataricus complete genome.
A.Reference number: A99139
A.Accession: D90387
                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1077 <KUR>
A;Cross-references: UNIPROT:Q97WN1; UNIPARC:UPI00006467E; GB:AE006641; NID:g13815479; I
C;Genetics:
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C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
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55.0%; Pred. No. 94;
tive 5; Mismatches
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Best Local Similarity 55.0°
Matches 11; Conservative
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DOI=10.1128/IAI.69.11.6931-6941.2001;
Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus mutans.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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Peruzzi F., Piggot P.J., Daneo-Moore L.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
EMBL; U78607; AAD00288.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jin S., Duncan M.J., Taubman M.A., Smith D.J.; "Cloning of the gbpB gene from Streptococcus mutans."; J. Dent. Res. 79:224-224 (2000).
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211 AA; 22803 MW; 4ACE331159CFAFC6 CRC64;
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061M99-PHOPR
097R645-PLAYO
07R0H5-PLAYO
06M7F1 MYCMS
054GB1 DICDI
0514G5-BYDVP
090CY8-BLUTE
YRPD BACSU
0811M7-BACCK
0613A3-BACCK
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Q81V20
Q63FW1
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2004 (TrEMBLrel. 26,
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Q9ZAS7;
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NUCLEOTIDE SEQUENCE.
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STRAIN=55M3;
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Best Local Similarity
  NCBI_TaxID=1309;
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd
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Q9AG98_STRMU
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OSM212_STRT1
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Maximum DB seq length: 200000000
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STRAIN=GS-5;
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  Duncan M.J.; "Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in
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100.0%; Score 94; DB 2; Length 431;

Best Local Similarity 100.0%; Pred. No. 5.1e-07;

Matches 20; Conservative 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOI=10.1128/IAI.69.11.6931-6941.2001;
Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
                                                                                                                                             Length 431;
                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                          Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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PROSITE; PS50911; CHAP; 1.
SEQUENCE 431 AA; 44620 MW; 464FE3B563FB7E51 CRC64;
                                                                                     Pfam; PF05257; CHAP; 1.
PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 14650 NW; 05D38D8BC4609F CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                          Query Match 100.0%; Score 94; DB 2; L. Best Local Similarity 100.0%; Pred. No. 5.1e-07; Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                431 AA
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Infect. Immun. 69:6931-6941(2001).
EMBL; AX046410; AX694500.1; -; Genomic_DNA.
Interpro; IPR007921; CHAP.
Interpro; IPR0094148; SibA.
Pfam; PF05257; CHAP; 1.
                                          Infect. Immun. 69:6931-6941(2001).
EMBL; AY04641; AAK94504.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
                                                                                                                                                                                                                                                                PRT;
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MEDLINE=21481971; PubMed=11598068;
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                                                                                                                                                                                                                                                                Q938V3_STRMU PRELIMINARY;
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                                  clinical isolates."
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431 AA.

Q9AG98 STRMU PRELIMINARY; PRT; Q9AG98; 1.JUN-2001 (TrEMBLrel. 17, Created)

STRMU

RESULT 4
Q9AG98 ST
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Duncan M.J.;

Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates.",

Infect. Immun. 69:6931-6941(2001).

EMBL; AR3384451.1; -; Genomic_DNA.

EMBL; AX046411; AAX08104.1; -; Genomic_DNA.

InterPro; IRR007921; GHAP.

InterPro; IRR009148; SibA.

FRINTS; PRO1852; SIBARPROTEIN.

PRINTS; PRO1852; SIBARPROTEIN.

PROSITE; PSS0911; CHAP; 1.

SEQUENCE 431 AA; 44592 MW; 3EBE21FC5E47232E CRC64;
                                                                                                                                                                                                                                                                                                   MEDLINE=21153617; PubMed=11254612;
DOI=10.1128/IAI.69.4.2493-2501.2001;
Chia J.S., Lee Y.Y., Huang P.T., Chen J.Y.;
"Identification of Stress-responsive genes in Streptococcus mutans by differential display reverse transcription-PCR.";
Infect. Immun. 69:2493-2501(2001).
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MEDLINE=21481977; PubMed=11598074;
DOI=10.1128/IAI.69.11.6987-6998.2001;
Chia J.S., Chang L.Y., Auro C.T., Chang Y.Y., Chen J.Y.;
The Government of the moderniant glycoprotein is essential for cell as a serification immunodominant glycoprotein is essential for cell wall integrity and the maintenance of cell shape in Streptococcus
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Immunodominant glycoprotein IDG-60 (Glucan-binding protein B).
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                                                                                                                        Streptococcus mutans.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chia J.-S., Chang L.-Y., Lee Y.-Y., Chen J.-Y.; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=3VF4;
Jin S., Duncan M.J., Taubman M.A., Smith D.J.;
"Cloning of the gbpB gene from Streptococcus mutans.";
J. Dent. Res. 79:224-224(2000).
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DOI=10.1128/IAI.69.11.6931-6941.2001;
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QBDWM3;
QHAR-2003 (TrEMBLrel. 23,
QL-MAR-2003 (TREMBLrel. 23,
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Best Local Similarity
Local Similarity
Local 20; Conservative
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                                                                                                                                                                                                          NCBI_TaxID=1309;
                                                                                                                                                                                Streptococcus
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ID Q8
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Gaps

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Indels

Length 432;

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"Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in Clinical isolates.";

Linical isolates.";

EMBL; AY046412; AAK94502.1; -; Genomic_DNA.

PREPART PRO19251; CHAP.

PRINTS; PRO19252; CHAP; 1.

PROSTIE; PSS50911; CHAP; 1.

SEQUENCE 432 AA; 44648 MW; E769B2504AEES0E9 CRC64;
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Bolotin A., Quinquis B., Renault P., Sorokin A., Ehrlich S.D.,
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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DOI=10.1128/IAI.69.11.6931-6941.2001,
Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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1-FEB-2005 (TrEMBLrel. 29, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Glucan binding protein (PCSB).
                                        Score 94; DB 2; 1
Pred. No. 5.2e-07;
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                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                        100.0%;
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Q938V2;
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QSM6K4;
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                                     Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
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"Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of Streptococcus mutans UA159, a cariogenic dental
                                                                                                                                                                                                                                                                                               STRAIN=UAIS9 / ATCC 700610 / Serotype c; MEDLINE=22295063; PubMed=12397186; DOI=10.1073/pnas.172501299; Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J., Carson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P., Qian Y., Li S., Zhu H., Najar F.Z., Lai H., White J., Roe B.A., Perretti J.J.;
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Putative secreted antigen GbpB/SagA; putative peptidoglycan
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MEDLINE=21481971; PubMed=11598068;
DOI=10.1128/IAI.69.11.6931-6941.2001;
Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                        Streptococcus mutans.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jin S., Duncan M.J., Taubman M.A., Smith D.J.; "Cloning of the gbpB gene from Streptococcus mutans."; J. Dent. Res. 79:224-224 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     431 AA; 44620 MW; 2D1CA685248CCD3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             432 AA; 44652 MW; 3P88ECB9A1F3BE4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Glucan-binding protein B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pathogen.";
Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 94; DB 2; I Pred. No. 5.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 94; DB ilarity 100.0%; Pred. No. 5.1 Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Infect. Immun. 69:6931-6941(2001).

EMBL. AXV64613; AXV64603.1; -; Genomic_DNA.

InterPro; IPR00921; CTAP.

InterPro; IPR009148; SibA.

Pfam; PF02577; CTAP; 1.

PRINTS; PR01852; SIBAPROTEIN.

PROSITE; PS50911; CHAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE014855; AAN57811.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
                                                                hydrolase.
Name=gbpB; OrderedLocusNames=SMU.22;
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PROSITE; PS50911; CHAP; 1.
COmplete proteome.
SEQUENCE 431 AA; 44620 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q938V1_STRMU PRELIMINARY;
Q938V1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus mutans.
                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
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Best Local Similarity
---- 20; Conserve
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                                                                                                                                                                                                               NCBI_TaxID=1309;
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                                                                                                                                                                                   Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=3SN1;
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Gaps

110 QNNTATSYINSILNSKSISE 129

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RESULT 10
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Decaris B., Leblond-Bourget N.;
Decaris B., Leblond-Bourget N.;
Incse, a Chimeric and Variable Gene, Encodes an Extracellular Protein Involved in Cellular Segregation in Streptococcus thermophilus.";
J. Bacteriol. 187:2737-2746(2005).
EMBL; CP000023; AAV5975.1; -; Genomic_DNA.
EMBL; AY730643; AAW82375.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
PubMed=15543133; DOI=10.1038/nbt1034;
Bolotin A., Quinquis B., Renault P., Sorokin A., Ehrlich S.D.,
Kulakauskas S., Lapidus A., Goltsman E., Mazur M., Pusch G.D.,
Fonstein M., Overbeek R., Kyprides N., Purnelle B., Prozzi D.,
Ngui K., Masuy D., Hancy F., Burteau S., Boutry M., Delcour J.,
Goffeau A., Hols P.;
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Nat. Biotechnol. 22:1554-1558(2004).
Kulakauskas S., Lapidus A., Goltsman E., Mazur M., Pusch G.D., Fonstein M., Overbeek R., Kyprides N., Purnelle B., Prozzi D., Ngui K., Masuy D., Hancy F., Burteau S., Boutry M., Delcour J., Goffeau A., Hols P., "Complete sequence and comparative genome analysis of the dairy bacterium Streptococcus thermophilus.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77.7%; Score 73; DB 2; Length 474; 65.0%; Pred. No. 0.0019;
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Pred. No. 0.002;
6; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus thermophilus (strain CNRZ 1066).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               485 AA; 49165 MW; 8665E4B1FC6CF7CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     474 AA; 48142 MW; 1BAC6A9E0A0A200D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          485 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; CP000024; AAV61641.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glucan binding protein.
Name=pcsB; OrderedLocusNames=str0022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KSNAATSYINAIINSKSVSD 20
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PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77.78;
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PROSITE; PS50911; CHAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QSM212_STRT1 PRELIMINARY;
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Best Local Similarity 65.0
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 65.0
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF05257; CHAP; 1.
                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
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NCBI_TaxID=299768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome. SEQUENCE 474 AA;
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SEQUENCE 485 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
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STRAIN=SF370 / ATCC 700294 / Serotype M1; MEDLINE=2119264; PubMed=11296296; DOI=10.1073/pnas.071559398; MEDLINE=2119264; PubMed=11296296; DOI=10.1073/pnas.071559398; Perretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar P.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.B., "Complete genome sequence of an M1 strain of Streptococcus pyogenes."; Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Banks D.J., Porcella S.F., Barbian K.D., Beres S.B., Philips L.B., Voyich J.M., DeLeo F.R., Martin J.M., Somerville G.A., Musser J.M.; "Progress toward characterization of the group A Streptococcus metagenome: complete genome sequence of a macrolide-resistant serotype
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 69; DB 2; Length 320,
Pred. No. 0.0076;
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pyogenes (Berotype M6).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MG Strain..;
MG St
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Q9A128; Q7BH59;
01-JUN-2001 (TYEMBLrel. 17, Created)
10-MAY-2001 (TYEMBLrel. 17, Last sequence update)
10-MAY-2005 (TYEMBLrel. 30, Last annotation update)
                                                                                                                                                                   25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                      398 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=MGAS10394;
PubMed=15272401; DOI=10.1086/422697;
                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                          OrderedLocusNames=M6_Spy0017;
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Best Local Similarity 60.09
1 STRP6
Q5XEL1 STRP6 PRELIMINARY;
Q5XEL1;
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                                                                                                                                                                                                                                                                                                                                                         Secreted protein.
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"Genome sequence of an M3 strain of Streptococcus pyogenes reveals a large-scale genomic rearrangement in invasive strains and new insights into phage evolution.";
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                                                                                                                                                                                                                                                                                                                                                         STRAIN=MGAS315 / Serotype M3;
MEDLINE=2213808; Pubmed=1212206; DOI=10.1073/pnas.152298499;
Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlitevert P.M., Musser J.M.;
Genome sequence of a serotype M3 strain of group A Streptococcus:
phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                           STRAIN=SSI-1 / Serotype M3;
MEDLINE=22683278; PubMed=1279345; DOI=10.1101/gr.1096703;
Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
Hayashi H., Hattori M., Hamada S.;
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J. Bacteriol. 183:5709-5717(2001).
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Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
    Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        398 AA; 42028 MW; 5DCEDA78CB863B60 CRC64;
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1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
General stress protein GSP-781.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             emergence.",
proc. Natl. Acad. Sci. U.S.A. 99:10078-10083 (2002)
EMBL; BA000034; BAC63110.1; -; Genomic DNA.
EMBL; AE014136; AAM78621.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR007921, CHAP.
PF05257; CHAP; 1.
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Pred. No. 0.0076;
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                                                                                                                                                                                                                                                                                          Genome Res. 13:1042-1055(2003).
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PROSITE; PS50911; CHAP; 1.
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SEQUENCE 398 AA:
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                                            NCBI_TaxID=301448;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pyogenes (Serotype M18).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                      28A9B3F7195E969B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  398 AA; 42028 MW; 5DCEDA78CB863B60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative secreted protein.
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Last annotation update)
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EMBL, AE009955; AAL56849.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
EMBL; AE006474; AAK33158.1; -; Genomic_DNA.
EMBL; AF31999; AL73135.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
Pfam; PF05257; CHAP; 1.
                                                                                                                                                                                 Potential
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OrderedLocusNames=SPB0015, SpyM3_0014;
Streptococcus pyogenes (serotype M3).
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                                                                                                           PRINTS; PRO1852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
Complete proteome; Signal.
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PROSITE; PS50911; CHAP; 1.
Complete proteome.
SEQUENCE 398 AA; 42028 MW;
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QBP318 Q7CFL7;
01-OCT-2002 (TYEMBLFEL: 22,
01-OCT-2002 (TYEMBLFEL: 22,
13-SEP-2005 (TYEMBLFEL: 31,
                                                                                                                                                                                                                                                                       60.08;
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Best Local Similarity 60.00
-00 12; Conservative
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Matches 12; Conservative
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NCBI_TaxID=301451;
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05-JUL-2004
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STRAIR=ATCC BAA.334 (TIGR4;
STRAIR=ATCC BAA.334 (TIGR4;
MEDLINE=21357209; PubMed=11463916; DOI=10.1126/science.1061217;
Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
Peterson S.N., Heidelberg J.F., DeBoy R.T., Haft D.H., Dodson R.J.,
Durkin A.S., Gwinn M.L., Kolonay J.F., Nelson W.C., Peterson J.D.,
Umayam L.A., White O., Salberg S.L., Lewis M.R., Radune D.,
Holtzapple E.K., Khouri H.M., Wolf A.M., Utterback T.R., Hansen C.L.,
McDonald L.A., Feldblyum T.V., Angiuoli S.V., Dickinson T.,
Mickey E.K., Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
Complete genome sequence of a virulent isolate of Streptococcus
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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InterPro; IPR009148; SibA.
PFam; PF05257; CHAP; 1.
PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS0911; CHAP; 1.
Complete proteome.
SEQUENCE 392 AA; 41697 MW; B5A5A860FABEA77DD CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                392 AA
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EMBL; AE07059; AEX76264.1; -; Genomic_DNA.
PIR; B98124; B98124.
PIR; G95258; G95258.
EMBL; AE008566; AAL00823.1; -; Genomic_DNA.
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114 NGAVTSYINTIVNSKSITE 132
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              PIR; B98124; B98124.
PIR; G95258; G95258.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
Pfam; PF05257; CHAP; 1.
PROSITE; PS50911; CHAP; 1.
Complete proteome.
SEQUENCE 392 AA; 41697 MW;
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OrderedLocusNames=SP2216;
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Q97N55;
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NCBI_TaxID=1313;
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Sequence 2, Appl
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        GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-08-186-223-2
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US-08-243-082-24
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US-09-248-796A-18679
US-09-625-188-10
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US-09-107-433-3230
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1 KSNAATSYINAIINSKSVSD 20
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VS-09-583-110-4374

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VS-09-583-110-4374

Sequence 4374, Application US/09583110

FREENTAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al.

TITLE OF INVENTION: Nocleic Acid and Amino Acid Sequences Relating to Streptococcus

TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

FILE REFERENCE: PATHOG-07A

CURRENT APPLICATION NUMBER: US 09/107,433

FRIOR APPLICATION NUMBER: US 60/085,131

PRIOR FILING DATE: 1998-06-30

FRIOR PELING DATE: 1998-06-12

PRIOR FILING DATE: 1998-06-12

PRIOR FILING DATE: 1997-07-02

NUMBER: OF SEQ ID NOS: 5322

SEQ ID NO 4374

LENGTH: 392
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14799, A
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29, Appl
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| Sequence 67, Application US/09222938A
| Patent No. 6437A10N:
| GENERAL INFORMATION:
| APPLICANT: Youngman, Philip
| APPLICANT: Wurphy, Christopher
| APPLICANT: Murphy, Christopher
| APPLICANT: Guzman, Luz-Maria
| APPLICANT: Guzman, Luz-Maria
| TITLE OF INVENTION: ESSENTIAL BACTERIAL GENES AND THEIR USE
| TIER REPERENCE: 07334/060001
| CURRENT APPLICATION NUMBER: US/09/222,938A
| CURRENT FILING DATE: 1998-12-30
| NUMBER OF SEQ ID NOS: 102
| NUMBER OF SEQ ID NOS: 102
| SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 67.0%; Score 63; DB 2; Length 210; I Similarity 57.9%; Pred. No. 0.026; 11; Conservative 5; Mismatches 3; Indels
US-09-489-039A-13109
US-08-704-398-2
PCT-US95-05966-2
US-09-248-796A-14799
US-09-270-767-44725
US-09-220-939-29
US-10-023-528-29
US-10-023-528-29
US-10-423-330-29
US-08-243-082-3
US-08-243-082-3
US-09-830-230A-294
US-09-830-230A-294
US-09-830-230A-293
US-09-830-230A-293
US-09-830-230A-293
US-09-830-230A-293
US-09-830-230A-293
US-09-830-230A-293
US-09-830-230A-293
US-09-830-230A-293
US-09-9308-003-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) ORGANISM: Streptococcus pneumoniae US-09-222-938A-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 SNAATSYINAIINSKSVSD 20
         Query Match
Best Local Similarity
Matches 11; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/186,222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62.8%; Score 59; DB 1
47.4%; Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Mismatches
                                          Sequence 2, Application US/08186222;
Patent No. 5559007
GENERAL INFORMATION:
APPLICANT: Suri, Bruno
APPLICANT: Suri, Bruno
TITLE OF INVENTION: Bacterial Vectors
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GRIGY Corporation
STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PILING DATE:
CLASSIFICATION: 435
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 07/672,205
PRIOR DATE: 19-MR-1991
APPLICATION NUMBER: GB 9006400.7
FILING DATE: 22-MR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Villamizar, John
REGISTRATION NUMBER: 30,598
REFERENCE/DOCKET NUMBER: 4-17994/A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914)347-5769
INFORMATION FOR SEC ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 461 amino acids
TYPE: amino acid
TOPLOCKY: linear
TOPLOCKY: linear
TYPE: amino acid
TYPE: amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 NSSATNYMDAVVNSKSLTD 131
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STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 62.8
Best Local Similarity 47.4
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-08-186-222-2
                                                                                                                                                                                                                                                                          STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-107-532A-5095
                                 US-08-186-222-2
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                    Gaps
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                                                                          Query Match 67.0%; Score 63; DB 2; Length 392; Best Local Similarity 57.9%; Pred. No. 0.053; Matches 11; Conservative 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 67.0%; Score 63; DB 2; Best Local Similarity 57.9%; Pred. No. 0.054; Matches 11; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: CD/ROM SYSTEM: CD/ROMON>
OPERATING SYSTEM: CD/ROMON>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/085131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...399
; SEQUENCE DESCRIPTION: SEQ ID NO: 3230:
US-09-107-433-3230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMÁTION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                   Sequence 3230, Application US/09107433 Patent No. 6800744 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (781) 893-5007
TELEFAX: (781) 893-8277
INFORMATION FOR SEQ ID NO: 3230:
              ; ORGANISM: Streptococcus pneumoniae US-09-583-110-4374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 399 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : | ||||| |:||||:::
114 NGAVTSYINTIVNSKSITE 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
                                                                                                                                                                                                                                                               RESULT 3
US-09-107-433-3230
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TYPE: PRT
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Pred. No. 12;
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ZIP: Z0036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,082
FILING DATE:
CLASSIFICATION NUMBER: US/07/853,754
FILING DATE:
FILING DATE:
APPLICATION NUMBER: US/07/853,754
FILING DATE:
TELESTATION NUMBER: 26.031
REFERENCE/DOCKET NUMBER: CON.
REGISTRATION: NUMBER: CON.
RESTERENCE/DOCKET NUMBER: KUWAT 0010
TELEFRAX: (202) 828-8000
TELEFRAX: (202) 828-8038
TELEFRAX: SEDIE RECOMMUNICATION DOCKET NUMBER: REPREMENCE/DOCKET NUMBER: RUMAT 0010
TELEFRAX: (202) 828-8038
TELEFRAX: SPENCER 64267
INPORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: YAMAHITA, Kunihiko
TITLE OF INVENTION: METHOD OF PRODUCING PEPTIDES OR
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spencer, Frank & Schneider
STREET: 1111 Nineteenth Street, N.W.
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: <1
OTHER INFORMATION: /note= "Frotein A(1-402)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                          KUWAT 0010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-243-082-18
; Sequence 18, Application US/08243082
; Patent No. 5506120
; GENERAL INFORMATION:
                                        REFERENCE/DOCKET NUMBER: XUM
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 828-8030
TELEFAX: (202) 828-8038
TELEFAX: SPENCER 64267
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
TENDEN: 152 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KSNAATSYINAIINSKSVSD 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 KOMÁVKKÝLNSÍLNGKRHSD 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 45.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                   : 152 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 172 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: peptide US-08-243-082-24
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                         REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 24, Application US/08243082
| Patent No. 5506120
| GENERAL INFORMATION:
| APPLICANT: YAWAMOTO, HITOAKI
| APPLICANT: YAWAMOTO, HITOAKI
| TITLE OF INVENTION: METHOD OF PRODUCING PEPTIDES OR
| TITLE OF INVENTION: METHOD OF PRODUCING PEPTIDES OR
| TITLE OF INVENTION: METHOD OF PRODUCING PEPTIDES OR
| TITLE OF INVENTION: METHOD OF PRODUCING PEPTIDES OR
| TITLE OF INVENTION: APPLICANCES: 26
| CORRESPONDENCE ADDRESS: 26
| CORRESPONDENCE ADDRESS: 36
| CORRESPONDENCE ADDRESS: 36
| CONTINENT OF SAME OF SAM
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,082
COMPUTER: PC

OPERATING SYSTEM: «Unknown»
SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/05151
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/05151
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/05151
FILING DATE: 1019 2. 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEPHONE: (781)893-507
TELEPHONE: (781)893-607
TELEPHONE: (781)893-607
TELEPHONE: (781)893-6277
INFORMATION FOR SEQ ID NO: 5095:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...525
SEQUENCE DESCRIPTION: SEQ ID NO: 5095:
US-09-107-532A-5095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/853,754
FILING DATE: 05-UN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Schneller, John W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 525 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    || :::||:|::|
115 SNTSSNYIDAVLNADSLAD 133
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Best Local Similarity 42.19
Matches 8; Conservative
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Pred. No. 42;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: NO. 6307037artis AG
APPLICANT: NO. 6307037artis AG
TITLE OF INVENTION: Fungal Target Genes and Methods
FILE REFERENCE: PB/5-31285p1
CURRENT APPLICATION NUMBER: US/09/625,188
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44; DB 2;
Pred. No. 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Mismatches
FILING DATE: 13-DEC-1996
PRIOR APPLICATION NUMBER: 19-136100/1994
APPLICATION NUMBER: 19-136100/1994
FILING DATE: 17-JUN-1994
PRIOR APPLICATION NUMBER: 19-136100/1994
APPLICATION NUMBER: 19-1361095
FILING DATE: 15-DEC-1995
PRIOR APPLICATION NUMBER: 18-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 081356/0116
TELECHONE: (202)672-5399
                                                                                                                                                                                                                                                                                                  081356/0116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-902-540-10793
; Sequence 10793, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
10S-09-625-188-10
Sequence 10, Application US/09625188
Patent No. 6307037
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Best Local Similarity 42.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 331 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||:||:|||
170 SNSASSYITPIIN 182
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Ashbya gossypii
US-09-625-188-10
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-094-557-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      646
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                                                                                                                                                                                                                                        Sequence 18679, Application US/09248796A

Requence 18679, Application US/09248796A

Redent No. 6747137

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-13
PRIOR FILING DATE: 1999-02-13
PRIOR FILING DATE: 1998-02-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 18679
LENGTH: 808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kakitani, Makoto
APPLICANT: Umemoto, Naoyuki
APPLICANT: Ishida, Isao
APPLICANT: Ishida, Isao
APPLICANT: Ishida, Isao
APPLICANT: Yamaota, Masaaki
APPLICANT: Yamaoka, Masoto
ITILE OF INVENTION: GLUCAN ELICITOR RECEPTOR, DNA MOLECULE
TITLE OF INVENTION: THE DNA MOLECULE AND METHOD FOR CREATING THE PLANTS
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
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Best Local Similarity 44.4%; Pred. No. 80;
Matches 8; Conservative 4; Mismatches 6; Indels
         DB 1; Length 172;
14;
                                                       8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/094,557
FILING DATE: 15-UW-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Washington STATE: D.C.
           Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 34, Application US/09094557 Patent No. 6225531 GENERAL INFORMATION:
                                                                                                                          | | | |:|:|:| | || || 34 KQMAVKKYLNSILNGKRHSD 53
                                                                                                   1 KSNAATSYINAIINSKSVSD 20
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637 NAAQTVL/NLVINDKDILD 654
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         Query Match
Best Local Similarity 45.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Candida albicans
                                                                                                                                                                                                                                    US-09-248-796A-18679
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US-09-094-557-34
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APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA-
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1998-02-13
PRIOR PILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 19069
LENGTH: 815
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TILLE ORIVERNY BAN, G

FILE REFERENCE: PCI0343AAK

CURRENT APPLICATION NUMBER: US/09/708,392

CURRENT FILING DATE: 2000-11-08

PRIOR PILING DATE: 1999-11-08

PRIOR PILING DATE: 2000-02-18

PRIOR PILING DATE: 2000-02-18

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-07-05

PRIOR PILING DATE: 2000-07-05

PRIOR PILING DATE: 2000-07-05

PRIOR PILING DATE: 2000-07-12

PRIOR PILING DATE: 2000-07-12

PRIOR PILING DATE: 2000-07-12

PRIOR PILING DATE: 2000-07-12

PRIOR PILING DATE: 2000-07-14

PRIOR PILING DATE: 2000-07-17

PRIOR PILING DATE: 2000-07-27

NUMBER: OF SEQ ID NOS: 20

SEQ ID NO 15

LENGTH: 170
                                                                                                                                                          . WS-09-248-796A-19069

; Sequence 19069, Application US/09248796A

; Patent No. 6747137

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15, Application US/09708392
Patent No. 6734186
GENERAL INFORMATION:
APPLICANT: Pfizer Inc
APPLICANT: Pfizer Limited
APPLICANT: Wayman, Chris
APPLICANT: Maw, G
                                              21 SDSSISFLRSIINSKNRGD 39
             2 SNAATSYINAIINSKSVSD 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Candid
US-09-248-796A-19069
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US-09-708-392-15
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US-09-543-681A-5625
Sequence 5625, Application US/09543681A
Sequence 5625, Application US/09543681A
Sequence 5625, Application US/09543681A
Sequence 5625, Application US/09543681A
Sequence 5625, Application:
GENERAL INFORMATION:
TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: UNMERE: US/09/543,681A
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 1099-04-09
PRIOR PILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 5625
LENGTH: 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6586197
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ADANG, MICHAEL J
APPLICANT: LIO, KE
TITLE OF INVENTION: METHODS AND MATERIALS FOR IDENTIFYING NOVEL PESTICIDE AGENTS
FILE REPERENCE: UGS-101, K
CURRENT APPLICATION NUMBER: US/09/657,931A
CURRENT FILING DATE: 2000-09-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 946
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                                                                                                                                                                                                                                                                                                                  Query Match 46.8%; Score 44; DB 2; Length 910; Best Local Similarity 71.4%; Pred. No. 1.3e+02; Matches 10; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
46.8%; Score 44; DB 2; Length 946;
Best Local Similarity 41.2%; Pred. No. 1.4e+02;
Matches 7; Conservative 7; Mismatches 3; Indels
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FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 10793
LENGTH: 910
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656 ANAAFNYLMSVLSGSSV 672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Plutella xylostella
                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-10793
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661 SNAITTINAIIDS 674
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; ORGANISM: Proteus mirabilis
US-09-543-681A-5625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-657-931A-10
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44.7%; Score 42; DB 2; Length 170;
Best Local Similarity 40.0%; Pred. No. 42;
Matches 8; Conservative 4; Mismatches 8; Indels
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-708-392-15
```

Search completed: January 25, 2006, 19:18:11 Job time : 16.6 secs

1 KSNAATSYINAIINSKSVSD 20 | | | | | | | | | | | | 139 KQMAVKKYLNSILNGKRSSE 158

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Sequence 196528, Sequence 122, App Sequence 126, App Sequence 116, App Sequence 17, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 1110, Ap Sequence 1110, App Sequence 57318, App Sequence 57318, App

Perfect score:

Title:

Run on:

Sequence:

Scoring table:

Searched:

Minimum DB seq Maximum DB seq

Database :

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## Squence 1, Application US/10797821
## Squence 1, Application US/10797821
## Squence 1, Application No. US2050031633A1
## Squence 1, Application No. US2050031633A1
## Squence 1, Application No. US205003163A1
## APPLICANT: Smith, Daniel J.
## APPLICANT: Smith, Daniel J.
## APPLICANT: Taubman, Martin A.
## TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens
## TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens
## TITLE OF INVENTION: 10/797, 821
## CURRENT APPLICATION NUMBER: US/10/797, 821
## PRIOR APPLICATION NUMBER: 60/363, 209
## PRIOR FILING DATE: 2002-08-08
## PRIOR PILING DATE: 2002-08-08
## PRIOR APPLICATION NUMBER: 09/290,049
## PRIOR APPLICATION NUMBER: 09/290,049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/10383930
; Publication No. US20040127400A1
; Sequence 1, No. US20040127400A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Daniel J
; APPLICANT: Taubman, Martin A
; TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
; FILE REPERENCE: 25669-018
; CURRENT APPLICATION NUMBER: US/10/383,930
; CURRENT FILING DATE: 2003-03-07
; PRIOR PLICATION NUMBER: 60/402,483
; PRIOR PLICATION NUMBER: 60/402,483
; PRIOR PLING DATE: 2002-08-08
; RIOR APPLICATION NUMBER: 60/363,209
; RIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 41
; SOPTWARE: Patentin version 3.2
US-10-437-963-196528
US-10-851-691-122
US-10-852-991A-126
US-10-686-390-15
US-10-686-390-17
US-10-686-282-17
US-10-686-282-17
US-10-686-282-17
US-10-686-282-17
US-10-686-349-15
US-10-686-349-15
US-10-686-349-17
US-10-32-585-7853
US-10-32-585-7853
US-10-369-493-10160
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100.0%; Score 94; DB 4; I
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-767-701-57338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT; OKGANISM: Streptococcus mutans US-10-383-930-1
      287
30
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1170
1170
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1170
218
371
30
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      RESULT 2
US-10-797-821-1
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Sequence 31, Appl
Sequence 31, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 11, Appl
Sequence 600, Appl
Sequence 465k, Appl
Sequence 3230, Appl
Sequence 576k8, Appl
Sequence 1, Appli
Sequence 21895, Appli
Sequence 21895, Appli
Sequence 226655, Sequence 226655,
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Sequence 33,
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cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

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cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
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Copyright (c) 1993 - 2006 Compugen Ltd.
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US-10-797-811-1

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US-10-383-930-30

US-10-797-821-29

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US-10-797-821-31

US-10-797-821-31

US-10-797-821-31

US-10-797-821-32

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US-10-425-115-225682
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Maximum Match 100%
Listing first 45 summaries
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113 KSNAATSYINAIINSKSVSD 132
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                                              ; TYPE: PRT; ORGANISM: Streptococcus mutans
US-10-383-930-30
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Matches 20; Conservative
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US-10-797-821-29
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SEQ ID NO 30
LENGTH: 43
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; Sequence 29, Application US/10383930
; Publication No. US20040127400A1
; GENERAL INFORMATION:
    APPLICANT: Smith, Daniel J
    APPLICANT: Taubman, Martin A
    TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
    FILE REFERENCE: 25669-018
; CURRENT APPLICATION NUMBER: US/10/383,930
; CURRENT FILING DATE: 2003-03-07
; PRIOR FILING DATE: 2002-08-08
; PRIOR FILING DATE: 2002-08-08
; PRIOR PLICATION NUMBER: 60/402,483
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH 431
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Sequence 30, Application US/10383930;
Fublication No. US20040127400A1;
GENERAL INFORMATION:
APPLICANT: Taubman, Martin A;
TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
FILE REFERENCE: 2566-018
CURRENT APPLICATION NUMBER: US/10/383,930
CURRENT APPLICATION NUMBER: 60/303.03
FRIOR FILING DATE: 2002-08-08
PRIOR FILING DATE: 2002-08-08
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100.0%; Score 94; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                               ; FEATURE:
; OTHER INFORMATION: GpbB-derived MHC class II (SYI) peptide US-10-797-821-1
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PRIOR PILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: 60/081,550
PRIOR PILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.2
SEQ ID NO 1
LENGTH: 20
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US-10-383-930-29
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Sequence 29, Application US/10797821
; Sequence 29, Application US/10797821
; Publication No. US20050031633A1
; Publication No. US20050031633A1
; APPLICANT: Smith, Daniel J.
; APPLICANT: Smith, Daniel J.
; APPLICANT: Taubman, Martin A.
; TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens
; FILE REFERENCE: 2569-02
; CURRENT APPLICATION NUMBER: US/10/797,821
CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: 60/363,209
; PRIOR PLLING DATE: 2002-08-08
; PRIOR PLLING DATE: 2002-08-08
; PRIOR PLLING DATE: 1999-04-12
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Sequence 33, Application US/10383930;
Publication No. US20040127400A1
GENERAL INFORMATION:
APPLICANT: Smith, Daniel J
APPLICANT: Taubman, Martin A
TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
FILE REPERBENCE: 25659-018
CURRENT APPLICATION NUMBER: 2003-03-07
FRIOR PIPLING DATE: 2003-08-08
PRIOR PILING DATE: 2002-08-08
PRIOR PILING DATE: 2002-08-08
PRIOR PILING DATE: 2002-03-07
PRIOR FILING DATE: 2002-03-07
PRIOR FILING DATE: 2002-03-07
SOFTWARE: Patentin version 3.2
SEQ ID NO 33
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Query Match 100.0%; Score 94; DB 4; Length 431; Best Local Similarity 100.0%; Pred. No. 1.3e-06; Matches 20; Conservative 0; Mismatches 0; Indels
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Sequence 31, Application US/10383930
; Sequence 31, Application US/10383930
; Publication No. US20040127400A1
; GENERAL INFORMATION:
    APPLICANT: Smith, Daniel J
    APPLICANT: Taubman, Martin A
    TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
    FILE REFERENCE: 25669-018
    CURRENT APPLICATION NUMBER: US/10/383,930
; CURRENT APPLICATION NUMBER: 60/402,483
; PRIOR APPLICATION NUMBER: 60/402,483
; PRIOR APPLICATION NUMBER: 60/363,209
; PRIOR PILING DATE: 2002-08-08
; PRIOR PILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin version 3.2
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| Sequence 32, Application US/10383930
| Publication No. US20040127400A1
| GENERAL INFORMATION:
| APPLICANT: Smith, Daniel J
| APPLICANT: Taubman, Martin A
| TITLE OP INVENTION: Immunogenicity of Glucan Binding Protein FILE REFERENCE: 25669-018
| CURRENT APPLICATION NUMBER: US/10/383,930
| CURRENT APPLICATION NUMBER: US/10/383,930
| PRIOR PILING DATE: 2002-08-08
| PRIOR PILING DATE: 2002-08-08
| PRIOR FILING DATE: 2002-03-07
| NUMBER OF SEQ ID NOS: 41
| SOFTWARE: Patentin version 3.2
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PRIOR APPLICATION NUMBER: 60/081,550
PRIOR FILING DATE: 1980-04-13
PRIOR PILING DATE: 1999-01-08
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOUTHWARE: PATCHIN VETBION 3.2
SEQ ID NO 33
LENGTH: 431
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ORGANISM: Streptococcus mutans
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US-10-383-930-31
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LENGTH: 432
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LENGTH: 432
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Fublication No. US20050031633A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Smith, Daniel J.
TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens
FILER EFFERENCE: 2569-200
CURRENT APPLICATION NUMBER: US/10/797,821
CURRENT PILING DATE: 2004-03-09
FRIOR APPLICATION NUMBER: 60/363,209
FRIOR FILING DATE: 2002-06-08
FRIOR FILING DATE: 2002-06-08
FRIOR FILING DATE: 2002-06-08
FRIOR FILING DATE: 1099-04-12
FRIOR PILING DATE: 1999-04-12
FRIOR PILING DATE: 1999-04-13
FRIOR FILING DATE: 1999-04-13
FRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SEQ ID NO 30
TEMPORTH OF SEQ ID NOS: 45
SEQ ID NO 30
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| Publication No. US20050031633A1
| GENERAL INFORMATION:
| APPLICANT: Smith, Daniel J.
| APPLICANT: Taubman, Martin A.
| TILLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens
| FILE REFERENCE: 25669-020
| CURRENT APPLICATION NUMBER: US/10/797,821
| CURRENT PILING DATE: 2004-03-09
| PRIOR FILING DATE: 2003-03-07
| PRIOR FILING DATE: 2002-03-07
| PRIOR FILING DATE: 2002-03-07
| PRIOR PILING DATE: 2002-03-07
| PRIOR PILING DATE: 2002-03-07
| PRIOR PILING DATE: 2002-03-07
| PRIOR FILING DATE: 1099-04-12
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                                                                                                                                       100.0%; Score 94; DB 5; Length 431; Lonstry 100.0%; Pred. No. 1.3e-06; Conservative 0; Minmatcher
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                                TYPE: PRT
; ORGANISM: Streptococcus mutans
US-10-797-821-29
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Best Local Similarity
Matches 20; Conserv
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US-10-797-821-33
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   LENGTH: 431
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Best Local Similarity
Matches 20; Conserv
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                                                                                              TYPE: PRT
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Publication No. US20050031633A1

GENERAL INFORMATION

APPLICANT: Smith Daniel J.

APPLICANT: Taubman, Martin A.

TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens

FILE REFERENCE: 25669-020

CURRENT APPLICATION NUMBER: US/10/797,821

CURRENT FILING DATE: 2004-03-09

PRIOR APPLICATION NUMBER: 60/363,209

PRIOR FILING DATE: 2002-03-07

PRIOR PILING DATE: 2002-03-07

PRIOR APPLICATION NUMBER: 60/402,483

PRIOR PILING DATE: 1999-04-12

PRIOR APPLICATION NUMBER: 60/081,550

PRIOR APPLICATION NUMBER: 60/081,550

PRIOR PILING DATE: 1998-04-13

PRIOR FILING DATE: 1998-04-13

PRIOR FILING DATE: 1999-01-08

NUMBER OF SEQ ID NOS: 45

SOFTWARE: Patentin version 3.2
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                                               Query Match
100.0%; Score 94; DB 4; I
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 20; Conservative 0; Mismatches 0;
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; ORGANISM: Streptococcus mutans
US-10-383-930-32
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US-10-797-821-31
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APPLICANT: Smith, Daniel J.
APPLICANT: Smith, Daniel J.
APPLICANT: Taubman, Martin A.
TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens
FILE REFERENCE: 2569-020
CURRENT APPLICATION NUMBER: US/10/797,821
CURRENT APPLICATION NUMBER: US/0399
PRIOR FILING DATE: 2003-039
PRIOR PLILING DATE: 2003-0307
PRIOR PLILING DATE: 2002-03-07
PRIOR PLILING DATE: 2002-03-07
PRIOR PLILING DATE: 2002-03-07
PRIOR PLILING DATE: 2002-08-08
PRIOR PLILING DATE: 2002-08-08
PRIOR PLILING DATE: 2999-04-12
PRIOR PLILING DATE: 1999-04-12
PRIOR PLILING DATE: 1999-04-13
PRIOR PLILING DATE: 1998-04-13
PRIOR PLILING DATE: 1998-04-13
PRIOR PLILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/081,550
PRIOR APPLICATION NUMBER: 60/115,142
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Sequence 11, Application No. US20040127400A1

Sequence 11, Application No. US20040127400A1

SENERAL INFORMATION:

APPLICANT: Smith, Daniel J

TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein

FILE REFERENCE: 25669-018

CURRENT FILING DATE: 2003-03-07

PRIOR APPLICATION NUMBER: 60/402,483

PRIOR APPLICATION NUMBER: 60/402,483

PRIOR APPLICATION NUMBER: 60/402,483

PRIOR APPLICATION NUMBER: 60/363,209

PRIOR APPLICATION NUMBER: 60/363,209

PRIOR PILING DATE: 2002-03-07

NUMBER OF SEQ ID NOS: 41

SOFTWARE: PatentIn version 3.2

SEQ ID NO 11

LENGTH: 20
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Pred. No. 1.4e-06;
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PRIOR APPLICATION NUMBER: 60/115,142
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.2
SEQ ID NO 32
LENGTH: 432
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US-10-797-821-32
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| Publication No. US20040236072A1 |
| GENERAL INFORMATION |
| APPLICANT: Olmsted, Stephen |
| APPLICANT: Olmsted, Stephen |
| APPLICANT: Nickbarg, Robert |
| APPLICANT: Nickbarg, Riliot |
| APPLICANT: Nickbarg, Rilio
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PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.2
SEQ ID NO 11
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial
PRATURE:
CTHER INFORMATION: GDpB peptide
US-10-797-821-11
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US-10-474-792-600
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Search completed: January 25, 2006, 20:10:00 Job time : 60 secs

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27, Appl 7, Appl 114, Appl 27, Appl 27, Appl 46, Appl 171, App 34, Appl 185, Appl 185, Appl 185, Appl 145, Appl 145, Appl 146, Appl 7, Appli 146, Appl 167, Appl

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Sequence 252, Application US/11052554A
Publication No. US20050288866A1
GENERAL INFORMATION:
APPLICANT: Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
FILE REPRENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT APPLICATION NUMBER: US 60/589,227
PRIOR APPLICATION NUMBER: IN 133/DEL/2004
PRIOR APPLICATION NUMBER: IN 133/DEL/2004
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-20
NUMBER OF SEQ ID NOS: 763
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Sachdeva, et al.

TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT APPLICATION NUMBER: US 60/589,227
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR PLING DATE: 2004-07-20
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR PLING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
SOFTWARE: Patentin version 3.3
SEQ ID NO 210
LENGTH: 431
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US-10-401-386B-38

US-10-401-386B-34

US-10-916-827-45

US-10-667-255-7

US-11-069-551A-27

US-11-156-084-28

US-11-156-084-171

US-11-156-084-171

US-11-156-084-171

US-11-082-389-36

US-11-082-389-36

US-11-082-389-36

US-10-495-664-3

US-11-082-389-36

US-10-485-517-145

US-10-877-346-7

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                                                                                                                                                                                                                                                                                                                              ; Sequence 210, Application US/11052554A; Publication No. US20050288866A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Streptococcus mutans UA159
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Sequence 14, Appl
Sequence 16, Appl
Sequence 170, Appl
Sequence 170, Appl
Sequence 170, Appl
Sequence 110, App
Sequence 146, App
Sequence 146, App
Sequence 112, App
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31, Appl
1702, Ap
338, App
29, Appl
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Sequence 252, App
                                                                            January 25, 2006, 19:15:26; Search time 5.5 Seconds (without alignments) 39.378 Million cell updates/sec
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3: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
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7: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-11-212-443-163

US-11-212-443-164

US-11-212-443-164

US-11-196-475-170

US-11-196-475-170

US-11-196-475-164

US-11-196-475-164

US-11-196-475-164

US-11-196-475-146

US-11-196-475-146

US-11-196-475-146

US-11-136-475-146

US-11-133-039-282

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US-11-133-039-282

US-10-733-626-1702

US-10-733-626-1702

US-10-733-626-338

US-11-132-864-29

US-11-132-864-29

US-11-132-864-139

US-11-132-864-139
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Maximum Match 100%
Listing first 45 summaries
                                                           OM protein - protein search, using sw model
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                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                                              US-10-797-821-1
94
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Match
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                                                                                                                                                                                Scoring table:
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                                                                                                                                                         Sequence:
                                                                                                                                                                                                                    Searched:
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US-10-467-657-470
                                                                               US-11-212-443-14
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                                                                                                                                                 Query Match 73.4%; Score 69; DB 7; Length 398; Best Local Similarity 60.0%; Pred. No. 0.00033; Matches 12; Conservative 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 40.4%; Score 38; DB 7; Length 91; Best Local Similarity 53.8%; Pred. No. 7; Matches 7; Conservative 3; Mismatches 3; Indels
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Publication No. US20050287165A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Scalato, Enzo
APPLICANT: Rappuoli, Vega
APPLICANT: Rappuoli, Rino
APPLICANT: Elzza, Mariagrazia
APPLICANT: Grandi, Guido
ITTLE OF INVENTION: Meningococcal Antigens
FILE REFERENCE: CHIR0159
CURRENT APPLICATION NUMBER: US/11/212,443
CURRENT FILING DATE: 1999-04-30
PRIOR FILING DATE: 1999-04-30
PRIOR FILING DATE: 1999-01-14
NUMBER OF SEQ ID NOS: 195

SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Relation, 1920
APPLICANT: Rappuoli, Rino
APPLICANT: Rappuoli, Rino
APPLICANT: Rappuoli, Rino
APPLICANT: Braza, Mariagrazia
APPLICANT: Grandi, Guido
TITLE OF INVENTION: Meningococcal Antigens
FILE REFERENCE: CHIROLS9
CURRENT RPLICATION NUMBER: US/11/212,443
FRIOR RILING DATE: 1999-04-30
PRIOR FILING DATE: 1999-04-30
PRIOR FILING DATE: 1999-01-14
NUMBER OF SEQ ID NOS: 195
SOFTWARE: Patentin Ver. 2.1
SENGTH: 91
                                                                                    ), ORGANISM: Streptococcus pyogenes MGAS8232
US-11-052-554A-252
                                                                                                                                                                                                                                                                                                                                                        RESULT 3
US-11-212-443-163
US-11-212-443-163
Sequence 163, Application US/11212443
Publication No. US20050287165A1
GENERAL INFORMATION:
APPLICANT: Scalato, Enzo
                                                                                                                                                                                                                                                                   |:| : ||||::||||:||
110 KNNETSGYINALLNSKSISD 129
                                                                                                                                                                                                                                        1 KSNAATSYINAIINSKSVSD 20
SOFTWARE: Patentin version 3.3
SEQ ID NO 252
LENGTH: 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 TSYINAIINSKSV 18
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                                                                                                                                     DB 7; Length 124;
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Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNAIV Vega
APPLICANT: MASIGNAIV Vega
APPLICANT: MASIGNAIV Vega
APPLICANT: MASIGNAION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 16, Application US/11212443
; Publication No. US20050287165A1
; Publication No. US20050287165A1
; GENERAL INFORMATION:
; APPLICANT: Scalato, Enzo
; APPLICANT: Masignani, Vega
APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagrazia
APPLICANT: Pizza, Mariagens
; TITLE OF INVENTION: UNINGER: US/11/212,443
CURRENT APPLICATION NUMBER: US/09/302,626
; PRIOR APPLICATION NUMBER: US/09/302,626
; PRIOR APPLICATION NUMBER: PCT/1B99/00103
; PRIOR FILING DATE: 1999-04-30
; PRIOR FILING DATE: 1999-01-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PALENTIN Ver. 2.1
                                                                                                                                     Score 38; DB 7
Pred. No. 10;
3; Mismatches
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CURRENT FILING DATE: 2003-08-11
PRIOR PILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 470
LENGTH: 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Neisseria meningitidis
SEQ ID NO 14
LENGTH: 124
TYPE: PRT
ORGANISM: Neisseria meningitidis
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Best Local Similarity 53.8%;
Matches 7; Conservative
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US-11-212-443-16
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                                                                                                                                                                                                                                                                                                                                                    8; Indels
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US-11-196-475-164

Sequence 164, Application US/11196475

Publication No. US20050271682A1

GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Luft, Benjamin J.
CURRENT FILING DATE: 2006-09.1

PRIOR PILING DATE: 1993-11-01

PRIOR APPLICATION NUMBER: US 08/148,191

PRIOR APPLICATION NUMBER: US 09/666,017

PRIOR APPLICATION NUMBER: US 09/666,017

PRIOR PILING DATE: 2000-09-19

PRIOR PILING DATE: 2001-08-18

PRIOR PILING DATE: 2001-08-18

NUMBER OF SEQ ID NOS: 213

SOFTWARE: FastSQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Indels
                                                                                                                                                                                                                                                                                                40.4%; Score 38; DB 7; 38.9%; Pred. No. 34;
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Pred. No. 45;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                              NUMBER OF SEQ ID NOS: 213
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 170
TAYET: PRT
ORGANISM: Artificial Sequence
PRIOR APPLICATION NUMBER: PCT/US01/24736
PRIOR FILING DATE: 2001-08-07
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                                                                                                                                                                                              FEATURE: OTHER INFORMATION: Chimeric protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Chimeric protein US-11-196-475-164
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                                                                                                                                                                                                                                                                                                                                                                                                                                 286 NSGISTLTITVNSKKTKD 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  378 NSGTSTLTITVNSKKTKD 395
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Best Local Similarity 38.9%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                     Best Local Similarity 38.9
Matches 7; Conservative
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                       Score 38; DB 6; Length 186; Pred. No. 16; 3; Mismatches 3; Indels
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Sequence 170, Application US/11196475

Publication No. US20050271682A1

Sequence 170, Application US/11196475

Publication No. US20050271682A1

SERERAL INFORMATION:

APPLICANT: Dattwyler, Raymond J.

APPLICANT: Luft, Benjamin J.

APPLICANT: Luft, Benjamin J.

TITLE OF INVENTION: Recombinant Constructs of Borrelia TITLE OF INVENTION: Burgdorfer!

FILE REFERENCE: 2631.1001-011

CURRENT FILING DATE: 2005-08-03

PRIOR APPLICATION NUMBER: US 08/148,191

PRIOR PILING DATE: 1993-11-01

PRIOR FILING DATE: 1994-04-29

PRIOR PLILING DATE: 1994-04-29

PRIOR PLILING DATE: 2000-09-19

PRIOR PLILING DATE: 2000-09-19

PRIOR PLILING DATE: 2000-09-18
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Daturyler, Raymond J.
APPLICANT: Deduces Solecki, Maria J. C.
APPLICANT: Genes Solecki, Maria J. C.
APPLICANT: Lufft, Benjamin J.
APPLICANT: Lufft, Benjamin J.
TITLE OF INVENTION: Recombinant Constructs of Borrelia FITLE OF INVENTION: Burgdorferi
FILE REPERBANG: 2611.1001-011
CURRENT APPLICATION NUMBER: US/11/196,475
CURRENT APPLICATION NUMBER: US 08/148,191
PRIOR FILING DATE: 1993-11-01
PRIOR FILING DATE: 1993-11-01
PRIOR FILING DATE: 1994-04-29
PRIOR FILING DATE: 1994-04-29
PRIOR FILING DATE: 2000-08-19
PRIOR FILING DATE: 2000-08-18
PRIOR FILING DATE: 2000-08-18
PRIOR FILING DATE: 2001-08-07
NUMBER: OF SEQ ID NOS: 213
SOUTWARE FASE FASESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                        Sequence 7, Application US/11196475
Publication No. US20050271682A1
GENERAL INFORMATION:
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ORGANISM: Borrelia burgdorferi
                    Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
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118 TTYASAVINGKRV 130
                                                                                                                   6 TSYINAIINSKSV 18
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LENGTH: 273
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40.4%; Score 38; DB 7; Length 450;
Best Local Similarity 38.9%; Pred. No. 46;
Matches 7; Conservative 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
40.4%; Score 38; DB 7; Length 446;
Best Local Similarity 38.9%; Pred. No. 46;
Matches 7; Conservative 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Burgdorferi
FILE REFERENCE: 2631.1001.001
FILE REFERENCE: 2631.1001.001
CURRENT APPLICATION NUMBER: US/11/196,475
CURRENT FILING DATE: 2005-08-03
FRIOR PEDITOCATION NUMBER: US 08/148,191
PRIOR FILING DATE: 1993-11-01
PRIOR FILING DATE: 1993-11-01
PRIOR FILING DATE: 1993-01-01
PRIOR PELING DATE: 1994-04-29
PRIOR PLING DATE: 1994-04-29
FRIOR PLING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-08-18
PRIOR FILING DATE: 2000-08-18
PRIOR FILING DATE: 2000-08-18
PRIOR FILING DATE: 2001-08-07
PRIOR FILING DATE: 2001-08-07
NUMBER OF SEQ ID NOS: 213
SOFTWARE: FASTERE for Windows Version 4.0
TITLE OF INVENTION: Recombinant Constructs of Borrelia TITLE OP INVENTION: Burgdorferi; FILIE REPRERENCE: 2631.1001-011; FULLE REPRENCE: 2631.1001-011; FULLE REPRENCE: 2631.1001-011; FULLE REPLICATION NUMBER: US 08/148,191; FRIOR APPLICATION NUMBER: US 08/148,191; FRIOR APPLICATION NUMBER: US 08/235,836; FRIOR FILING DATE: 1994-04-29; FRIOR APPLICATION NUMBER: US 09/666,017; FRIOR FILING DATE: 2000-09-19; FRIOR FILING DATE: 2001-08-07; NUMBER: PCT/USO1/24736; FRIOR APPLICATION NUMBER: PCT/USO1/24736; FRIOR FILING DATE: 2001-08-07; NUMBER: PCT/USO1/24736; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 148, Application US/11196475
Publication No. US20050271682A1
GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Gomes Solecki, Maria J. C.
APPLICANT: Luff, Benjamin J.
APPLICANT: Dunn, John J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Chimeric Protein US-11-196-475-148
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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3 NAATSYINAIINSKSVSD 20

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RESULT 12
US-11-196-475-146
; Sequence 146, Application US/11196475
; Publication No. US20050271682A1
; GENERAL INFORMATION:
; APPLICANT: Dattwyler, Raymond J.
; APPLICANT: Dattwyler, Raymond J.
; APPLICANT: Duft, Benjamin J.
; APPLICANT: Duft, Benjamin J.
; APPLICANT: Duft, Benjamin J.
; TITLE OF INVENTION: Recombinant Constructs of Borrelia
; TITLE OF INVENTION: Recombinant Constructs
; TITLE OF INVENTION: Burgdorferi
; FILLE REFERENCE: 261.1001-01
; FILLE REFERENCE: 261.1001-01
; FRIOR FILLING DATE: 1993-11-01
; PRIOR FILLING DATE: 1994-04-29
; PRIOR FILLING DATE: 1994-04-29
; PRIOR FILLING DATE: 2000-09-19
; PRIOR FILLING DATE: 2000-09-19
; PRIOR FILLING DATE: 2000-09-19
; PRIOR PAPLICATION NUMBER: US 66/226,484
; PRIOR PLILING DATE: 2000-09-19
; PRIOR PLILING DATE: 2001-09-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Recombinant Constructs of Borrelia TITLE OF INVENTION: Burgdorferi FILE REFERENCE: 2631.1001.011
CURRENT APPLICATION NUMBER: US/11/196,475
CURRENT APPLICATION NUMBER: US/11/196,475
CURRENT FILING DATE: 2005-08-03
PRIOR PELING DATE: 1993-11-01
PRIOR PELING DATE: 1993-11-01
PRIOR PELING DATE: 1994-04-29
PRIOR FILING DATE: 1994-04-29
PRIOR PELING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-08-18
PRIOR FILING DATE: 2001-08-07
NUMBER OF SEQ ID NOS: 213
SOFTWARE: FRASES FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 213
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 146
LENGTH: 453
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APPLICANT: Gomes Solecki, Maria J. C.
APPLICANT: Luft, Benjamin J.
APPLICANT: Dunn, John J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 112, Application US/11196475 Publication No. US20050271682A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Chimeric Protein US-11-196-475-146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 397 NSGTSTLTITVNSKKTKD 414
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Best Local Similarity 38.9*
The Conservative
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Fublication No. US2006002947A1
GENERAL INCRMATION:
GENERAL INCRMATION:
APPLICANT: HUMPHREVS.
FILE APPLICANT: KU, MINZHEN
FILE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
FILE REPERENCE: REH-2017US01
CURRENT APPLICATION NUMBER: 10/245,871
PRIOR APPLICATION NUMBER: 10/245,871
PRIOR FILING DATE: 2002-09-17
PRIOR PILING DATE: 2002-09-17
PRIOR PILING DATE: 2002-09-17
PRIOR PILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 1452
SOFTWARE: Patentin version 3.3
SSEQ ID NO 282
LENGTH: 702
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                                                                                                                                                                              Query Match 40.4%; Score 38; DB 7; Length 573; Best Local Similarity 38.9%; Pred. No. 62; Matches 7; Conservative 3; Mismatches 8; Indels
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Publication No. US20050256299A1
GEMERAL INFORMATION:
APPLICANT: University of Sheffield
APPLICANT: Biosynexus Incorporated
APPLICANT: Biosynexus Incorporated
APPLICANT: Mond, James
ITILE OF INVENTION: Antigenic Polypeptides
ITILE OF INVENTION: Antigenic Polypeptides
FILE REFERENCE: P100629WO
CURRENT PPLICATION NUMBER: US/10/485,517
CURRENT PILING DATE: 2004-02-02
FRIOR APPLICATION NUMBER: GB 0118825.9
FRIOR APPLICATION NUMBER: GB 020349.9
FRIOR PILING DATE: 2000-09
NUMBER OF SEQ ID NOS: 424
SEQFTWARE: PatentIn version 3.1
SEQ ID NO 146
DENGTH: 706
                                                                                                            OTHER INFORMATION: Chimeric Protein
                                                                                                                                                                                                                                                                                                      200 NSGISTLTITVNSKKTKD 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 NAATSYINAIINSKSVSD 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 SNAATSYINAIINSKSVS 19
                                                               ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
US-11-033-039-282
                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
US-11-033-039-282
                                                                                                                                   US-11-196-475-112
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SEQ ID NO 112
LENGTH: 573
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; ORGANISM: Staphylococcus aureus
US-10-485-517-146
Query Match
Best Local Similarity 35.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 6; Mismatches 7; Indels 0;
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Gaps

Search completed: January 25, 2006, 20:11:07 Job time : 6.5 secs

1 KSNAATSYINAIINSKSVSD 20
: | | | : | : | : | : | 347 QKNALTQQVNSAQNVQAVND 366

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January 25, 2006, 18:48:24; Search time 68.2 Seconds (without alignments) 128.850 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
                                                                                                            OM protein - protein search, using sw model
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2443163 Total number of hits satisfying chosen parameters: 2443163 seqs, 439378781 residues 1 KHKLITIQGQVSALQTQQAG 20 Gapop 10.0 , Gapext 0.5 US-10-797-821-2 97 **BLOSUM62** Scoring table: Perfect score: Sequence: Searched:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Listing first 45 summaries geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2003bs:* geneseqp2004s:* geneseqp2003as:* Post-processing: Minimum Match 08 Maximum Match 1008 geneseqp2001s:* geneseqp2002s:* Geneseq 21:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2005s:*

SUMMARIES

	Description		Add93622 Streptoco	Adx37245 Streptoco	Add93629 Streptoco	Adx37252 Streptoco	Add93649 Streptoco	Add93650 Streptoco	Add93653 Streptoco	Adx37272 Streptoco	Adx37273 Streptoco	Adx37276 Streptoco	Aeb91500 Microbial	Add93651 Streptoco	Add93652 Streptoco	Adx37274 Streptoco	Adx37275 Streptoco	Add93628 Streptoco	Adx37251 Streptoco	Abp03636 Human ORF	Aae36324 Arabidops	Abp29684 Streptoco	Adu69524 S agalact	Adv88392 Streptoco	Adv81808 Streptoco	Adv79645 Streptoco
	q		ADD93622	ADX37245	ADD93629	ADX37252	ADD93649	ADD93650	ADD93653	ADX37272	ADX37273	ADX37276	AEB91500	ADD93651	ADD93652	ADX37274	ADX37275	ADD93628	ADX37251	ABP03636	AAE36324	ABP29684	ADU69524	ADV88392	ADV81808	ADV79645
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	Query Match Length DB		20	20	20	20	431	431	431	431	431	431	431	432	432	432	432	20	20	100	604	447	447	447	447	447
de	Query		100.0	100.0	67.0	67.0	67.0	67.0	67.0	67.0	67.0	67.0	67.0	67.0	67.0	67.0	67.0	52.6	52.6	49.5	47.4	46.4	46.4	46.4	46.4	46.4
	Score		97	97	65	65	65	65	65	65	65	65	65	65	65	65	65	51	51	48	46	45	45	45	45	45
	Result No.		-	7	m	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

Abu47461 Protein e Aay93947 Amino aci Ady8748 Enterococ Aay16613 Amino aci Abu39026 Protein e Abb52485 Escherich Aab12448 Human hho Aab09968 Human hoa Aam39059 Human hoa Aam39059 Human hoa Aau28092 Novel hum Adf69106 Human MP5 Adx93182 Plant ful Ads2433 Bacterial Abm88482 Rice abio Abg75918 Streptoco Abg77915 High leve Adm48066 Polypepti	
ABU47461 AAY333947 ADH88734 ADH88734 AAH19026 ABB12448 AAAB09968 AAAB09968 AAAB0959 AAAB095968 AAAB093182 ADF69106 ADF69109	ADA/9199 ABO83701 AAE03671
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1034 1115 295 410 410 410 789 789 789 789 789 789 831 1526 872 872 872	418 700 964
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ALIGNMENTS

RESULT 1

Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen. Streptococcus mutans glucan binding protein-B peptide fragment. ADD93622 standard; peptide; 20 AA. 07-MAR-2003; 2003WO-US006962 07-MAR-2002; 2002US-0363209P. (first entry) Taubman MA; (FORS-) FORSYTH INST. Streptococcus mutans WPI; 2003-845091/78. WO2003075845-A2 29-JAN-2004 18-SEP-2003 Smith DJ, ADD93622; ADD93622

Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.

Claim 11; Page 10; 49pp; English.

The present sequence is that of a peptide derived from the glucan binding protein-B (GbpB) of Streptococcus mutans strain SK32 ADD93649. The peptide blids to a major histocompatibility complex (MFC) class II protein. It was identified as a potential B cell epitope using a matrix-based algorithm for epitope prediction, which was used to search the primary amino acid sequence of GbpB for known MFC class II binding motifs. The peptide can be used in immunogenic compositions and subunit vaccines for dental caries. These comprise MFC class II binding GbpB peptides covalently linked with peptide subunits (preferably from the catalytic domain) of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Diepitopic or multiepitopic polypeptides can be prepared synthetically or

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The present sequence is that of a peptide comprising amino acid residues 52-71 of the glucan binding protein-B (GbpB) of Streptococcus mutans strain SK12 ADD93649. The peptide binds to a major histocompatibility complex (MHC) class II protein. It was identified as a potential B cell epitope using a matrix-based algorithm for epitope prediction, which was used to search the primary amino acid sequence of GbpB for known MHC class II binding motifier. The peptide can be used in immunogenic compositions and subunit vaccines for dental caries. These comprise MHC class II protein-binding GbpB peptides covalently linked with peptide subunits (preferably from the catalytic denain) of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Dispitopic or multispitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Autibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
                                                                                                                                                                                                                         Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   raised against MHC class II binding fragments of GbpB can be used in
                                                                                                                                                                              Streptococcus mutans glucan binding protein-B peptide fragment.
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                                                             ADD93629 standard; peptide; 20 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                             07-MAR-2002; 2002US-0363209F.
08-AUG-2002; 2002US-0402483F.
                                                                                                                                                                                                                                                                                                                                                                                       07-MAR-2003; 2003WO-US006962.
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                                                                                                                                                                                                                                                                   Streptococcus mutans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (FORS-) FORSYTH INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-845091/78.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                         WO2003075845-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20 AA;
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                                                                                                                                             29-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a composition comprising a fragment of a glucan binding protein-B (GbpB) and a biocompatible microparticle, where the fragment binds to a major histocompatibility complex (MrC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds to a Streptococcus mutans GbpB-derived peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MfC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in passive immunisation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunogenicity; immune stimulation; glucan binding protein-B;
microparticle; major histocompatibility complex; tooth disease.
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Pred. No. 6e-09;
; Mismatches 0; Indels
                                                                                                     20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus mutant glucan binding protein B peptide #2.
                                                                                                                                             0; Indels
                                                                                                       Length
                                                                                                     Score 97; DB 7;
Pred. No. 6e-09;
                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                            ADX37245 standard; peptide; 20 AA
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08-JAN-1999; 99US-0115142P.
12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-0462483P.
07-MAR-2003; 2003US-0402483P.
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                                                                                                     Query Match
Best Local Similarity 100.0%;
Matches 20; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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Best Local Similarity 100.
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus mutans,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SMIT/) SMITH D J.
(TAUB/) TAUBMAN M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2005-151644/16.
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                                                               Sequence 20 AA;
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                                    Gaps
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o. 0.0013;
o. 0.0013;
o. Indels
                                                                                                                                                                                                                             Streptococcus mutant glucan binding protein B peptide #9.
          67.0%; Score 65; DB
100.0%; Pred. No. 0.0
ive 0; Mismatches
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te= "HLA-binding peptide"
                                                                                                    "HLA-binding peptide"
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/note= "HLA-binding peptide"
          "HLA-binding peptide"
                                                                                   "HLA-binding peptide"
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248. .267
/note= "HLA-binding
                                                                                                                        "HLA-binding
                                                                                                                                  194. .213
/note= "HLA-binding
                                      38. .107
/note= "HLA-binding
113. .132
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                                                                 "HLA-binding
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08-AUG-2002; 2002US-0402483P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    class II protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 431 AA;
                                                                                                                                                                                                                                                                                                                                         WO2003075845-A2
                                                                                                                                                                                                                                                                                                                                                          18-SEP-2003.
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                                                                                                                                                                                                                                                                                                           The invention relates to a composition comprising a fragment of a glucan binding protein-B (GbpB) and a biocompatible microparticle, where the fragment binds to a major histocompatibility complex (MRC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds to a Streptococcus mutans GbpB-derived peptide of the invention.
                                                                                                                                                                                                                                         New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
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immunogenicity; immune stimulation; glucan binding protein-B;
microparticle; major histocompatibility complex; tooth disease.
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                                                                                                                                                                                                                                                                                                                                                                                                 67.0%; Score 65; DB 9; Length 20;
100.0%; Pred. No. 0.0013;
ive 0; Mismatches 0; Indels
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16. .35
'~re= "HLA-binding
                                                                                                                                                                                                                                                                                        Claim 4; SEQ ID NO 9; 73pp; English.
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'note= "HLA-binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADD93649 standard; protein; 431 AA.
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                                                                                                              08-JAN-1999; 99US-0115142P.
12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-0363209P.
08-AUG-2002; 2002US-0402483P.
                                                                                   09-MAR-2004; 2004US-00797821
                                                                                                      98US-0081550P
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es 14; Conservative
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/note=
37.
                                                                                                                                                                                                      Taubman MA;
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                              Streptococcus mutans
                                                                                                                                                                         (SMIT/) SMITH D J. (TAUB/) TAUBMAN M A.
                                                                                                                                                                                                                        WPI; 2005-151644/16.
                                               US2005031633-A1
                                                                                                                                                                        SMITH D
                                                                                                                                                                                                                                                                                                                                                                               Sequence 20 AA;
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The present sequence is the protein sequence of the glucan binding protein-B (GbpB) of Streptococcus mutans strain SX32. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions comprise major histocompatibility complex (WHC) class II protein-binding GbpB peptides, especially HLA-binding peptides, cowplently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Dispitopic or multiphtopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex

DB 7; Length 431;

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The present sequence is the protein sequence of the glucan binding protein-B (GbpB) of Streptococcus mutans strain 5SM3. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The includes a number of muman leucocyte antigen (HLA)-binding epitopes. The caries. The compositions compositions and vaccines for dental caries. The compositions comprise major histocompatibilty complex (WHC) covalently linked with peptides unbunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Dispitopic or multipeptopic polypeptides can be prepared synthetically or by recombinant bNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
                                                                                                           Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
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microparticle; major histocompatibility complex; tooth disease.
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Pred. No. 0.047;
0; Mismatches 0; Indels
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                                                                      Streptococcus mutans glucan binding protein-B.
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tive 0;
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                                 29-JAN-2004 (first entry)
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nes 14, Conservative
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                                                                                                                                                        Streptococcus mutans
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GENBANK; AY046414.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
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                                     Indels
Pred. No. 0.047;
                                                                                                                                                                                                                                                                                                                                   Streptococcus mutans glucan binding protein-B.
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100.08; FL
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08-AUG-2002; 2002US-0402483P.
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                                                                        6 TIOGOVSALOTOOA 19
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Best Local Similarity 100.0
Matches 14, Conservative
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                                   14; Conservative
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              Best Local Similarity
Matches 14; Conserv
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10-PEB-2005

ADD93653;

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The invention relates to a composition comprising a fragment of a glucan binding protein-B (GbpB) and a biocompatible microparticle, where the fragment binds to a major histocompatibility complex (MHC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds to a Streptococcus mutans GbpB protein of the invention.
                                                                   New composition comprising a fragment of a glucan binding protein-B (dpbB) that binds to MfC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries
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                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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microparticle; major histocompatibility complex; tooth disease.
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                                                                                                                                                             Claim 3; SEQ ID NO 30; 73pp; English.
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08-JAN-1999; 99US-0115442P.
12-APR-1999; 99US-0029049.
07-MAR-2002; 2002US-0363209P.
08-AUG-2002; 2002US-0402483P.
07-MAR-2003; 2003US-00383930.
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Taubman MA;
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TAUBMAN M A.
                                WPI; 2005-151644/16.
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Smith DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADX37276;
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(TAUB/)
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                                                                                                                                                                                                                                                                                                         New composition comprising a fragment of a glucan binding protein-B (dppB) that binds to MfC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
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microparticle; major histocompatibility complex; tooth disease.
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100.0%; Pred. No. 0.047;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; SEQ ID NO 29; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADX37273 standard; protein; 431 AA.
                                              980S-0081550P.
990S-0115142P.
990S-00290049.
2002US-0363209P.
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99US-00290049.
2002US-0363209P.
               2004US-00797821
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TAUBMAN M A.
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TAUBMAN M A.
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                                            13-APR-1998;
08-JAN-1999;
12-APR-1999;
07-MAR-2002;
08-AUG-2002;
               09-MAR-2004;
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07-MAR-2003;
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12-APR-1999;
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fragment binds to a major histocompatibility complex (MHC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds to a streptococcus mutans GbpB protein of the invention.
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                                                                                                                                            67.0%; Score 65; DB 9; Length 431;
100.0%; Pred. No. 0.047;
ive 0; Mismatches 0; Indels
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Best Local Similarity
                                                                                                          Sequence 431 AA;
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6 TIOGOVSALOTOOA 19 57 TIQGQVSALQTQQA 70 δ 셤

AEB91500 standard; protein; 431 AA.

AEB91500;

(first entry) 20-OCT-2005 Microbial pathogen adhesin protein sequence, SEQ ID NO:210.

algorithm; adhesin; pharmaceutical; vaccine; drug screening; bordetella pertussis infection; antibacterial; pneumonia; antiinflammatory; respiratory-gen.; gastric ulcer; antiulcer; gastrointestinal-gen.; urinary tract infection; antimicrobial; uropathic.

Streptococcus mutans

WO2005076010-A2.

18-AUG-2005

07-FEB-2005; 2005WO-IN000037

06-FEB-2004; 2004IN-DE000173

20-JUL-2004; 2004US-0589227P

(COUL) COUNCIL SCI & IND RES

Jain P, Brahmachari SK, Ramachandran S; Kumar K, Sachdeva G,

SOUTH AFRICA.

WPI; 2005-597835/61.

Computational method for identifying adhesin and adhesin like molecules, comprises computing sequence-based attributes of protein sequences using neural network software and training an artificial neural network.

Claim 16; SEQ ID NO 210; 402pp; English.

The present invention relates to a computational method (M1) for identifying adhesin and adhesin-like proteins, by computing the sequence-based attributes of protein sequences using five attribute modules of a neural network software, training an artificial neural network (ANN) for each of the computed five attributes, and identifying the adhesin and adhesin-like proteins having probability of being an adhesin and adhesin-like proteins, having 274 fully defined 162 encoding adhesin and adhesin-like proteins, having 105 fully defined 306-15876 base pair (SEQ ID NO: 385-658) sequences; a set of 105 hypothetical adhesin and adhesin-like proteins, having 105 fully defined 306-15876 base pairs (SEQ ID NO: 365-763); a set of 279 annotated adhesin and adhesin-like proteins, having 105 fully defined 53-3716 base pair (SEQ ID NO: 1-279); a set of 105 hypothetical adhesin-like proteins, having 105 fully defined 166-5291 base pair (SEQ ID NO: 280-384) sequences; and a fully connected multilayer feed forward ANN (I) based on (M1). (M1) is useful for identifying adhesin and adhesin-like proteins, based on the connected multilayer feed forward ANN (I) based on the connected multilayer feed forward ANN (I) based on the connected multilayer feed forward ANN (I) based on the connected multilayer feed forward ANN (I) based on the connected multilayer feed forward ANN (I) based on the connected multilayer feed forward ANN (I) based on the connected multilayer feed forward ANN (I) based on the connected multilayer feed forward ANN (I) based on the connected multilayer feed forward ANN (I) based on the connected multilayer feed forward ANN (I) based on the connected multilayer feed forward ANN (I) based on the connected multilayer feed forward ANN (I) based on the connected multilayer feed forward ANN (I) based on the connected multilayer feed forward ANN (I) based on the connected multilayer feed forward ANN (I) based on the connected multilayer feed forward ANN (I) based on the connected multilayer feed forward ANN (I) based on t

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useful for identifying putative adhesins that are important in drug discovery and preventing therapeutics for whooping cough, pneumonia, gastric uleer and urinary tract infections. (M.) identifies adhesins from distantly related organisms, and from bacteria belonging to a wide phylogenetic spectrum. (M.) is capable of predicting adhesive nature of unique proteins. The present sequence is a microbial pathogen adhesin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is the protein sequence of the glucan binding protein.B (GbpB) of Streptococcus mutans strain 1572. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions comprise major histocompatibility complex (MHC) class II protein-binding GbpB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Diepitopic or multiepitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
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nes 14; Conservative
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                                                                                                    protein sequence.
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ADD93652;

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New composition comprising a fragment of a glucan binding protein-B (dpbB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental cartes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a composition comprising a fragment of a glucan binding protein-B (GbpB) and a biocompatible microparticle, where the fragment binds to a major histocompatibility complex (MHC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds to a Streptococcus mutans GbpB protein of the invention.
                                                     immunogenicity; immune stimulation; glucan binding protein-B;
microparticle; major histocompatibility complex; tooth disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunogenicity; immune stimulation; glucan binding protein-B;
microparticle; major histocompatibility complex; tooth disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 432;
                  Streptococcus mutant glucan binding protein B variant #3.
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Pred. No. 0.047;
0; Mismatches 0; Indels
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08-7AN-1999; 99US-0115142P.
12-APR-1999; 99US-0020049.
07-VMXR-2002; 2002US-032309P.
08-AUG-2002; 2002US-0402483P.
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                                                                                                      Streptococcus mutans
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex
                                                                                                                                                                                                                                                                                  Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
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Pred. No.
                                                                                                                                    ADD93652 standard; protein; 432 AA.
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08-AUG-2002; 2002US-0402483P
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Best Local Similarity
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Smith DJ,

ADX37274;

RESULT 14

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                                                                                                                                                                                                                                                                     New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
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               13-APR-1999; 98US-0081550P.
08-JAN-1999; 99US-0115142P.
12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-036209P.
08-AUG-2002; 2002US-0402483P.
07-MAR-2003; 2003US-0402483P.
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57 TIQGQVSALQTQQA 70
                                                                                                                                                                                                   Smith DJ, Taubman MA;
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(TAUB/) TAUBMAN M A.
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Search completed: January 25, 2006, 19:01:40 Job time : 69.2 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

January 25, 2006, 18:48:55; Search time 9.1 Seconds (without alignments) 211.465 Million cell updates/sec

US-10-797-821-2 97

1 KHKLITIQGQVSALQTQQAG 20 score: Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 283416 segs, 96216763 residues Searched:

283416

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		de			SUMMAKIES	
Result No.	Score	Query	Query Match Length	DB	ID	Description
1	46	47.4	636	~	A86248	protein T23J18.9
71	45	46.4	142	~	C81359	hypothetical prote
М	45	46.4	1034	~	AB0551	exonuclease SbcC [
4	45	46.4	1115	7	D69617	TO.
ഗ	43	44.3	214	N	D70673	hypothetical prote
9	43	44.3	216	~	T45430	hypothetical prote
7	43	44.3	326	7	D95309	probable UDP-Bluco
œ	43	44.3	872	7	S76197	endopeptidaseClp
6	42	43.3	192	7	G95072	conserved hypothet
10	42	43.3	192	7	D97940	conserved hypothet
11	42	43.3	234	N	T00931	O
12	42	43.3	709	7	T00664	hypothetical prote
13	42	43.3	1020	Н	Огнин	μ
14	42	43.3	4957	~	T03455	ALR protein - huma
	42	43.3	5262	N	T03454	ALR protein - huma
16	41	42.3	177	Н	E22102	phycocyanin-645 be
17	41	42.3	465	N	AE1568	hypothetical prote
18	41	42.3	491	7	AC1816	hypothetical prote
19	41	42.3	735	7	T00850	probable receptor-
20	41	42.3	1115	~	T19137	hypothetical prote
21	40	41.2	275	0	S75994	hypothetical prote
22	40	41.2	334	~	T28832	hypothetical prote
23	40	41.2	384	~	A84012	N-acetylornithine
24	40	41.2	408	~	D64857	aminotripeptidase
25	40	41.2	408	N	D90825	probable peptidase
	40	41.2	408	~	G85683	
27	40	41.2	409	~	A42363	
28	40	41.2	409	N	AD0646	aminotripeptidase
29	40	41.2	412	~	C64118	aminotripeptidase

alpha-amylase (EC	choline binding pr choline-binding pr	hypothetical prote	CAT8 protein - yea	conserved hypothet	conserved hypothet	probable flagellar	probable oxidoredu	secreted 45 kd pro	general stress pro	peptidase T VCA018	vdcC protein [impo	u	beta-galactoside a	T-box_protein 2 -
S60040	A95250 F98114	875935	S54587	H69820	C83502	E81420	C95988	G95258	B98124	C82491	AD3629	S27962	JC5898	G01840
0	N N	0	N	N	N	~	7	~	~	N	N	N	~	7
611	621	720	1433	237	278	294	376	392	392	410	504	614	675	702
41.2	41.2	41.2	41.2	40.2	40.2	40.2	40.2	40.2	40.2	40.2	40.2	40.2	40.2	40.2
40	4 4 0 0	40	40	39	39	39	39	39	39	39	39	39	39	39
30	3 7 3 7	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

protein T23J18.9 [imported] - Arabidopsis thaliana protein T23J18.9 [imported] - Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: A86248
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jin, Y.; Liu, X.; Liu, X

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-636 <STO>
A;Residues: 1-636 <STO>
A;Cross-references: UNIPROT:Q9LPZ2; UNIPARC:UPI0000A908F; GB:AE005172; NID:g6554201; P

C,Genetics: A,Gene: T23J18.9 A,Map position: 1

Gaps ; 0 Length 636; 4; Indels ore 46; DB 2; ed. No. 14; Mismatches Score 46; Pred. No. 5, 47.4%; Query Match
Best Local Similarity 50.0
Matches 9; Conservative

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1 KHKLITIQGQVSALQTQQ 18

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|||:| :| | :||: 576 KHKIIELQRQEAALKEQK 593 g

CB1359

CB1359

CB1359

CB1359

CSpecial protein Cj0859c [imported] - Campylobacter jejuni (strain NCTC 11168)

CSpecial campylobacter jejuni

CSPECIAL CB1359

REPAIRAILI, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilli, C.; W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000

A; Reference number: A81250; MUID:20150912; PMID:10688204

A; Accession: C81359

A; Accession: C81359

A,Status: preliminary A,Molecule type: DNA A,Residues: 1-142 <PAR> A,Erosidues: 1-142 <PAR> A,Cross-references: UNIPROT:Q9PP64; UNIPARC:UPI00000C1D68; GB:AL139076; GB:AL111168; NIF A,Experimental source: serotype O2, strain NCTC 11168

2

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Gaps

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Indels

Length 1115;

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R.Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, E.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A. Mature 393, 537-544, 1998
A. Anthors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A.Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A.Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A.Title: Dropper A.Toson, Mulb:98295987; PMID:9634230
A.Status: preliminary; nucleic acid sequence not shown; translation not shown A.Mesidues: 1-214 <COL>
A.Residues: 1-214 <COL>
A.Residues: 1-214 <COL>
A.Residues: 1-214 <COL>
A.Residues: Born A.Residues: Strain H37Rv
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A;Experimental source: cosmid B637
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein Rv2983 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 43; DB 2; Length 214;
Pred. No. 14;
5; Mismatches 3; Indels
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46.7%; Pred. No. 14;
ive 5; Mismatches 3; Indels
                                        A;Gene: dnaE
C;Superfamily: DNA-directed DNA polymerase III alpha chain
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R;Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, September 1997
A;Reference number: 216918
A;Accession: T45430
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Roicule type: DNA
A;Residues: 1-216 <PAR>
                                                                                                                                                             Query Match 46.4%; Score 45; DB Best Local Similarity 58.8%; Pred. No. 36; Matches 10; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         933 KOLTAÇGAVSILQAÇRA 949
                                                                                                                                                                                                                                                                                                                                             3 KLITIQGQVSALQTQQA 19
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112 IVVLQGDLPALQTQE 126
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Best Local Similarity 46.7%;
Matches 7; Conservative
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110 IVVLQGDLPALQTQE 124
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Best Local Similarity 46...
7; Conservative
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C,Genetics:
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R; Kunst, F:; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G; Azevedo, V.; Berter C; Runst, F:; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G; Azevedo, V.; Berter C; Brunst, S.; Brusillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Changare, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapddus, A.; Lardinois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Maguda, S.; Maueel, Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portor, N.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wigher, A.; Yamamoto, K.; Yasumoto, K.; Yata, Yata, K.; Yata, K.; Yata, K.; Yata, Yata, K.; Yata, Yata, K.; Yata, Y
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A;Cross-references: UNIPROT:034623; UNIPARC:UPI0000608C4; GB:Z99118; GB:AL009126; NID:q
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: AB0551
R; Parkhill, J; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
Nature 413, 848-852, 2001
Nature 413, 848-852, 2001
N;Ruthers: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Accession: AB0502; MUD:21534947; PMID:11677608
N;Reference number: AB0502; MUD:21534947; PMID:11677608
N;Reference number: AB0502; MUD:21534947; PMID:11677608
N;Residues: 1-1034 <-PR>
N;Residues: 1-1034 <-PR>
N;Residues: 1-1034 <-PR>
N;CGGenetics: UNIPARC:UPI00000CDAFF; GB:AL513382; PIDN:CAD08850.1; PID:g16501663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exonuclease SbcC [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
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C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                Gaps
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C,Genetics:
A,Gene: Cj0859c
C,Superfamily: Campylobacter jejuni hypothetical protein Cj0859c
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                                                                                                                                                             Query Match
46.4%; Score 45; DB 2; Length 142;
Best Local Similarity 64.3%; Pred. No. 4.2;
Matches 9; Conservative 2; Mismatches 3; Indels
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2; Mismatches
                               Pred. No.
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                                                                                                                                                         3 KLITIQGQVSALQTQQA 19
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                               58.88;
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                                                                   10; Conservative
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                      Best Local Similarity
Matches 10; Conserv
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-192 <KUR>
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probable UDP-glucose 4-epimerase [imported] - Sinorhizobium meliloti (strain 1021) magapy C; Species: Sinorhizobium meliloti
C; Species: Sinorhizobium meliloti
C; Species: Sinorhizobium meliloti
C; Species: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C; Accession: D95309
R; Barnett, M.J.; Pisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowe S; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A; Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot A; Reference number: A95262; MUID:21396509; PMID:11481432
A; Accession: D95309
A; Status: preliminary
A; Wolecule type: DNA
A; Residues: 1-326 Acura
A; Cross-references: UNIPROT: Q92ZR9; UNIPARC:UPI00000CB09F; GB:AE006469; PIDN:AAK65038.1;
A; Cross-references: UNIPROT: Q92ZR9; UNIPARC:UPI00000CB09F; GB:AE006469; PIDN:AAK65038.1;
A; Residues: 1-326 Acura
A; Cross-references: UNIPROT: Q92ZR9; UNIPARC:UPI0000CB09F; GB:AE006469; PIDN:AAK65038.1;
A; Residues: 1-326 Acura
A; Conserimental source: strain 1021, megaplasmid pSymh
A; R; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Adola, P.; Rape, F.; Barloy-Hubler, D.; Rahn, D.; Rahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Weiser R.A; Title: The composite genome of the legume symbiont Sinorhizobium mellloti.
A; A; Title: The composite genome of the legume symbiont Sinorhizobium mellloti.
A; A; Consering annotation
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A; Reference number: S74322; MUID:97061201; PMID:8905231
A; Accession: S76197
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-872 < KAN>
A; 
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A; Variety: PCC 6803
C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C; Accession: 876197
B; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Owimura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yahada, M.; Yasuda DNA Res. 3, 109-136, 1996
A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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N;Alternate names: ATP-dependent Clp proteinase regulatory chain; protein slr1641
N;Contains: adenosinetriphosphatase (EC 3.6.1.3)
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50.0%; Pred. No. 22;
iive 6; Mismatches 1
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145 ELVTFQGRVSSMET 158
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Best Local Similarity 50.0
Matches 7; Conservative
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A;Genome: plasmid
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Cispedies: Streptococcus protein SP0624 [imported] - Streptococcus pneumoniae (strain TIG Cispedies: Streptococcus pneumoniae cjspedies: Streptococcus pneumoniae cjspedies: O3-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004 CjAccession: G95072 RjTettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heivon, J.J.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001 R.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
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A;Experimental source: strain TIGR4
C;Genetics:
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C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Accession: D97940
R;Hoskins, U.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.;
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.;
y. P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
A;Reference number: A97872; MUID:21429245; PMID:11544234
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C;Genetics:
A;Gene: spr0548
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56.2%; Pred. No. 18;
ive 2; Mismatches 5; Indels
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Indels
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2; Mismatches
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A;Molecule type: DNA
A;Residues: 1-1020 cLEE>
A;Cross-references: UNIPROT:P12036; UNIPARC:UPI000012FFBF; EMBL:X15306; NID:G35028; PID1
A;Note: it is uncertain whether Met-1 or Met-2 is the initiator
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A Map position: 22q12.1-22q13.1
A Map position: 22q12.1-22q13.1
C,Superfamily: neurofilament triplet H protein
C,Superfamily: neurofilament triplet H protein
C,Superfamily: neurofilament triplet H protein
C,Keywords: coiled coil; heterotrimer; intermediate filament; nerve; phosphoprotein
C,Keywords: coiled coil; heterotrimer; intermediate filament; nerve; phosphoprotein
C,Keywords: coiled coil; heterotrimer (*RD)
F;101-410/Domain: cod #status predicted (*RD)
F;101-410/Domain: carboxyl-terminal (*CTD)
F;101-410/Domain: carboxyl-terminal (*CTD)
F;101-1020/Domain: carboxyl-terminal (*CTD)
F;101-1020/Do
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R; Prasad, R.; Zhadanov, A.B.; Sedkov, Y.; Bullrich, F.; Druck, T.; Rallapalli, R.; Yano Nocogene 15, 549-560, 1997
A; Title: Structure and expression pattern of human ALR, a novel gene with strong homoloma, Reference number: Z14954; MUID:97388474; PMID:9247308
A; Recession: T03455
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C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T0454
R;Prasad, R.; Zhadanov, A.B.; Sedkov, Y.; Bullrich, F.; Druck, T.; Rallapalli, R.; Yano
Oncogene 15, 549-560, 1997
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A;Molecule type: mRNA
A;Residues: 1-4957 <PRA>
A;Cross-references: UNIPROT:014686; UNIPARC:UPI00001100F1; EMBL:AF010404; NID:G2358286;
                                                                                                                                                A,Title: The structure and organization of the human heavy neurofilament subunit (NF-H) A;Reference number: S00979; MUID:88328981; PMID:3138108 A;Accession: S00979
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C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004 C;Accession: S00979 R;Lees, J.F.; Shneidman, P.S.; Skuntz, S.F.; Carden, M.J.; Lazzarini, R.A. EMBO J. 7, 1947-1955, 1988
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Pred. No. 5.5e+02;
2; Mismatches 8; Indels
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C;Reywords: alternative splicing
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43.3%; Score 42; DB
Best Local Similarity 46.7%; Pred. No. 1.1e
Matches 7; Conservative 6; Mismatches
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124 SLEGEAAALRQQQAG 138
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Local Similarity 47.4%;
les 9; Conservative ;
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        C;Accession: T00664
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R;Federsalon: M.G.; Ecker, J.; Theologis, A.; Davis, R.W.
R;Federsalon: Longer, J.; Theologis, A.; Davis, R.W.
R;William, V.S.; Yu, G.; Ecker, J.; Theologis, A.; Davis, R.W.
R;Meference number: Z14197
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 31-Dec-2004
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A,Map postition:
A,Introns: 17/3; 53/3; 441/2
C,Superfamily: U-box and arm repeat containing protein ARC1/SPL11
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N;Alternate names: neurofilament protein, 112K
C;Species: Homo sapiens (man)
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194 KAGLITIQGKISAV 207
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Matches 9; Conservative
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A, Map position: 2
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Best Local Similarity
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RESULT 12

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RESULT 13

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A;Title: Structure and expression pattern of human ALR, a novel gene with strong homolog A;Reference number: Z14954; MUID:97388474; PMID:9247308
A,Rocession: T03454
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1.5262 <PRA>
A,Gross-references: UNIPROT:014686; UNIPARC:UPI0000110107; EMBL:AF010403; NID:g2358284; C;Genetics:
A,Gene: ALR
A,Map position: 12
C;Superfamily: acute lymphoblastic leukemia protein, ALR type
C;Keywords: alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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DOI=10.1128/IAI.69.11.6931-6941.2001;
Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
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Bacteria, Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
NCBI_TaxID=1309;
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Peruzzi F., Piggot P.J., Daneo-Moore L.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U78607; AAD00288.1; -; Genomic_DNA.
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211 AA; 22803 MW; 4ACE331159CFAFC6 CRC64;
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093814_ENTFA
08FX8_HHILU
08FX22_BARQU
PEPT_PASMU
08FBE3_ECOL6
0596K4_STRT2
05M212_STRT1
064D30_SARCH
060271_XENLA
LRFN2_NOUSE
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LRFN2_MACFA
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0938VO_STRMU PRELIMINARY;
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STRAIN=5SM3;
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  NCBI_TaxID=1309;
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200.719 Million cell updates/sec
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Copyright (c) 1993 - 2006 Compugen Ltd
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Q9AG98_STRMU
Q8DWM3_STRMU
Q938V1_STRMU
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
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97
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Maximum DB
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Immunodominant glycoprotein IDG-60 (Glucan-binding protein
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                                                                          Nаше=ваqA;
      DD THE STATE OF STATE
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Infect. Immun. 69:6931-6941(2001).

EMBL; AY046410; AX949500.1; -; Genomic_DNA.

InterPro; IPR007921; CHAP.

InterPro; IPR009148; SibA.
      Duncan M.J.;
"Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates.";
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DOI=10.1128/IAI.69.11.6931-6941.2001;
Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
Duncan M.J.;
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100.0%; Pred. No. 0.046;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                         Query Match 67.0%; Score 65; DB 2; Length 431; Best Local Similarity 100.0%; Pred. No. 0.046; Matches 14; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                  431 AA; 44650 MW; 05D38D8D8BC4609F CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Glucan-binding protein B.
                                                                                 Infect. Immun. 69:6931-6941(2001).

EMBL; AY046414; AAX94504.1; -; Genomic_DNA.
InterPro; IRRO07921; CHAP.
InterPro; IRRO09148; SibA.
Pfam; PF05257; CHAP; 1.
PRINTS; PR01852; SIBARROTEIN.
PROSITE; PS50911; CHAP; 1.
SEQUENCE 431 AA; 44650 MW; 05D38D8D8BC4605
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09AG98 STRMU
09AG98_STRMU PRELIMINARY; PRT;
AC 09AG98_
DT 01-JUN-2001 (TEWBLrel: 17, Created)
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Best Local Similarity 100.0
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Q938V3;
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431 AA.

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Duncan M.J.;

Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates.';

Infect. Immun. 69:6931-6941(2001).

EMBL; AF338445; AAK08104.1; -; Genomic_DNA.

EMBL; AY046411; AAF45501.1; -; Genomic_DNA.

InterPro; IRR007921; CHAP.

InterPro; IRR007921; CHAP.
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MEDI=10.1128/IAI.69.4.2493-2501.2001;
Chia J.S., Lee Y.Y., Huang P.T., Chen J.Y.;

"Identification of stress-responsive genes in Streptococcus mutans by differential display reverse transcription-PCR.";

Infect. Immun. 69:2493-2501(2001).
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MEDLINE-21401977; PubMed=11598074;
DOI=10.1128/IAI.69.11.6987-6998.2001;
Chia J.S., Chang L.Y., Shun C.T., Chang Y.Y., Chen J.Y.;
Chia J.S., Chang L.Y., Shun C.T., Chang Y.Y., Chen J.Y.;
A 60-kilodalton immunodominant glycoprotein is essential for cell
wall integrity and the maintenance of cell shape in Streptococcus
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Chia J.-S., Chang L.-Y., Lee Y.-Y., Chen J.-Y.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
Streptococcus mutans.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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QBDWM3 STRMU
ID QBDWM3 STRMU PRELIMINARY; PRT; 431 AA.
AC QBDWM3.
T 01-WAR-2003 (TrEMBLrel. 23, Created)
DT 01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
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MEDLINE=21481971; PubMed=11598068;
DOI=10.1128/IAI.69.11.6931-6941.2001;
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PRINTS; PR01852; SIBAROTEIN.
PROSITE; PS50911; CHAP; 1.
SEQUENCE 431 AA: 44592 Mm.
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Local 14; Conservative
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                                                                                    NCBI_TaxID=1309;
                                                            Streptococcus.
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NCBI_TaxID=1309;
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10 938V2 ST
10 0938
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AC 0938
DD 01-D
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OC Barr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=UALS9 / ATCC 700610 / Serotype c;
MEDLINE=22295063; PubMed=12397186; DOI=10.1073/pnas.172501299;
Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Carson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P.,
Qian Y., Li S., Zhu H., Najar F.Z., Lai H., White J., Roe B.A.,
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Putative secreted antigen GbpB/SagA; putative peptidoglycan
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Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 65; DB 2; Length 431;
Pred. No. 0.046;
0; Mismatches 0; Indels
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                      Streptococcus mutans.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Jin S., Duncan M.J., Taubman M.A., Smith D.J.;
"Cloning of the gbpB gene from Streptococcus mutans.";
J. Dent. Res. 79:224-224(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         432 AA; 44652 MW; 3F88ECB9A1F3BE4F CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Glucan-binding protein B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
RBL; ARO14985; AAN57811.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 67.0%; Score 65; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 14; Conservative 0; Mismatches
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EMBL; AYO46413; AXC94503.1; -; Genomic_DNA.
InterPro; 1PR007921; CHAP.
InterPro; 1PR009148; SibA.
Pfam; PF05257; CHAP; 1.
PRINTS; PRO1852; SIBAPROTRIÑ.
PROSITE; PS50911; CHAP; 1.
SEQUENCE 432 AA; 44652 MW; 3F88ECB9A1F3
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                                                                                       hydrolase.
Name=gbpB; OrderedLocusNames=SMU.22.
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PROSITE; PS50911; CHAP; 1.
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                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF05257;
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"Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates.";
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Suzuki N., Okayama S., Nonaka H., Tsuge Y., Inui M., Yukawa H.;
"Large-Scale Engineering of the Corynebacterium glutamicum Genome.";
                                                       Gaps
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21481971; PubMed=11598068;
DOI=10.1128/IAI.69.11.6931-6941.2001;
Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.0%; Score 65; DB 2; Length 432;
100.0%; Pred. No. 0.046;
ive 0; Mismatches 0; Indels
     Length 432;
  67.0%; Score 65; DB 2; Length 432
100.0%; Pred. No. 0.046;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus mutans.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
                                                                                                                                                                                                                                                                                 432 AA
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InterPro; IPR007921; CHAP.
InterPro; IPR007921; CHAP.
InterPro; IPR001948; SibA.
Pfam; PF05257; CHAP; 1: AR01852; SIBAPROTRIN.
PROSTITE; PS50911; CHAP; 1.
SEQUENCE 432 AA; 44648 MW; E769B2504AEE
                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Guery Match
Best Local Similarity 100...
These 14; Conservative
                                                                                                       6 TIQGOVSALOTOQA 19
                                                                                                                                       57 TIQGQVSALQTQQA 70
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                                                                                                                                                                                                                                                                                                                                                                                                              Glucan-binding protein B.
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QSKRH3;
Query Match
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                 Q938V2 STRMU PRELIMINARY;
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NUCLEOTIDE SEQUENCE.
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PubMed=1529592; DOI=10.1018/nature02579;

PubMed=1529592; DOI=10.1018/nature02579;

PubMed=1529592; DOI=10.1018/nature02579;

Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,

Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,

Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,

Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,

Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,

Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Groppi A.,

Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,

Micaud J.-M., Nikolski M., Lebur I., Ma L., Muller H.,

Nicaud J.-M., Nikolski M., Oztas S., Ozter-Kalogeropoulos O.,

Pellenz S., Potier S., Richard G.-P., Straub M.-L., Suleau A.,

Swennen D., Tekaia F., Wesolowski-Louvel M., Westhof E., Witth B.,

Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,

Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,

"Genome evolution in yeasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Micaud S., Jaffe D., Fisher S., Intfalla G., Dossat C., Segurens B., Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castellia V., Katinka M., Vacherie B., Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V., Biemont C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J., Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S., Kallis M., Volff JN., Guigo R., Zody M.C., Mesirov J., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tetraodon nigroviridis (Green puffer).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes,
Tetraodontoidea, Tetraodontidae, Tetraodon.
Debaryomyces hansenii (Yeast) (Torulaspora hansenii).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAR7749, whole genome shotgun sequence.
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Pred. No. 59;
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PROSITE; PS00678; WD_REPEATS_1; 4.

PROSITE; PS50294; WD_REPEATS_2; 3.

PROSITE; PS50294; WD_REPEATS_REGION; 1.

Complete protecome; Repeat; WD_repeat.

SEQUENCE 529 AA; 58922 MW; A96740E45515E0E CRC64;
                        Eukaryota, Fungi, Ascomycota, Saccharomycotina, Sacc
Saccharomycetales, Saccharomycetaceae, Debaryomyces
                                                                                           [1]
NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
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InterPro; IPR001680; WD40.
Pfam; PR00400; WD40; 7.
PRINTS: PR00320; GPROTEINBRPT.
ProDom; PD000018; WD40; 2.
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70 QHKIIDLEGEVSNLRT 85
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Q4T8Q5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
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                                                                NCBL_TaxID=4959;
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pubmed=15305914; DOI=L0.1111/j.1462-2920.2004.00665.x;
Rabus R., Ruepp A., Prickey T., Rattei T., Partmann B., Stark M.,
Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,
Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
Klenk H.-P.,
"The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapa
                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Desulfotalea psychrophila.
Bacteria; Proteboacteria; Deltaproteobacteria; Desulfobacterales;
Desulfobulbaceae; Desulfotalea.
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                                                                                                           Length 130;
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                                                                                                                                                          3; Indels
                        EMBL; AB193035; BAD84114.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 130 AA; 14770 MW; 35B97ABE54D5E7CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             448 AA; 50258 MW; B16366C6AB032B48 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No DEBHA PRELIMINARY; PRT; 529 AA.

OBUNG, DEBHA PRELIMINARY; PRT; 529 AA.

OSUGO COT-2004 (TYEMBLE-1. 28, Created)

25-OCT-2004 (TYEMBLE-1. 28, Last sequence update)

25-OCT-2004 (TYEMBLE-1. 28, Last annotation update)

Similar to CA5768 | CAPACI Candida albicans.

OrderedLocusNames=DEHAOC133439;
                                                                                                                                                                                                                                                                                                                                                                                               25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Probable exodeoxyribonuclease VII, large chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF02601; Exonuc VII L; 1.
Pfam; PF01316; tRNA_anti; 1.
TIGRFAMB; TIGR00237; xseA; 1.
PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
COMPLETE PROCECOME.
SEQUENCE 448 AA; 50258 MW; B16366C6AB032B48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49.5%; Score 48; DB 2; 45.0%; Pred. No. 34;
                                                                                                                DB 2;
  Appl. Environ. Microbiol. 71:3369-3372(2005).
                                                                                                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                            4; Mismatches
                                                                                                                Score 51;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KHKLITIQGQVSALQTQQAG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | : |||:|:|::| |::| KPRFITIRGEISNLKTPYSG 44
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                                                                                                                                                                                                                             102 LVQLQNKLSALQTQAAG 118
                                                                                                                                                                                                     20
                                                                                                                  52.6%;
                                                                                                                                                                                                     4 LITIOGOVSALQTOOAG
                                                                                                                                                                                                                                                                                                                                                      QEALVI DESPS PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OrderedLocusNames=DP1945;
                                                                                                                Query Match 52.6
Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=84980;
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RESULT 10 Q6BUA6

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Gaps

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2; Indels

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Shinn P., Brooks S., Buehler B., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi B., Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J., Ler Z., Liu J., Liu A., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II; Brassicales, Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                   STRAIN=SC5314;
Jubmed=15123810; DOI=10.1073/pnas.0401648101;
Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
Bayis R.W., Scherer S.,
"The diploid genome sequence of Candida albicans.";
Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O., Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W., Jones T., Scherer S., Agabian N.; "Annotation of the Genome of Candida albicans.";
                                                                                                                                                                              Bukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBI TaxID=237561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 46; DB 2; Length 592;
Pred. No. 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AACQ01000129; EAK94204.1; -; Genomic_DNA.
EMBL; AACQ01000128; EAK94251.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00539; PYROKININ; UNKNOWN_1.
PROSITE; PS50005; TPR; 4.
PROSITE; PS50293; TPR REGION; 1.
SECEPICY; REPEAT; TPR REPEAT.
SEQUENCE 592 AA; 67324 MW; PASB271F220B38E6 CRC64;
                                                                                        Last sequence update)
Last annotation update)
.ng sequence receptor Pex5.
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Last annotation update)
                            592 AA.
                                                                                                                           Potential peroxisome targeting sequence recer
Name=PEX5; ORFNames=CaO19.13085, CaO19.5640;
Candida albicans SC5314.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO, GO:0004872; F:receptor activity; IEA.
InterPro; IPR001484; Pyrokinin.
InterPro; IPR001440; TPR.
InterPro; IPR011990; TPR-like_helical.
Pfam; PP00515; TPR 1; 4.
SMART; SM00028; TPR; 4.
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                                                                      Created)
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80 RHELNTIQNQPNAIHQQQS 98
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                                                                  10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.48;
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                          QS9UTO_CANAL PRELIMINARY;
QS9UTO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9LPZ2_ARATH PRELIMINARY;
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Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C., Wincker P., Lander B.S., Weissenbach J., Roest Crollius H.; "Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S.;
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis."; Nat. Biotechnol. 21:526-531(2003).
                                                                                                                       NUCLEOTIDE SEQUENCE.
Genoscope, Whitehead Institute Centre for Genome Research,
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                Score 46; DB 2; Length 223;
Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47.4%; Score 46; DB 2; Length 465; 44.4%; Pred. No. 76;
                                                                                                                                                                                                                                                                                                                                                                                                            5; Indels
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                                                                                                                                                                                                                                                                                                                      223 AA; 24595 MW; OFFF76D0E6AAEEDA CRC64;
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465 AA; 49845 MW; P6B451DEED9170A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22608306; PubMed=12692562; DOI=10.1038/nbt820
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EMBL; BA000030; BAC69811.1; -; Genomic DNA.
Complete proteome; Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                   preliminary data.

EMBL; CAAE01007749; CAF90727.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      465 AA.
                                                                                                                                                                                                                                                                                                                                                                                                        7; Mismatches
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HRLVPVHGRPSSLHTAQA 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OrderedLocusNames=SAV2100;
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Best Local Similarity 30.0.
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OB2LB1_STRAW PRELIMINARY;
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nes 8; Conserv
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SEQUENCE
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STRAW Q82LB1;

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SEQUENCE Query Match

Best Loc Matches

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RESULT 13

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Search completed: January 25, 2006, 19:13:34
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                                                          Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi B., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Tortiumi M., Vayaberg M., Yu G., Davis R., Federspiel N., Theologis A., Ecker J.; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                               Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C., Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C., Shinn P., Altafi H., Bei B., Chio J., Choi E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Triniumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A.,
                                                                                                                                                                                                                             Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C., Shinn P., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Muyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tetraodon nigroviridis (Gren puffer).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes;
Tetradontoidea, Tetraodontidae, Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47.4%; Score 46; DB 2; Length 636; illarity 50.0%; Pred. No. 1e+02; Conservative 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                 Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 10 SCAF14571, whole genome shotgun sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00133; CARBOXYPEPT ZN 2; UNKNOWN 1.
SEQUENCE 636 AA; 73691 MW; A394CEC482D0A3E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; ACOLIG61; AAFL6647.1; -; Genomic_DNA. PIR; A86248; A86248. Binding; IEA. GO; GO:0003723; F:RN binding; IEA. InterPro; IPR006393; Agenet. InterPro; IPR007930; DUF724. InterPro; IPR00684; Peptidase_M14. Pfam; PF05641; Agenet; 2. Pfam; PF0566; DUF724; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KHKLITIQGQVSALQTQQ 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q4SK16_TETNG PRELIMINARY;
Q4SK16;
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                                                                                                                                                                                                     [3]NUCLEOTIDE SEQUENCE.
                                                 NUCLEOTIDE SEQUENCE.
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Best Local Similarity
Matches 9; Conserv
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Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Bismont C., Skali Z., Cattolico L., Poulain J., De Berardinis V.,
Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Hincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
Wincker P., Lander E.S., Reissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genoscope; Whitehead Institute Centre for Genome Research; Submitted (FBS-2004) to the RWBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           794 AA; 87677 MW; 67DACF43B24FF862 CRC64;
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InterPro; IPR003051; FN III.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR001599; Ig.
InterPro; IPR001599; Ig.
InterPro; IPR001599; Ig.
InterPro; IPR001599; Ig.
InterPro; IPR001699; IRR Cterm.
InterPro; IPR001699; IRR Cterm.
InterPro; IPR00105; Myb_DNA_bd.
Pfam; PF00560; IRR 1; 6.
Pfam; PF00560; IRR 1; 6.
PRINIS; PR005019; IEURICHRPT.
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SWART; SM00409; IG2; 1.
SWART; SM00409; IG2; 1.
SWART; SM00082; IGR: TYP; 6.
SWART; SM00082; IRR_TYP; 6.
PROSITE; PS50853; FN3; 1.
PROSITE; PS50037; MYB 1; UNKXOWN 1.
Immunoglobulin domain; Leucine-rich repeat.
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                                                                                                                                                                                                                                                                                                                                   the early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
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Best Local Similarity 35.0.
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
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RESULT 2

US-09-205-448-1

i Sequence 1, Application US/09205448

patent No. 6537746

i GENERAL INVORMATION:

APPLICANT: Arnold, Frances

APPLICANT: Arnold, Frances

APPLICANT: California Institute of Technology

TITLE OF INVENTION: Method for Creating Polynucleotide and Polypeptide

TITLE OF INVENTION: Sequences

FILE REPRENCE: 01809-025710PC

CURRENT APPLICATION NUMBER: US/09/205,448

CURRENT PILING DATE: 1998-12-04

PRIOR PILING DATE: 1998-12-04

NUMBER OF SEQ ID NOS: 11

SOFTHARE: Patentin Ver. 2.0

SEQ ID NO 1

LENGTH: 410
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45.4%; Score 44; DB 2;
Best Local Similarity 45.0%; Pred. No. 9.6;
Matches 9; Conservative 3; Mismatches
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LENGTH: 295
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                                                                                                                                            January 25, 2006, 18:50:05; Search time 16.6 Seconds (without alignments) 99.609 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/H_CTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                     GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-09-212-448-1

US-09-270-767-42554

US-09-252-991A-32447

US-09-583-110-5295

US-09-107-433-4762

US-09-107-433-4762

US-09-134-001C-3479

US-09-134-001C-3479

US-09-562-777-45

US-09-562-777-45

US-09-562-777-65

US-09-548-0139

US-09-348-0139

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US-09-252-991A-19366

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US-09-583-110-4263
US-09-107-433-2948
US-09-171-878-1
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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No.
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Gaps

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Length 295; Indels

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US-09-134-000C-6619

US-05-134-000C-6619

SEQUENCE 6619, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE REFERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1997-08-15
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR PLING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812

SOFTWARE: PatentIn version 3.1
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32899, A
61632, A
11, Appli
46079, A
41998, A
44, Appl
2579, A
                                               Sequence 1
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US-09-270-767-41750

US-09-712-363-214

US-09-62-737-43

US-09-489-039A-12533

US-09-252-91A-32899

US-09-270-767-61632

US-08-270-767-61632

US-09-270-767-46079

US-09-270-767-46079

US-09-270-767-41998

US-09-270-767-41998

US-09-270-767-41998

US-09-270-767-41998

US-09-252-991A-25793

US-09-252-991A-26940

US-08-885-291-51

US-09-496-652-11

US-09-496-672-51
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US-09-252-991A-32447
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LENGTH: 192
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Patent No. 6703491
GENERAL INFORMATION:
APPLICANT Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
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llarity 56.2%; Pred. No. 19;
Conservative 4; Mismatches
                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                             FEATURE:
OTHER INFORMATION: Xaa means any amino acid
                                                                                                                                                                   Query Match 45.4%; Score 44; DB Best Local Similarity 40.0%; Pred. No. 14; Matches 12; Conservative 3; Mismatches
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                                         ; OTHER INFORMATION: flagellin A (FlaA) US-09-205-448-1
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Patent No. 6852836
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Matches 7; Conservative
ORGANISM: Rhizobium lupini
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 9; Conserv
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US-09-270-767-42554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-270-767-42554
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LENGTH: 371
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NS-09-252-991A-32447

Sequence 32447, Application US/09252991A

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

SEQ ID NO 3447

LENGTH: 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INCORMATION:
APPLICANT: Lynn Doucette-Stamm et al.
APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Nucleic Acid and Therapeutics
FILE REFERENCE: PATION OND
FILE REFERENCE: PATION OND
FILE REFERENCE: 100 Number: 109/583,110
CURRENT FILING DATE: 1098-06-30
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1997-00-02
NUMBER OF SEC ID NOS: 5322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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llarity 56.2%; Pred. No. 13;
Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
43.8%; Score 42.5; D
Best Local Similarity 45.0%; Pred. No. 50;
Matches 9; Conservative 5; Mismatches
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; Sequence 4762, Application US/09107433
; Patent No. 6800744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 5295, Application US/09583110; Patent No. 6699703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |:|: | | |:||
147 HRLVEVAGDQQQAVQARQAG 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Pseudomonas aeruginosa
                                  |||::||:||:
134 KLISLEGQLCAICTQQ 149
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3 KLITIQGQVSALQTQQ 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 iniigoapgiktoras
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Matches 9; Conserv
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Gaps
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Patent No. 6753314

GENERAL INFORMATION:
APPLICANT: Giot, Loic
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same:
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same:
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same:
TITLE OF INVENTION: 1996-542
CURRENT APPLICATION NUMBER: 08/09538,092
CURRENT PILING DATE: 1999-04-01
PRIOR FILING DATE: 1999-04-01
PRIOR FILING DATE: 2000-02-01
PRIOR FILING DATE: 2000-02-01
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Pred. No. 24;
6; Mismatches 2; Indels
                                                           COMPUTER KEALAMALE FURNIT
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,306A
PILING DATE: 02-0ct-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 95/20080.4
PILING DATE: 02-0ct-1995
PRIOR APPLICATION NUMBER: US 60/009,832
PILING DATE: 01-Jan-1996
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REGISTRATION NUMBER: 34,380
REGISTRATION NUMBER: 34,380
REGISTRATION NUMBER: 34,380
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; OTHER INFORMATION: Polypeptide Accession Number P12036
US-09-538-092-911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version 0.9
SEQ ID NO 911
LENGTH: 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 345-9100
TELEPAX: (617) 345-9110
INFORMATION FOR SEQ ID NO: 168:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 46.7%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 TIQGQVSALQTQQAG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 317 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: peptide US-08-726-306A-168
                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown
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US-09-538-092-911
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GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPBUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Fatent No. 5958684
GENERAL INFORMATION:
APPLICANT: Van Leeuwen, Frederik Willem
APPLICANT: Burbach, Johannes Peter Henri
APPLICANT: Graveld, Franklin G.
ITTLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS
NUMBER OF SEQUENCES: 189
CORRESPONDENCE ADDRESS:
ADDRESSEB: Banner & Witcoff, Ltd.
STREET: 1 Financial Center
CITY: Boston
STATE: MA
COUNTRY: US
                                                                                                                                   NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                            ZIP: 02354

COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROW ISO9660
COMPUTER: <UNKnown>
OPERATING SYSTEM: <UNKnown>
SOFTWARE: <UNKnown>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/ 085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Denek
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...192
SEQUENCE DESCRIPTION: SEQ ID NO: 4762:
                                                                                                                                                                                                             STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4762:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 ITIQGOVSALQTQQAG 20
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                                       CITY: Waltham
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US-08-726-306A-168
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US-09-902-540-13091

; Sequence 13091, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENION: Myxococcus xanthus Genome Sequences and Uses Thereof; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR PRILICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
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APPLICANT: Holadar, A. Scott
TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
FILE REFERENCE: 201304/1000
CURRENT APPLICATION NUMBER: US/09/394,272
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATCHIIN Ver. 2.0
SEQ ID NO 14
LENGTH: 720
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                                                                                                                                                                                                                                                                                                                                                                                    Length 430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Indels
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Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                    Score 40; DB 2;
Pred. No. 79;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
      CURRENT APPLICATION NUMBER: US/09/489,039A CURRENT FILING DATE: 2000-01-27 PRIOR APPLICATION NUMBER: US 60/117,747 PRIOR FILING DATE: 1999-01-29 NUMBER OF SEQ ID NOS: 14342 SEQ ID NO 7776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; sequence 14, Application US/09394272; Patent No. 6472588; GENERAL INFORMATION:
                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 LITIOGOVSALOTOOAG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 47.1%;
Matches 8; Conservative
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401 KHEFVTLEGMEKAVQ 415
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 40.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Myxococcus xanthus US-09-902-540-13091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KHKLITIQGQVSALQ 15
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; ORGANISM: Synechocystis sp.
US-09-394-272-14
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                                                                                                                                                                                                                              LENGTH: 430
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APPLICANT: Lyan Doucette-Stamm et al
APPLICANT: Lyan Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-08-14
PRIOR FILING DATE: 1997-10-8
PRIOR FI
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Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Pred. No. 33;
2; Mismatches 3; Indels
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APPLICANT: Gotthardt, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
TITLE OF INVENTION: LDL Receptor Signaling Pathways
TITLE OF INVENTION: LDL Receptor Signaling Pathways
TITLE OF INVENTION: DDL Receptor Signaling Pathways
CURRENT PILICATION NUMBER: US/09/562,737
CURRENT PILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 45
LENGTH: 1024
TYPE: PRT
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                                                                                                                                                            Sequence 3479, Application US/09134001C
Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3479
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Patent No. 6428967
GENERAL INFORMATION:
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Best Local Similarity 64.3%;
Matches 9; Conservative
124 SLEGEAAALRQQQAG 138
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269 TIKGQVSTVATGQA 282
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US-09-134-001C-3479
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RESULT 15
US-09-543-681A-6130

JS-09-543-681A-6130

Sequence 6130, Application US/09543681A

PATENT OF THE GOOD OF THE APPLICATION INCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: DATE: 1099-04-05

PRIOR PILIOR DATE: 1099-04-09

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 6130

LENGTH: 1267

TYPE: PRT

ORGANISM: Proteus mirabilis

US-09-543-681A-6130
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41.2%; Score 40; DB 2; Length 1267;
Best Local Similarity 53.3%; Pred. No. 2.9e+02;
Matches 8; Conservative 4; Mismatches 3; Indels
Best Local Similarity 56.2%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 7; Indels
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Job time : 17.6 secs
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       1867569 seqs, 417829326 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                         1 KHKLITIQGQVSALQTQQAG 20
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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97
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Ħ	2, Appli	2, Appli	9, Appli	9, Appli	29, Appl	30, Appl	33, Appl		30, Appl	33, Appl	31, Appl	32, Appl	31, Appl	32, Appl	8, Appli	8, Appli	338496,	9638, Ap	6, Appli	75385, A	1, Appli	31, Appl	1, Appli	31, Appl	66950, A	314, App	43 Appl
Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Semience
Q.	US-10-383-930-2	US-10-797-821-2	US-10-383-930-9	US-10-797-821-9	US-10-383-930-29	US-10-383-930-30	US-10-383-930-33	US-10-797-821-29	US-10-797-821-30	US-10-797-821-33	US-10-383-930-31	US-10-383-930-32	US-10-797-821-31	US-10-797-821-32	US-10-383-930-8	US-10-797-821-8	US-10-425-115-338496	US-10-156-761-9638	US-10-171-404A-6	US-10-282-122A-75385	US-09-205-448-1	US-10-125-692-31	US-10-371-168-1	US-10-991-347-31	US-10-282-122A-66950	US-10-238-075-314	US-10-004-378A-43
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42, Appl 261, App 261, App 27, Appl 24, Appl 261, Appl 209227, 309227, 313,69, Appl 426, Appl 42	
Sequence Seq	
US-10-004-378A-42 US-10-291-172-261 US-10-211-278-261 US-10-212-278-261 US-10-004-378A-41 US-10-004-378A-41 US-10-004-378A-41 US-10-0425-114-55846 US-10-425-115-309227 US-10-369-491-3369 US-10-369-491-3369 US-10-369-491-369 US-10-369-491-369 US-10-369-491-369 US-10-369-491-369 US-10-472-923-426 US-10-425-114-48565 US-10-425-114-48565 US-10-425-114-48565 US-10-425-114-48565 US-10-425-114-48565 US-10-425-114-48565 US-10-425-114-48565 US-10-473-127-424	
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                                                                                                                                                                                                                                                                                                 1 KHKLITIQGQVSALQTQQAG 20
                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/10797821; Publication No. US20050031633A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                      1 KHKLITIQGQVSALQTQQAG 20
                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-10-383-930-2
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US-10-383-930-2
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APPLICANT: Smith, Daniel J.
APPLICANT: Taubman, Martin A.
APPLICANT: Taubman, Martin A.
TITLE OF INVENTIONS (Glucan Binding Protein and Glycosyltransferase Immunogens FILE REFERENCE: 25669-020
CURRENT APPLICATION NUMBER: US/10/797,821
CURRENT FILING DATE: 2004-03-09
PRIOR FILING DATE: 2003-03-07
PRIOR FILING DATE: 2002-03-07
PRIOR FILING DATE: 2002-03-07
PRIOR FILING DATE: 2002-08-08
PRIOR FILING DATE: 2002-08-08
PRIOR FILING DATE: 2002-08-08
PRIOR FILING DATE: 2002-08-08

Gaps

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RESULT 6
US-10-383-930-30
i Sequence 30, Application US/10383930
j Sequence 30, Application US/10383930
j Publication No. US20040127400A1
j GENERAL INFORMATION:
j APPLICANT: Smith, Daniel J
j TILE OP INFORMION: Immunogenicity of Glucan Binding Protein
j TILE OP INFORTION: Immunogenicity of Glucan Binding Protein
j TILE OP INFORTION: 25669-018
j CURRENT PRILING DATE: 2003-03-07
j PRIOR APPLICATION NUMBER: 60/402,483
j PRIOR APPLICATION NUMBER: 60/402,483
j PRIOR PILING DATE: 2002-08-08
j PRIOR FILING DATE: 2002-03-07
j RIUGE OF TELEMENT STATE: 2002-03-07
j RIUGE OF TELEMENT STATE: 2002-03-07
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US-10-383-30-29

US-10-383-30-29

Sequence 29, Application US/10383930

Publication No. US20040127400A1

GENERAL INFORMATION:

APPLICANT: Smith, Daniel J

TILLE OF INVENTION: Immunogenicity of Glucan Binding Protein

FILE REPERBACE: 25669-018

CURRENT FILING DATE: 2003-03-07

PRIOR PULICATION NUMBER: 60/402,483

PRIOR PPLICATION NUMBER: 60/402,483

PRIOR PPLICATION NUMBER: 60/363,209

PRIOR PLING DATE: 2002-08-08

PRIOR PLING DATE: 2002-03-07

NUMBER OF SEQ ID NOS: 41

SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 67.0%; Score 65; DB 4; Length 431; Best Local Similarity 100.0%; Pred. No. 0.029; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     67.0%; Score 65; DB 5; Length 20; 100.0%; Pred. No. 0.00091; tive 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: 09/290,049
PRIOR PILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: 66/081,550
PRIOR PILING DATE: 1998-04-13
PRIOR PILING DATE: 1999-01-08
PRIOR PILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.2
SEQ ID NO 9
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: GbpB peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORGANISM: Streptococcus mutans US-10-383-930-29
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Best Local Similarity
                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 29
LENGTH: 431
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Publication No. US20050031633A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION OF Glucan Binding Protein and Glycosyltransferase Immunogens

TITLE OF INVENTION Glucan Binding Protein and Glycosyltransferase Immunogens

TITLE OF INVENTION NUMBER: US/10/797,821

CURRENT PILING DATE: 2004-03-09

PRIOR APPLICATION NUMBER: 60/363,209

PRIOR PILING DATE: 2003-03-07

PRIOR PILING DATE: 2002-03-07

PRIOR FILING DATE: 2002-03-07

PRIOR FILING DATE: 2002-03-07

PRIOR FILING DATE: 2002-08-08
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; Publication No. US20040127400A1
; Publication No. US20040127400A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Daniel J
; APPLICANT: Taubman, Martin A
; TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
; FILE REPERENCE: 25669-018
; CURRENT APPLICATION NUMBER: 60/402,483
; PRIOR FILING DATE: 2002-03-07
; PRIOR FILING DATE: 2002-08-08
; PRIOR PLICATION NUMBER: 60/402,483
; PRIOR FILING DATE: 2002-03-07
; PRIOR PLICATION NUMBER: 60/363,209
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 9
; LINGTH: 20
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Best Local Similarity 100.0%; Pred. No. 0.00091;
Matches 14; Conservative 0; Mismatches 0;
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100.0%; Score 97; DE
Best Local Similarity 100.0%; Pred. No. 3.6
Matches 20; Conservative 0; Mismatches
     PRIOR FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: 60/081,550
PRIOR PILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR PILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.2
SEQ ID NO 2
LENGTH: 20
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                                                                                                                                                                                                                                                                       ORGANISM: Artificial
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US-10-383-930-9
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Sequence 30, Application US/10797821

Sequence 30, Application US/10797821

Sequence 30, Application US/2050031633A1

SENERAL INFORMATION:

APPLICANT: Smith, Daniel J.

APPLICANT: Taubman, Martin A.

TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens

FILE REFERENCE: 2569-020

CURRENT FILING DATE: 2004-03-09

PRIOR APPLICATION NUMBER: US/10/797,821

CURRENT FILING DATE: 2003-03-07

PRIOR PLILNG DATE: 2003-03-07

PRIOR FILING DATE: 2002-03-07

PRIOR APPLICATION NUMBER: 60/402,483

PRIOR PLING DATE: 1099-04-12

PRIOR FILING DATE: 1999-04-12

PRIOR FILING DATE: 1999-04-13

PRIOR FILING DATE: 1999-04-13

PRIOR FILING DATE: 1999-04-13

PRIOR FILING DATE: 1999-04-13

PRIOR PLING DATE: 1999-04-13

PRIOR FILING DATE: 1999-04-13
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APPLICANT: Taubman, Martin A.
APPLICANT: Taubman, Martin A.
TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens FILE REPERENCE: 25669-020
CURRENT APPLICATION NUMBER: US/10/797,821
CURRENT FILING DATE: 2004-03-09
PRIOR APPLICATION NUMBER: 60/363,209
PRIOR APPLICATION NUMBER: 60/402,483
PRIOR PILING DATE: 2002-08-08
PRIOR APPLICATION NUMBER: 09/402,483
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                                                                                                                                                                                                                                                     Length 431;
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                                                                                      ; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-10-797-821-29
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US-10-797-821-30
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    SEQ ID NO 29
LENGTH: 43
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| Sequence 29, Application US/10797821
| Sequence 29, Application No. US20050031633A1
| GENERAL INFORMATION:
| APPLICANT: Smith, Daniel J. |
| APPLICANT: Taubman, Martin A. |
| TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens FILE REFERENCE: 25669-200 |
| FILE REPERENCE: 25669-200 |
| FRIOR PILING DATE: 2004-03-09 |
| PRIOR PILING DATE: 2003-03-07 |
| PRIOR FILING DATE: 2002-08-08 |
| PRIOR FILING DATE: 2002-08-08 |
| PRIOR FILING DATE: 1999-04-12 |
| PRIOR FILING DATE: 1999-04-12 |
| PRIOR FILING DATE: 1999-04-12 |
| PRIOR FILING DATE: 1999-04-13 |
| PRIOR FILING DATE: 1999-04-10 |
| PRIOR FILING DATE: 1999-04
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### Sequence 33, Application US/10383930

### Publication No. 220040127400A1

### Sequence 33, Application US/10383930

### Sequence 33, Application No. 220040127400A1

### PELICANT: Smith, Daniel J

### PELICANT: Taubman, Martin A

### TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein

### PILE REFERENCE: 25669-018

### CURRENT FILING DATE: 2003-07

### PRIOR APPLICATION NUMBER: 60/402,483

### PRIOR APPLICATION NUMBER: 60/363,209

### PRIOR APPLICATION NUMBER: 60/363,209

### PRIOR PILING DATE: 2002-03-07

### NUMBER OF SEQ ID NOS: 41

### SEQ ID NO 33

### LENGTH ### 131
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                                                                                                                                                           GORGANISM: Streptococcus mutans US-10-383-930-30
SOFTWARE: Patentin version 3.2
SEQ ID NO 30
LENGTH: 431
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; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-10-383-930-32
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US-10-797-821-32
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; Sequence 32, Application US/10383930
; Publication No. US20040127400A1
; GENERAL INRORMATION:
; APPLICANT: Smith, Daniel J
; APPLICANT: Taubman, Martin A
; TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
; FILE REFERENCE: 256-9-0.18
; CURRENT APPLICATION NUMBER: US/10/383,930
; CURRENT APPLICATION NUMBER: 60/402,483
; PRIOR APPLICATION NUMBER: 60/402,483
; PRIOR FILING DATE: 2002-08-08
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
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US-10-383-930-31
Sequence 31, Application US/10383930
Sequence 31, Application US/10383930
Sequence 31, Deplication US/10383930
Sequence 31, Deplication US/10383930
Sequence 31, Deplication US-103041
Sequence 32, Deplication US-1030404
Sequence 31, Deplication US-10304
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PRIOR FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: 60/081,550
PRIOR PILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PATENTIN VEFSION 3.2
SEQ ID NO 33
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SOFTWARE: Patentin version 3.2
SEQ ID NO 31
LENGTH: 432
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US-10-383-930-32
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Sequence 32, Application US/10797821
; Bublication No. US20050031633A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Daniel J.
; APPLICANT: Taubman, Martin A.
; TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens;
; TITLE OF INVENTION NUMBER: US/10/797,821
; CURRENT APPLICATION NUMBER: US/10/797,821
; CURRENT APPLICATION NUMBER: 10/383,930
; PRIOR APPLICATION NUMBER: 60/403-09
; PRIOR APPLICATION NUMBER: 60/402,483
; PRIOR FILING DATE: 2002-08-08
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: 60/401,550
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 Length 432;
Query Match 67.0%; Score 65; DB 4; Length 432 Best Local Similarity 100.0%; Pred. No. 0.029; Matches 14; Conservative 0; Mismatches 0; Indels
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                                                                   6 TIQGOVSALQTOOA 19
                                                                                                    57 TIOGOVSALOTOGA 70
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Best Local Similarity 100.0
Matches 14; Conservative
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Sequence 8, Application US/10383930;
Publication No. US20040127400A1
GENERAL INFORMATION:
APPLICANT: Smith, Daniel J
APPLICANT: Taubman, Martin A
TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
FILE REFERENCE: 25669-018
CURRENT APPLICATION NUMBER: US/10/383,930
CURRENT FILING DATE: 2003-03-07
FRIOR PILING DATE: 2002-08-08
PRIOR PILING DATE: 2002-08-08
PRIOR PILING DATE: 2002-03-07
PRIOR FILING DATE: 2002-03-07
SOFTWARE: Patentin version 3.2
SEQ ID NO 8
LENGTH: 20
TENGTH: 20
                                                                                                                                                                                                                                     Query Match 67.0%; Score 65; DB 5; Length 432; Best Local Similarity 100.0%; Pred. No. 0.029; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 52.6%; Score 51; DB 4; Length 20; Best Local Similarity 100.0%; Pred. No. 0.21; Matches 11; Conservative 0; Mismatches 0; Indels
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.2
LENGTH: 432
                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-10-797-821-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT; ORGANISM: Streptococcus mutans US-10-383-930-8
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US-10-383-930-8
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Db 10 TİĞĞQVSÄLĞT 20 Search completed: January 25, 2006, 20:10:01 Job time : 61 secs

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RESULT 2
US-11-052-554A-252
US-11-052-554A-252
US-11-052-554A-252
Sequence 252, Application US/11052554A
Publication No. US20050288866A1
GENERAL INFORMATION:
APPLICANTON: Sachdeva, et al.
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIFYING ADHESIN ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US 60/589,227
PRIOR PLIING DATE: 2004-07-20
PRIOR PLIING DATE: 2004-07-20
PRIOR PLIING DATE: 2004-07-20
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
NUMBER OF SEQ ID NOS: 763
US-11-052-554A-210
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Query Match
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Sequence 252, App
Sequence 232, App
Sequence 294, App
Sequence 294, Appli
Sequence 341, Appli
Sequence 318, App
Sequence 318, App
Sequence 318, App
Sequence 1009, App
Sequence 1009, App
Sequence 1282, App
Sequence 1282, App
Sequence 1282, App
Sequence 1282, App
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Sequence 104, App
Sequence 105, App
Sequence 5304, App
Sequence 344, App
Sequence 1116, App
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2, Appli
5, Appli
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                                                                   January 25, 2006, 19:15:26; Search time 5.5 Seconds (without alignments) 39.378 Million cell updates/sec
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Sequence
Sequence
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1: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
        GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-11-052-554A-252

US-11-052-554A-232

US-10-467-657-5510

US-11-194-246-294

US-11-091-668-4

US-110-467-652-3418

US-10-467-652-3418

US-10-714-887-338

US-10-714-887-338

US-10-467-657-7612

US-10-95-561-1010

US-10-95-561-1010

US-11-074-176-36

US-11-074-176-36

US-11-074-176-316

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US-11-194-246-344
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                                                                                                                                                                                         75621 seqs, 10829074 residues
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                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                 OM protein - protein search, using sw model
                                                                                                                                   1 KHKLITIQGQVSALQTQQAG 20
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
                                                                                                            US-10-797-821-2
97
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Sequence 210, Application US/11052554A

Publication No. US2005028866A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
TITLE OF INVENTION WINBER: US 11/052,554A
CURRENT FILING DATE: 2005-02-07
FRIOR PILING DATE: 2006-02-07
FRIOR PILING DATE: 2004-02-06
FRIOR PILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NOS: 763
SEQ ID NOS: 763
SEQ ID NOS: 763
SEQ ID NOS: 763
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 1, Appli
1, Appli
1, Appli
12, Appli
12, Appl
13, Appl
13, Appl
13, Appl
13, Appl
1228, Ap
1238, Ap
1238, Ap
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Sequence 12, Appl
Sequence 464, App
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 Sequence 1, Sequence 1, Sequence 2 Sequence 2 Sequence 2 Sequence 6 Sequence 6 Sequence 6 Sequence 7 Sequence 7 Sequence 7 Sequence 7 Sequence 9
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Sequence 1
Sequence 6
Sequence 4
Sequence 2
Sequence 2
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100.0%; Pred. No. 0.00048;
tive 0; Mismatches 0; Indels
US-10-875-800-1
US-10-299-977-1
US-10-299-977-1
US-10-875-800-2
US-11-045-590-12
US-11-045-557-6198
US-11-045-657-6198
US-11-055-822-528
US-10-821-234-957
US-10-733-626-2288
US-10-733-626-2288
US-10-733-626-2288
US-10-733-626-2288
US-10-733-626-2288
US-11-000-463-454
US-11-000-463-464
US-11-000-463-464
                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Streptococcus mutans UA159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 TIQGOVSALQTQQA 70
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Matches 14; Conservative
 108
1344
1334
1334
161
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161
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172
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DEBLICANT: Trepod, Catherine
APPLICANT: Trepod, Catherine
TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MET
TITLE OF INVENTION: USE
TITLE OF INVENTION: USE
CURRENT APPLICATION NUMBER: US/11/194,246
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: US/10/274,586
PRIOR APPLICATION NUMBER: US 60/345,438
PRIOR FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 621
SOFTWARE: Patentin version 3.0
SEQ ID NO 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/11091668

Publication No. US20050262585A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: University of Nebraska
APPLICANT: Wackersity of Nebraska
APPLICANT: Wackersity of Nebraska
APPLICANT: Wackersity of Nebraska
APPLICANT: Wackersity of Nebraska
APPLICANT: Vaghchhipawala, Zarir Erach
TITLE OF INVENTION: Soybean FGAM Synthase Promoters Useful In Parasite Control
FILE REFERENCE: 1231-221
CURRENT APPLICATION NUMBER: US/11/091,668
CURRENT PILING DATE: 2005-03-28
PRIOR FILING DATE: 2004-03-26
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OTHER INFORMATION: The 'Xaa' at location 806 stands for Gly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION; (812)...(812)
; OTHER INFORMATION: The 'Xaa' at location 812 stands for Val.
US-11-091-668-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 38; DB 7; Length 318;
Pred. No. 20; 6; Indels
5; Mismatches 6; Indels
                       Indels
Best Local Similarity 47.1%; Pred. No. 71;
Matches 8; Conservative 3; Mismatches
                                                                                                                                                                                                                                                   ; Sequence 294, Application US/11194246; Publication No. US20050272089A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: HAEMOPHILUS INFLUENZAE
US-11-194-246-294
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349 HKPIMIAGGLGSIQAQQ 365
                                                                            2 HKLITIQGQVSALQTQQ 18
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 4
LENGTH: 1313
TYPE: PRT
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Best Local Similarity 38.9%;
Matches 7; Conservative
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LOCATION: (806)..(806)
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US-11-194-246-294
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US-11-052-554A-232
US-11-052-554A-232
Squarec 232, Application US/11052554A
Publication No. US2005028866A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TILLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TILLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
TILLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
TILLE OF INVENTION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR FILING DATE: 2004-02-06
PRIOR FILING DATE: 2004-02-06
PRIOR FILING DATE: 2004-02-06
PRIOR FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
SOFTWARE: PALENTIN VERSION 3.3
SEQ ID NO 232
LENGTH: 690
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                                                                                                                                                                              Score 40; DB 7; Length 398;
Pred. No. 12;
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Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIKON Sph
APPLICANT: FONTANA Maria Rita
APPLICANT: MASIGNAIN Vega
                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                     3;
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CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION UNMER: GB-0103424.8
FRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SOFTWARE: SeqWin99, version 1.04
LENGTH: 1259
                                                                                                                                                                                                                                     8; Mismatches
                                                                               TYPE: PRT
ORGANISM: Streptococcus pyogenes MGAS8232
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                                                                                                                                                                                                                                                                                        1 KHKLITIQGQVSALQTQQ 18
                                                                                                                                                                                                                                                                                                                                       49 QNOVSALOAOVSSLOSEO 66
                                                                                                                                                                                   41.2%;
     SOFTWARE: Patentin version 3.3
SEQ ID NO 252
LENGTH: 398
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60 KYKVLTVEGNIGTVQ 74
                                                                                                                                                                                   Query Match
Best Local Similarity 38.9
Matches 7; Conservative
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APPLICANT: HEARD, Jacqueline
APPLICANT: RIECHMANN, Jose Luis
APPLICANT: REELMANN, Jose Luis
APPLICANT: CREELMANN, Robert
APPLICANT: CREELMANN, Robert
APPLICANT: CANALES, Roger
APPLICANT: REPETTI, Peter
APPLICANT: RUBERTI, Peter
APPLICANT: RUBER, T. Lynne
APPLICANT: RUBER, T. Lynne
APPLICANT: SHERMAN, Bradley K
TITLE OF INTERN, DANAT TRANSCRIPTIONAL REGULATORS OF DROUGHT STRESS
FILE REFERENCE: MB10058-CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 430 SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THER INFORMATION: G3397 polypeptide Orthologous to G481 and G482
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Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNAI Vega
APPLICANT: MASIGNAI Vega
APPLICANT: MASIGNAI Vega
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Oryza sativa (japonica cultivar-group)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB 6;
Pred. No. 28;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/714,887
CURRENT FILING DATE: 2003-11-13
PRIOR APPLICATION NUMBER: 10/412,699
PRIOR FILING DATE: 2003-04-10
PRIOR PLILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: 09/506,720
PRIOR PLILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 09/394,519
PRIOR PLILING DATE: 1999-09-13
PRIOR PLILING DATE: 1999-09-13
PRIOR PLLING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/533,029
PRIOR APPLICATION NUMBER: 09/533,029
PRIOR APPLICATION NUMBER: 09/533,039
PRIOR PLLING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/533,030
PRIOR PLLING DATE: 2000-03-22
PRIOR PLLING DATE: 2000-03-22
PRIOR PLLING DATE: 2000-03-22
PRIOR PLLING DATE: 2000-03-22
PRIOR PLLING DATE: 2000-03-22
PRIOR PLLING DATE: 2000-03-22
PRIOR PLLING DATE: 2000-03-22
PRIOR PLLING DATE: 2000-11-16
                                                                                                                             APPLICANT: Mendel Biotechnology, Inc.
                                                    Sequence 338, Application US/10714887
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109 HKFREIEGERAASTTGAG 127
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Best Local Similarity 42.1%;
Matches 8; Conservative
                                                                                 US20060015972A1
                                                                         Publication No. US20
GENERAL INFORMATION:
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US-10-467-657-7612
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; Publication No. US20050246784A1
; GENERAL INFORMATION:
APPLICANT: Plesch, Gunnar
; APPLICANT: Blau, Astrid
; APPLICANT: Blau, Astrid
; APPLICANT: Mein, Mathieu
; TITLE OF INVENTION: Identification of Herbicidally Active Substances
; TILB REPRENCE: 2000 8857; CURRENT APPLICATION UNDERS: US/10/467,962B
; CURRENT APPLICATION NUMBER: PCT/EP02/01466
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 109
; SEQ ID NO 5: 109
; SEQ ID NO 5: 10466
; LENGTH: 804
                               Gaps
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                            Indels
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Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: FONTANA Maria Rita
APPLICANT: FONTANA Maria Rita
APPLICANT: PAZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
Best Local Similarity 38.9%; Pred. No. 1.1e+02; Matches 7; Conservative 4; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 38.1%; Score 37; DB Similarity 42.1%; Pred. No. 22; 8; Conservative 5; Mismatches
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CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
FRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, Version 1.04
SERGIH: 244
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                                                                                                        11 KEAQVKISGQIVBIQTEQ 28
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; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3418
                                                                         1 KHKLITIQGQVSALQTQQ 18
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Best Local Similarity
Matches 8; Conserv
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FILE REFERENCE:

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DB 6; Length 1141;

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Sequence 1010, Application US/10995561

Publication No. US20050272054A1

GENERAL INFORMATION:

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GENERAL INFORMATION:

TITLE OF INVENTION:

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Sequence 1282, Application US/10467657

Publication No. USCO05026051A1

GENERAL INFORMATION:

APPLICANT: FURINON SPA

APPLICANT: FOUTANM MATIA Rita

APPLICANT: FOUTANM MATIA RITA

APPLICANT: PIZZA MATIAGRAZIA

APPLICANT: MASIGNANI VOGGA

TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

FILE REFREENCE: 2003-08-11

CURRENT APPLICATION NUMBER: US/10/467,657

CURRENT FILING DATE: 2001-02-12

NUMBER OF SEQ ID NOS: 9218

SOFTWARE: SeqWin99, version 1.04

SEQ ID NO 1282

LENGTH: 177
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                    Score 36; DB 6; Pred. No. 2.1e+02;
                                                                                    3; Mismatches
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                    37.1%;
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197 VTIQQQVQTVQAQR 210
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Best Local Similarity 50.0
Matches 7; Conservative
                    Query Match
Best Local Similarity 50.0
Matches 7; Conservative
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Matches 6; Conservative
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Publication No. US2005027205431
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                           Length 680;
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Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SpA
APPLICANT: FONTANA MARIA Rita
APPLICANT: PASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REPRENCE:
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CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, Version 1.04
SEQ ID NO 9370
LENGTH: 716
CURRENT APPLICATION NUMBER: US/10/467,657
                CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: Seqwin99, version 1.04
SEQ ID NO 7612
LENGTH: 680
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                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7612
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628 LDTLRGELGTLRTRSSG 644
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Best Local Similarity 35.3%;
Matches 6; Conservative
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US-10-995-561-1009
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LENGTH: 1141
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AAB922486
ABB9285
ABB9589
AAG17150
AAG17149
AAG17148
AAG17148
AD114148
AD166732
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(without alignments)
128.850 Million cell updates/sec
                                        January 25, 2006, 18:48:24 ; Search time 68.2 Seconds
     GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd
                                                                                                          2443163 seqs, 439378781 residues
                            OM protein - protein search, using sw model
                                                                            TATEAQPSASSASTAAVAAN 20
                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                               US-10-797-821-3
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ALIGNMENTS

ADG74975

2443163

of hits satisfying chosen parameters:

Total number

Searched:

Title: Perfect score:

Run on:

Sequence:

Scoring table:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Geneseq 21:*

Database :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

	KW Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen. XX		ADD93623;	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

genesequ1980s:* genesequ200s:* genesequ2001s:* genesequ2001s:* genesequ2003s:* genesequ2003as:* genesequ2003as:* genesequ2003s:*

SUMMARIES

Query Match Length DB

Score

Result ě The present sequence is that of SAS peptide comprising amino acid residues 306-325 of the glucan binding protein-B (GbpB) of Streptococcus mutans strain SK22 ADD93649. The peptide binds to a major histocompatibility complex (MHC) class II protein. It was identified as a prediction, which was used to search the primary amino acid sequence of GbpB for known MHC class II binding motifs. The peptide can be used inmunogenic compositions and subunit vaccines for dental caries. These comprise MHC class II protein-binding GbpB peptides covalently linked with peptide subunits (preferably from the catalytic domain) of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Diepitopic or

ABB67831 ABU17126 ADX91331 ADX91493 ADY23867

291 371 189 231 132 151 151

AAG13790

Claim 12; Page 10; 49pp; English.

Add33623 Streptoco Add33649 Streptoco Add33649 Streptoco Add37273 Streptoco Add37273 Streptoco Add33651 Streptoco Add33651 Streptoco Add3652 Streptoco Add3652 Streptoco Add3653 Streptoco Add37275 Streptoco Add37276 Streptoco Add3726 Streptoco Add3726 Streptoco Add3726 Streptoco Add3726 Streptoco Add37261 Streptoco Adx37261 Streptoco Adx3731 Drant ful Ady23867 Plant ful Ady3781 Arabidops Aag13791 Arabidops

ADD93623 ADX37246 ADD93650 ADD93650 ADX37272 ADX937273 ADD93651 ADD93652 ADD93653 ADX37274 ADX37274 ADX37274 ADX37274 ADX97274 ADX37274 ADX97274 ADX37274

Matches

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RESULT 2 ADX37246

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Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
                                                                                                                              Streptococcus mutans glucan binding protein-B.
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403. .422
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383. .402
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/note= "HLA-binding peptide"
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note= "HLA-binding peptide"
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'note= "HLA-binding peptide"
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e= "HLA-binding peptide"
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'note= "HLA-binding peptide"
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:e= "HLA-binding peptide"
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:e= "HLA-binding peptide"
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                                                    ADD93649 standard; protein; 431 AA.
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08-AUG-2002; 2002US-0402483P.
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                                                                                                                                                                                    Streptococcus mutans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
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multiepitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in passive immunisation.
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                                                                                                                                                                                                                                                                                                                                  immunogenicity; immune stimulation; glucan binding protein-B;
microparticle; major histocompatibility complex; tooth disease.
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                                                                               Length 20;
                                                                                                                                                                                                                                                                                                            Streptococcus mutant glucan binding protein B peptide #3.
                                                                                                        0; Indels
                                                                              100.0%; Score 90; DB 7; I
100.0%; Pred. No. 2.1e-06;
                                                                                                         0; Mismatches
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08-JAN-1999; 99US-0115142P.
12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-0402483P.
07-MAR-2003; 2003US-0402483P.
                                                                                                                                                                                                                               ADX37246 standard; peptide; 20
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                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                            Streptococcus mutans.
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(TAUB/) TAUBMAN M A.
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                                                                                           Local Similarity
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                                                                                             The present sequence is the protein sequence of the glucan binding protein—B (GDBB) of Streptococcus mutans strain SR32. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions comprise major histocompatibility complex (WHC) class II protein-binding GDBB peptides, especially HLA-binding peptides, covalently linked with peptides ubunits of a glucosyltransferase. The antibods in a mammal- pieptide subunits of a glucosyltransferase. The antibods in a mammal- bieptopic or multiplitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GDpB can be used in
                        composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
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                                                                           Claim 6; Page 7; 49pp; English.
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Best Local Similarity 100.00
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Conservative
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2003-845091/78
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          GENBANK; AY046410
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caries. The compositions comprise major histocompatibility complex (MHC) class II protein-binding GDpB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an artibody in a mammal. Dispitopic or multiepitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GDpB can be used in
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microparticle; major histocompatibility complex; tooth disease.
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                                                                                                                                                                                                                                                                                                                                 Score 90; DB 7; Pred. No. 5.7e-05;
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Pred. No. 5.7e-05;
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Local Similarity 100.0%;
nes 20; Conservative 0;
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12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-0363209P.
08-AUG-2002; 2002US-0402483P.
07-MAR-2003; 2003US-00383930.
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(TAUB/) TAUBMAN M A.
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8 셤 ADX37273;

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The present invention relates to a computational method (MI) for identifying adhesin and adhesin-like proteins, by computing the sequence-identifying adhesin and adhesin-like proteins, by computing the sequence-compared to based attributes of protein sequences using five attribute modules of a certain network software, trainling an artificial neural network (ANN) for each of the computed five attributes, and identifying the adhesin and adhesin-like proteins, as set of 274 annotated genes encoding adhesin and adhesin-like proteins, having 274 fully defined 162 cencoding adhesin and adhesin-like proteins, having 274 fully defined 162 centering adhesin and adhesin-like proteins, having 274 fully defined 162 centering adhesin and adhesin-like proteins, having 279 fully defined 162 centering 165 fully defined 106-5291 base pair (SEQ ID NO: 1-279); a set of 105 hypothetical adhesin-like proteins, having 279 fully defined 53-3716 base pair (SEQ ID NO: 1-279); a set of 105 hypothetical adhesin-like proteins, having 105 fully defined 106-5291 base pair (SEQ ID NO: 280-384) sequences; and a fully connected multilayer feed forward ANN (I) based on (MI). (MI) is useful for identifying adhesin and adhesin-like proteins, of therapeutic potential, and identifying and short-listing proteins for further testing in development of new vaccine formulations concerns for further testing in development of new vaccine formulations concerns and adhesin-like for identifying and stating putative adhesins that are important in drug disconery and and and and adhesin-like for identifying attains that are important in drug disconery and and and and adhesin-like for identifying and are independent and adhesin-like for identifying and attains that are important in drug disconery and and adhesin-like for identifying that the proteins for wather thermandian and adhesin-like for identifying that the for wather the proteins for wather the proteins the proteins for the proteins for the proteins for the proteins for the proteins for the proteins for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                discovery and preventing therapeutics for whooping cough, pneumonia, gastric ulcer and urinary tract infections. (M1) identifies adhesins from fafteralty related organisms, and from bacteria belonging to a wide phylogenetic spectrum. (M1) is capable of predicting adhesive nature of unique proteins. The present sequence is a microbial pathogen adhesin
                                                                                                algorithm; adhesin; pharmaceutical; vaccine; drug screening; bordetella pertussis infection; antibacterial; pneumonia; antiinflammatory; respiratory-gen.; gastric ulcer; antiulcer; gastrointestinal-gen.; urinary tract infection; antimicrobial; uropathic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Computational method for identifying adhesin and adhesin like molecules, comprises computing sequence-based attributes of protein sequences using neural network software and training an artificial neural network.
                                              Microbial pathogen adhesin protein sequence, SEQ ID NO:210.
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100.0%; Pred. No. 5.7e-05;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (COUL ) COUNCIL SCI & IND RES SOUTH AFRICA.
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                                                                                                                                                                                                                                                                                                                                                                                                 07-FEB-2005; 2005WO-IN000037
                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-FEB-2004; 2004IN-DE000173
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20-OCT-2005 (first entry)
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                                                                                                                                                                                                                                         Streptococcus mutans
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les 20; Conser
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microparticle; major histocompatibility complex; tooth disease.
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           Mismatches
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                                                                                                   1 TATEAQPSASSASTAAVAAN 20
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Conservative 0;
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08-JAN-1999; 99US-0115142P.
12-ARR-1999; 99US-00290049.
07-WAR-2002; 2002US-0363209P.
08-MUG-2002; 2002US-0402483P.
07-WAR-2003; 2003US-00383930.
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                                                                                                                                                                                                                                                                                                                                                             (first entry)
             20; Conservative
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TAUBMAN M A.
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Best Local Similarity
Matches 20; Conser
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SMIT/) TAUB/)

Ramachandran S;

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Indels

ADD93651 ID ADD93651 Btandard; protein; 432 AA.

RESULT

AEB91500;

RESULT 7

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Length 431;

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The present sequence is the protein sequence of the glucan binding protein-B (GbpB) of Streptococcus mutans strain 3SN1. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions comprise major histocompatibility complex (MHC) class II protein-binding GbpB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an artibody in a mammal. Dispitopic or multiphtopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in
                                                                                                                                                                                                                                                                       Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
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microparticle; major histocompatibility complex; tooth disease.
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Pred. No. 0.00045;
0; Mismatches 1; Indels
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99US-0115142P.
99US-00290049.
2002US-0363209P.
2002US-0402483P.
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                                    07-MAR-2003; 2003WO-US006962
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                                                                                                                                  (FORS-) FORSYTH INST
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07-MAR-2002;
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07-MAR-2003;
  18-SEP-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is the protein sequence of the glucan binding protein. B (GbpB) of Streptococcus mutans strain 15JP2. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental? caries. The compositions comprise major histocompatibility complex (WHC) class II protein-binding GbpB peptides, especially HLA-binding peptides, covalently linked with peptides subminits of a glucosyltransferase. The antibody in a mammal. Dispitopic or multiplity production of an antibody an amamal. Dispitopic or multiplitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
                                                                                                                              Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
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                                                                                       Streptococcus mutans glucan binding protein-B.
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                                                     (first entry)
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                                                                                                                                                                     Streptococcus mutans
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GENBANK; AY046412.
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                ADD93651;
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                                                                                                                                           The invention relates to a composition comprising a fragment of a glucan binding protein-B (GbpB) and a biocompatible microparticle, where the fragment binds to a major histocompatibility complex (MrC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds to a Streptococcus mutans GbpB protein of the invention.
                                                              New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunogenicity, immune stimulation; glucan binding protein-B; microparticle; major histocompatibility complex; tooth disease
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                                                                                                                                                                                                                                            Length 432;
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0; Mismatches
                                                                                                                                                                                                                                             93.3%; Score 84;
95.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; SEQ ID NO 32; 73pp; English.
                                                                                                                        Claim 3; SEQ ID NO 31; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                      ADX37275 standard; protein; 432 AA.
                                                                                                                                                                                                                                                                                                       307 TATAAQPSASSASTAAVAAN 326
                                                                                                                                                                                                                                                                                         1 TATEAQPSASSASTAAVAAN 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              980S-0081550P.
990S-0115142P.
990S-0290049.
2002US-0363209P.
2003US-0402483P.
2003US-00383939.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-MAR-2004; 2004US-00797821
                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                        Local Similarity 95.0
nes 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smith DJ, Taubman MA;
                        Taubman MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus mutans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SMIT/) SMITH D J.
(TAUB/) TAUBMAN M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2005-151644/16.
   TAUBMAN M A.
                                            WPI; 2005-151644/16.
                                                                                                                                                                                                                          Sequence 432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2005031633-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-APR-1998;
08-JAN-1999;
12-APR-1999;
07-MAR-2002;
08-AUG-2002;
07-MAR-2003;
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                        Smith DJ,
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   (TAUB/)
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The invention relates to a composition comprising a fragment of a glucan binding protein-B (GbpB) and a biocompatible microparticle, where the fragment binds to a major histocompatibility complex (MrG) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds to a Streptococcus mutans GbpB protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
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                                                                                                                                                                                                                                                                                         Length 432;
                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                      93.3%; Score 84; DB 9; I
95.0%; Pred. No. 0.00045;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus mutans glucan binding protein-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADD93653 standard; protein; 431 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Page 8-9; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                    1 TATEAQPSASSASTAAVAAN 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-MAR-2002; 2002US-0363209F.
08-AUG-2002; 2002US-0402483P.
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Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                       19; Conservative
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The present sequence is that of a peptide comprising amino acid residues 311-330 of the glucan binding protein-B (GpBB) of Streptococcus mutans Strain SK32 ADD93649. The peptide binds to a major histocompatibility complex (MHC) class II protein. It was identified as a potential B cell epitope using a matrix-based algorithm for epitope prediction, which was used to search the primary amino acid sequence of GbpB for known MHC class II binding motifs. The peptide can be used in immunogenic compositions and subunit vaccines for dental caries. These comprise MHC class II protein-binding GbpB peptides covalently linked with peptide subunits (preferably from the catalytic domain) of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Diepitopic or multipation; polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                   Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
                                         Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
  Streptococcus mutans glucan binding protein-B peptide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunogenicity; immune stimulation; glucan binding protein-B;
microparticle; major histocompatibility complex; tooth disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus mutant glucan binding protein B peptide #18
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Pred. No. 0.0054;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                      07-MAR-2002; 2002US-0363209P.
                                                                                                                                                                                                 07-MAR-2003; 2003WO-US006962
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                                                                                Streptococcus mutans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing
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                                                                                                                                                                                                                                                                                              immunogenicity; immune stimulation; glucan binding protein-B;
microparticle; major histocompatibility complex; tooth disease.
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                                                                                                                                                                                                                                                         Streptococcus mutant glucan binding protein B variant #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; SEQ ID NO 33; 73pp; English.
                                                                                                                                 ADX37276 standard; protein; 431 AA.
                    TATEAQPSASSASTAVVTAN 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADD93638 standard; peptide; 20 AA.
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TATEAQPSASSASTAAVAAN 20
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08-JAN.1999; 99US-0115142P.
12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-0363209P.
08-AUG-2002; 2002US-0402483P.
07-MAR-2003; 2003US-00383930.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mammals against dental caries.
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Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Taubman MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMITH D J.
TAUBMAN M A.
                                                                                                                                                                                                                                                                                                                                                         Streptococcus mutans
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                                                                                                                                                                                                                                                                                                                                                                                              US2005031633-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smith DJ,
                                  306
                                                                                                                                                                          ADX37276;
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ADD93638
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Gaps

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PF 09-MAR-2004; 2004US-00797821.

XX
13-APR-1999; 99US-0115142P.
PR 06-JAR-2009; 99US-0115142P.
PR 06-JAR-2009; 99US-012510P.
PR 07-MAR-2009; 2002US-0363209P.
PR 07-MAR-2009; 2002US-0363930.

XX
(SMIT/) SMITH D J.
PA (TAUB) TAUBMAN M A.

XX

WPI; 2005-151644/16.

XX

WPI; 2005-151644/16.

XX

WPI; 2005-151644/16.

XX

WPI; 2005-151644/16.

XX

The invention comprising a fragment of a glucan binding protein-B acroparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.

XI

The invention relates to a composition comprising a fragment of a glucan comparaticle, where the binding protein-B (GbpB) and a biocompatible microparticle, where the circumpartials and an antibody (claimed) for immunizing mammals against dental caries.

CC fragment binds to a major histocompatiblity complex (RGC) claimed corresponds to a composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds to a corresponde corresponds to a corresponde of the invention.

XX

Sequence 20 AA;
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Search completed: January 25, 2006, 19:01:41 Job time : 69.2 secs

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0; Gaps

Query Match 74.4%; Score 67; DB 9; Length 20; Best Local Similarity 100.0%; Pred. No. 0.0054; Matches 15; Conservative 0; Mismatches 0; Indels

6 QPSASSASTAAVAAN 20 |||||||||||||||| 1 QPSASSASTAAVAAN 15

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GenCore version 5.1.6
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OM protein - protein search, using sw model

; Search time 9.1 Seconds (without alignments) 211.465 Million cell updates/sec January 25, 2006, 18:48:55 Run on:

US-10-797-821-3 90 Perfect score:

1 TATEAQPSASSASTAAVAAN 20 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SUMMAKIES STATES	Match Length DB ID Description	53.3 172 2 H86837 hypothetical prote	828	384 2 D86448	2 402 2 A86194	494 2 A42170 zinc finger	497 2 JC5076	2 S39356	825 1 EDBEXD	125 2 G72716	347 2 JC7178	364 2 T02801	372 2 T45524	2 T14007	1446 1 A45344	317 2 T00500	331 2 B47236	439 1 VHBPCL minor	439 2 A99833 minor	439 2 C85690	439 2 H90900 probab	477 2 A47236		503 2 S63257	.9 503 2 S63257 .9 724 2 S57604	503 2 S63257 724 2 S57604 797 1 VGBEX1	503 2 563257 probable 724 2 557604 probable 794 1 VGBEX1 glycoprot 866 2 T45462 membrane	503 2 S6257 724 2 S57604 791 VGBEX1 866 2 T45462 867 2 T45463	503 2 S63257 723 2 S57604 797 1 VGBEX1 866 2 T45462 867 2 T45463	503 2 862257 724 2 857604 797 1 VGBEX1 866 2 T45462 867 2 T45463 1156 2 T34852
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* 6	Match	53.3	53.3	52.	52.	52.3	52.3	52.3	52.3	51.1	51.1	51.1	51.1	51.1	20.0	48.	48.	48.	48.	48.	48.	48.	48.5	48		48.	8 4	4 4 4 8 8 8	4 4 4 4 8 8 8 8	4 4 4 4 4 8 8 8 8 8
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Regult	No.	г	7	m	4	Ŋ	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23		24	24 25	2 5 4 2 5 4	24 25 26 27	22 2 2 2 2 4 4 2 4 4 4 4 4 4 4 4 4 4 4

spalt protein - fr	ZK688.5 protein -	transcription fact	antifreeze protein	antifreeze protein	translocation prot	acetolactate decar	protein C43E11.1 [hypothetical prote	antifreeze glycope	dihydrolipoamide a	hydrogenase (EC 1.	earl protein - mai	hemagglutinin, pha	antifreeze glycopr	hypothetical prote
\$40022	S44920	T13751	FDFL4W	A22592	H83011	A37757	F87754	H87373	T44768	H83018	S11777	T01573	T09491	A38420	T46422
0	Н	8	Н	~	~	-	~	~	~	~	٦	~	7	~	7
1355	1799	2061	82	91	141	285	363	453	507	547	601	929	785	822	1013
48.9	48.9	48.9	47.8	47.8	47.8	47.8	47.8	47.8	47.8	47.8	47.8	47.8	47.8	47.8	47.8
44	44	44	43	43	43	43	43	43	43	43	43	43	43	43	43
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Angeles and protein yrgA [imported] - Lactococcus lactis subsp. lactis (strain IL1403) C,Species: Lactococcus lactis subsp. lactis C,Species: Lactococcus lactis subsp. lactis C,Species: Lactococcus lactis subsp. lactis C,Species: Lactococcus lactis subsp. lactis C,Species: Lactococcus lactis con 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004 C,Accession: H8637 R,Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrl Genome Res. 11, 731-753, 2001 A,Aitle: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s A,Accession: H8637 A,Accession: H8637 A,Accession: H8637 A,Accession: H8637 A,Accession: H8637 A,Accession: H8637 A,Accession: L172 <STO> A,Estion C,Complete type: DNA A,Estion DNA A,Estion L172 <STO> A,Experimental source: strain IL1403 C,Genetics: A,Gene: yrgA
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Gaps ö Length 172; 4; Indels 53.3%; Score 48; DB 2; 50.0%; Pred. No. 7.6; iive 6; Mismatches Query Match 53.3 Best Local Similarity 50.0 Matches 10; Conservative

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protein HOSCOS.1 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenor C8402
R;Accession: C84402
R;anonymous, The C. elegans Sequencing Consortium.
R;anonymous, The C. elegans Sequencing Consortium.
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolomary Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an A;Status: preliminary

A; Molecule type: DNA A; Residues: 1-828 <STO>

A;Cross-references: UNIPROT:Q9TXU2; UNIPARC:UP1000007CE2B; GB:chr_III; PIDN:AAC68790.1; A;Genetics: A;Gene: H05C05.1

A; Map position: 3

ö Gaps ö Length 828; 6; Indels Query Match 53.3%; Score 48; DB 2; Best Local Similarity 57.9%; Pred. No. 35; Matches 11; Conservative 2; Mismatches

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R.Pyrc, J.J.; Moberg, K.H.; Hall, D.J.
Biochemistry 31, 4102-4110, 1992
Biochemistry 31, 4102-4110, 1992
Affille: faolation of a novel cDNA encoding a zinc-finger protein that binds to two site A; Reference number: A42170; MUID:92232709; PMID:1567856
A; Accession: A42170
                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-694 cPYRA.
A; Cross-references: UNIPROT:P56270; UNIPARC:UPI000017C427; GB:J05371
A; Note: it is uncertain whether Met-18 is the initiator or whether translation is initial R; Bossone, S.A.; Asselin, C.; Patel, A.J.; Marcu, K.B.
Proc. Natl. Acad. Sci. US.A. 89, 7455-7456, 1992
A; Title: MAZ, a zinc finger protein, binds to c-MYC and C2 gene sequences regulating translating translation number: A46153; MUID:92366479; PMID:1502157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-497 <TSU3
A; Cross-references: UNIPARC: UPI0000163B39; DDBJ: DB5131; NID: 91752741; PIDN: BAA12728.1;
A; Experimental source: pancreatic islet
C; Comment: This protein plays a role in the control of transcriptional initiation of gei
and between the introns of the mouse gene for immunoglobulin M-D.
C; Keywords: phosphoprotein; zinc finger
F;146,204,480/Binding sitc: phosphate (Ser) (covalent) (by casein kinase II) #status pr:
F;349/Binding site: phosphate (Tyr) (covalent) #status predicted
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                                                                                   N,Alternate names: MYC-associated zinc finger protein MAZ; zinc finger protein ZF87
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NyAlternate names: MAZ protein
Cispecies: Homo sapiens (man)
Cipace 31.Jan.1997 #sequence_revision 31.Jan.1997 #text_change 05-Nov-1999
Cibacession: JCS076
Rifsuteui, H.; Sakatsume, O.; Itakura, K.; Yokoyama, K.K.
Biochem. Biophys. Res. Commun. 226, 801-809, 1996
A;ritle: Members of the MAZ family: A novel cDNA clone for MAZ from human pa
                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004
C;Accession: A42170; A46153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 18-417, 'L', 419-494 <BOS>
A; Cross-references: UNIPARC:UP1000012ECF8; GB:M94046
A; Experimental source: HeLa cells
A; Note: sequence extracted from NCBI backbone (NCBIN:110666, NCBIP:110667)
C; Reywords: DNA binding: Zinc finger
F; 113-125/Region: alamine-rich
F; 113-125/Region: alamine-rich
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Pred. No. 29;
2; Mismatches 5; Indels
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Pred. No. 29;
2; Mismatches
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Best Local Similarity 61.1%;
Matches 11; Conservative
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61.1%;
                                                              zinc finger protein MAZ - human
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F;296-318/Region: zinc finger
F;324-346/Region: zinc finger
F;354-368/Region: zinc finger
F;373-405/Region: zinc finger
F;409-430/Region: zinc finger
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Matches 11; Conserv
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C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Comway, A.B.; Comway, A.R.; Creasy, T.H.; Dewar, K.; Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.; Li, J.J., Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Roney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Reference and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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C; Genetics:
                                                                                                                                                                                                                                                                                                                                                         Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Sansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Lin, X.; Liu, X.; Liu, Z.X.; Liu, Z.X.; Liu, Z.X.; Liu, Z.A.; Maiti, R.; Marziali, Rizzo, M.; Roney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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A, Molecule type: DNA
A, Residues: 1-384 <STO>
A, Residues: 1-384 <STO>
C, Genetics: UNIPROT: Q9LQM3; UNIPARC: UPI0000AC169; GB: AE005172; NID: 98920610; C, Genetics: A, Map position: 1
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Species: Arabidopsis thaliana (mouse-ear cress)
Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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Pred. No. 24;
2; Mismatches
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                                                           766 AASAQPSESSSATAASGDN 784
2 ATEAQPSASSASTAAVAAN 20
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TRGSPSSSATTTSAASN 82
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Best Local Similarity 50.0%;
Matches 9; Conservative
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Best Local Similarity 62.5
Matches 10; Conservative
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A Molecule type: DNA
A Residues: 1-402 <STO>
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: G72116
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Taka awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; A;Tile: Caralli, 1999
A;Tile: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                       A;Accession: G72716
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-125 <KAW>
A;Cross-references: UNIPROT:Q9YCM2; UNIPARC:UPI00005DE24; DDBJ:AP000060; NID:g5104188;
A;Experimental source: strain Kl
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C;Species Streptomyces thermoviolaceus
C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 09-Jul-2004
C;Accession: JC7178
R;Tsujibo, H:; Hatano, N:; Endo, H:; Miyamoto, K:; Inamori, Y.
Biosci. Biotechnol. B
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C;Comment: This enzyme, involved in chitin degradation system, hydrolyzing chitin by an
he conversion of insoluble chitin to its monomeric component.
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C; Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 05-Oct-2004
C; Accession: E81456; T02801
R; Myler, P.J.; Audleman, L.; deVos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C.;
Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999
A; Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protein-A; Reference number: A81455; MUID:99178987; PMID:10077609
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A;Molecule type: DNA
A;Residues: 1-364 <PYL>
A;Cross-references: UNIPROT:060974; UNIPARC:UPI000007B776; GB:AE001274; NID:G3264B50; P
A;Experimental source: strain MHOM/IL/81/Friedlin
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A,Start codon: GTG
C,Keywords: chitin biosynthesis; glycosidase; hydrolase
P,50-347/Product: 30K chitinase #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chitinase (BC 3.2.1.14) - Streptomyces thermoviolaceus
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58.8%; Pred. No. 11;
ive 4; Mismatches
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Matches 10; Conservative
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A; Residues: 1-347 <TSU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: APE1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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NyAlternate names: RL2 protein
C;Species: human herpesvirus 2
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: JQ1501
R;McGeoch, D.J; Cunningham, C.; McIntyre, G.; Dolan, A.
J. Gen. Virol. 72, 3057-3075, 1991
A;Title: Comparative sequence analysis of the long repeat regions and adjoining parts of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: JQ1501
A;Accession: JQ1501
A;Molecule type: DNA
A;Molecule type: DNA
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
C;Genetics:
A;Gene: RL2
A;Gene: RL2
A;Introns: 25/3; 252/1
C;Superfamily: herpesvirus immediate-early protein; tandem repeat; transcription regulation
F;122-172/Domain: RING finger C3HC4 motif
F;122-172/Domain: Ainc finger C3HC4 motif
F;589-623/Region: 5-residue repeats (A-S-S-S-S)
                                                                                                                                                                                                                                                                                                                                                                                 C;Specide: Drosophila sp.
C;Date: 18-Peb-1994 #sequence_revision 01-Dec-1995 #text_change 07-May-1999
C;Date: 18-Peb-1994 #sequence_revision 01-Dec-1995 #text_change 07-May-1999
C;Accession: S39356
Nature 366, 690-694, 1993
A;Title: A Drosophila homologue of human Spl is a head-specific segmentation gene. A;Reference number: S39356; MUID:94081952; PMID:8259212
A;Recession: S39356
A;Recession: S39356
A;Residues: preliminary
A;Rolecule Yppe: DNA
A;Residues: 1-644 <WIM>A;Residues: 1-644 <WIMPARC:UPIO000124C17; EMBL:Z29361; NID:g441283; PID:g441284 A;Rosse-references: Flybase:FBgn0000233
A;Introns: 245/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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C;Species: Aeropyrum pernix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4;
                                                                                                                                                                                                                                                                                                                                                          transcription factor btd - fruit fly (Drosophila sp.)
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Pred. No. 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 52.2%; Score 47; 1 Similarity 58.8%; Pred. No. 310; Conservative 3; Mismatcl
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170 AAEAAPPASAATIAAAA 187
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197 TSSPSSSAASAAAAA 213
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                                              ATEAQPSASSASTAAVAA
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Best Local Similarity 63.2
Matches 12; Conservative
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Matches 10; Conserv
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Length 1446;

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C;Accession: A45344
R;Vlcek, C;; Kozmik, Z.; Paces, V.; Schirm, S.; Schwyzer, M.
N;Vology 179, 365-377, 1990
A;Title: Pseudorables virus immediate-early gene overlaps with an oppositely oriented of A;Reference number: A45344; MUID:91021039; PMID:2171211
A;Accession: A45344
                                                                                                                                                                                                                                                                                                   A; COSSEreferences: UNIPROT: P33479; UNIPARC: UPI000012D219; GB: M34651; NID: G334070; PIDN: C; Superfamily: herpesvirus immediate-early protein IE175
C; Keywords: DNA binding; early protein; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable elicitor response element-binding protein WRKY3 - Arabidopsis thaliana C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Species: Ol-Feb-1999 #squence_revision 01-Feb-1999 #text_change 31-Dec-2004
C'SAccession: T00500; C84623
R'Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaulsubmitted to the EMBL Data Library, November 1997
A'Description: Arabidopsis thaliana chromosome II BAC T20D16 genomic sequence.
A'Reference number: Z14164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Rosidues: 1-317 <ROU>
A; Rosidues: 1-317 <ROU>
A; Essidues: 1-317 <ROU>
A; Essidues: 1-317 <ROU>
A; Experimental source: Cultivar Columbia
A; Experimental source: cultivar Columbia
B; Lin, X; Kaul, S; Rounsley, S.D; Shea, T.P; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R; Lin, X; Kaul, S; Cronin, L.A.; Shen, M; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, L.
Nature 402, 761-768, 199
A; Ttle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A64420; MUID: 20083487; PMID: 10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: UNIPARC: UPI0000138F7D; GB: AE002093; NID: 92642432; PIDN: AAB87100.1; (
30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 45; DB 1; I
Pred. No. 1.6e+02;
4; Mismatches 4;
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Pred. No. 51;
2; Mismatches
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Job time : 9.1 secs
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C;Superfamily: DNA-binding protein WRKY3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       424 AAAPRPSASSASSSAAS 441
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Best Local Similarity 71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 50.0%;
Best Local Similarity 55.6%;
Matches 10; Conservative
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48 OPSSSSASASASAA 61
                                                                                                                                                                                                                  A;Status: translation not shown A;Molecule type: DNA A;Residues: 1-1446 <VLC>
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A;Molecule type: DNA
A;Residues: 1-317 <STO>
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R; Bao, W.G.; Fukuhara, H.
Bubmitted to the EMBL Data Library, July 1999
Winder of the EMBL Data Library, July 1999
A; Bescription: The ubiquitin-encoding genes of Kluyveromyces lactis.
A; Rescription: The ubiquitin-encoding genes of Kluyveromyces lactis.
A; Recession: T4552
A; Rocession: T4524
A; Residue: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-372 < BAO>
A; Residues: 1-372 < BAO>
A; Residues: 1-372 < BAO>
A; Experimental source: strain 2359/152
C; Genetics:
A; Gene: rim101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      regulatory protein rim101 homolog [imported] - yeast (Kluyveromyces marxianus var. lacti
C;Species: Kluyveromyces marxianus var. lactis, Candida sphaerica
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004
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R,Shiina, N.; Tsukita, S.
Mol. Biol. Cell 10, 597-608, 1999
A;Title: Mutations at phosphorylation sites of Xenopus microtubule-associated protein 4
A;Reference number: 217855; MUID:99169009; PMID:10069806
A;Accession: T14007
A;Accession: T14007
A;Residue: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-124 - <AIN.
A;Residues: 1-124 - <AIN.
A;Cross-references: UNIPROT:09Y190; UNIPARC:UPI00000FDDE8; EMBL:AB021705; NID:d1252552; C;Reywords: microtubule binding
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C,Species: Xenopus laevis (African clawed frog)
C,Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
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                                              A;Gene: L549.13
A/Map position:
C;Superfamily: Leishmania major probable membrane protein L549.13
C;Keywords: transmembrane protein
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Pred. No. 31;
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Best Local Similarity 83.3
Matches 10; Conservative
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immediate-early protein - suid herpesvirus 1 (strain Kaplan) C;Species: suid herpesvirus 1

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"Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates."

Infect. Immun. 69:6931-6941(2001).

EMBL; AX046410; AX094500.1; -; Genomic_DNA.

InterPro; IPR007921; CHAP.

InterPro; IPR007921; CHAP.

PFfam; PF0527; CHAP.

PRINTS; PR01852; SIBARROTEIN.

PROSITE; PS50911; CHAP; 1.
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Q9AG98;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-FBB-2005 (TrEMBLrel. 29, Last annotation update)
Immunodominant glycoprotein IDG-60 (Glucan-binding protein B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=SJ32;
MEDLINE=21481971; PubMed=11598068;
DOI=L0.1128/IAI.69.11.6931-6941.2001;
Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jin S., Duncan M.J., Taubman M.A., Smith D.J.; "Cloning of the gbpB gene from Streptococcus mutans."; J. Dent. Res. 79:224-224(2000).
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Q91XME HUMAN
Q91XM2 HUMAN
Q91XW2 HUM1
Q97XW2 CHW1
Q97XW2 CAREL
G6HBY4 STRSU
G6HBY4 STRSU
Q6CW93 CRYPY
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 NCBI_TaxID=1309;
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               GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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Duncan M.J.; "Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in
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                                  Streptococcus mutans.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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EMBL; AE014855; AAN57811.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
Interpro; IPR001948; SibA.
FRAN; PF05257; CHAP; 1.
PRINTS; PR01852; SIBARROTEIN.
PROSITE; PS50911; CHAP; 1.
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SEQUENCE 431 AA; 44620 MW; ZDICA685248CCD3B CRC
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Pred. No. 0.0012;
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Infect. Immun. 69:6931-6941(2001).
EMBL, AY046413; AX04493.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SiDA.
Pfam; PF05257; CHAP; 1.
PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
SEQUENCE 432 AA; 44652 MW; 3F88ECB9AlF3BE4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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MEDLINE=21481971; PubMed=11598068;
DOI=10.1128/IAI.69.11.6931-6941.2001;
Name=gbpB; OrderedLocusNames=SMU.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      306 TATEAOPSASSASTAAVAAN 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q938V1_STRMU PRELIMINARY;
Q938V1;
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nes 20; Conservative
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                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
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Best Local Similarity
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                                                                                                                           NCBI_TaxID=1309;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     pathogen."
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                                                                                                                                                                                                                       STRAIN=GS-5;
MEDLINE=2115617; PubMed=11254612;
MEDLINE=21128/IAI.69.4.2493-2501.2001;
Chia J.S., Lee Y.Y., Huang P.T., Chen J.Y.;
"Identification of stress-responsive genes in Streptococcus mutans by differential display reverse transcription-PCR.";
Infect. Immun. 69:2493-2501(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=GS-5;
MEDLINE=21481977; PubMed=11598074;
DOI=10.1128/IAI.69.11.6987-6998.2001;
Chiad J.S., Chang L.Y., Shun C.T., Chang X.Y., Chen J.Y.;
Chiad J.S., Chang L.Y., Shun G.T., Chang M.Y., Chen J.Y.;
what immunodominant glycoprotein is essential for cell
wall integrity and the maintenance of cell shape in Streptococcus
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Putative secreted antigen GbpB/SagA; putative peptidoglycan hydrolase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21481971; PubMed=11598068;
DOI=10.1128/IAI.69.11.6931-6941.2001;
Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
                                  Streptococcus mutans.
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=GS-5;
Chia J.-S., Chang L.-Y., Lee Y.-Y., Chen J.-Y.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jin S., Duncan M.J., Taubman M.A., Smith D.J.; "Cloning of the gbpB gene from Streptococcus mutans."; J. Dent. Res. 79:224-224 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      431 AA; 44592 MW; 3EBE21FC5E47232E CRC64;
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EMBL, AR338445; AAK08104.1; -; Genomic_DNA.

EMBL, AV046411; AAK94501.1; -; Genomic_DNA.

InterPro; IPR007921; CHAP.

InterPro; IPR009148; SibA.
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PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
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QBDWM3 STRMU PRELIMINARY;
QBDWM3;
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les 20; Conservative
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                                                                                                                                 NCBI_TaxID=1309;
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               Name=sagA;
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Best Loc Matches

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RESULT 3 **СММОВО**

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Length 432;

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Gaps

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Gaps

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Duncan M.J.;

"Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates.";

Infect. Immun. 69:6931-6941(2001).

EMBL; AY046414; AAK94504.1; -; Genomic_DNA.

InterPro; IPR007921; CAAP.

InterPro; IPR00148; SibA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OSJNBb0043P23.4).
Name=OSJNBb0043P23.4;
Name=OSJNBb0095M04.140; Synonyms=OSJNBb0043P23.4;
Name=OSJNBb0095M04.140; Synonyms=OSJNBb0043P23.4;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M., Overcon II L.L., Taitrin T., Kim M., Bera J.J., Jin S.S., Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M., Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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Buell C.R., Yuan Q., Cuyang S., Liu J., Gansberger K., Jones K.M., Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S., Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V., Wang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J., White O., Salaberg S.L., Fraser C.M.; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Hypothetical protein OSJNBb0096M04.140 (Hypothetical protein
                  MEDLINE=21481971; PubMed=11598068;
DOI=10.1128/IAI.69.11.6931-6941.2001;
Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
                                                                                                                                                                                                                                                                                                                                      Length 431;
                                                                                                                                                                                                                                                                                                                                    91.1%; Score 82; DB 2; Length 431
90.0%; Pred. No. 0.0023;
ive 0; Mismatches 2; Indels
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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AC092559; AAO37944.1; -; Genomic DNA.
EMBL; AC09324; AAO73278.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buell R.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                     PRINTS; PRO1852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
SEQUENCE 431 AA; 44650 MW; 05D38D8BBC4609F CRC64;
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InterPro; IPR000095; PAKbox/Rhobndng.
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PROSITE; PS50108; CRIB; 1.
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Best Local Similarity 90.09
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NUCLEOTIDE SEQUENCE.
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  Gape
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DOI=10.1128/IAI.69.11.6931-6941.2001;
Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
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                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Glucan-binding protein B.
Streptococcus mutans.
Bacteria, Firmicutes; Lactobacillales; Streptococcaee;
    Indels
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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STRAIN=15JP2;
Jin S., Duncan M.J., Taubman M.A., Smith D.J.;
"Cloning of the gbpB gene from Streptococcus mutans.";
J. Dent. Res. 79:224-224 (2000).
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Glucan-binding protein B.
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                                                                                                                                                                           432 AA.
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Infect. Immun. 69:6931-6941(2001).
EMBL, AV046412; AAK94502.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
0; Mismatches
                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                           307 TATAAQPSASSASTAAVAAN 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 307 TATAAQPSASSASTAAVAAN 326
                                     1 TATEAQPSASSASTAAVAAN 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TATEAQPSASSASTAAVAAN 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR01852; SIBAPROTEIN.
                                                                                                                                                                       Q938V2_STRMU PRELIMINARY;
Q938V2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q938V0 STRMU PRELIMINARY;
Q938V0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50911; CHAP; 1
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF05257; CHAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                    Streptococcus.
NCBI_TaxID=1309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1309;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=15JP2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=5SM3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Duncan M.J.;
19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                        STRMU
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Matches

ò 셤 Oggashoo

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Query Match
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셤
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REALINE-20196006; Pubbed=10731132; DOI=10.1126/science.287.5461.2185; RADINE-20196006; Pubbed=10731132; DOI=10.1126/science.287.5461.2185; RADINE-20196006; Pubbed=10731132; DOI=10.1126/science.287.5461.2185; RADINE-20196006; Pubbed=10731132; DOI=10.1126/science.287.5461.2185; RADINER Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F., Gutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Bratch R.C., Rogers R.A., Barel R.G., Champe M., Pfeiffer B.D., RADILLOW R.M., Baru A., Bartle R.G., Champe M., Pfeiffer B.D., RADILLOW R.M., Baru A., Bartle R.J., Barder R.G., Champe M., Pfeiffer B., Beeson K.Y., Bence P.V., Barman B.P., Bhandari D., Bolahakor S., Burtis K.C., Busam D.A., Parller H., Cadieu E., Center A., Chadra I., RADICA E., Dougley S., Dahlke C., Davemport L.B., Davise P., Brottler P., Burtis K.C., Busam D.A., Lauller H.M., Cadieu E., Center A., Chadra I., RADININ K.J., Brangeliste C.C., Ferraz C., Ferra C., Ferra C., Ferra C., Ferra C., Ferra C., Ferra C., Ferra C
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Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=CGI31144; ORFNames=CG13144;
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bphydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                      DB 2; Length 166;
                                                                                                                      Indels
                           17181 MW; 6EC080E8429A16DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                           291 AA.
                                                                                               5.9;
                                                                                                                      3; Mismatches
                                                                        Score 55;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                     1 TATEAQPSASSASTAAVAA 19
                                                                                                                                                                                                    35 TTTQNDPSSSSASAAAMAA 53
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                                                                   y Match 61.1%;
Local Similarity 63.2%;
les 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                         Q9VKU4_DROME PRELIMINARY;
Q9VKU4;
     protein.
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                         166 AA;
     Hypothetical
SEQUENCE 10
                                                                           Query Match
                                                                                                                                                                                                                                                                                                                  DROME
                                                                                                                           Matches
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MEDDINE-22426070; PubMed-12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R., Fatel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae;
Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren B.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; "Finishing a whole-genome shotgun: release 3 of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Derkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ø
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9VFW7:CG32473; NDExp=1; IntAct=EBI-149908, EBI-140143; P13496:G1; NDExp=1; IntAct=EBI-149908, EBI-157742; EMBL; AE003628; AAF52965.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.1%; Score 55; DB 2; Length 291; 66.7%; Pred. No. 11; 3; Indels ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001337; TMV coat.
SEQUENCE 291 AA; 33122 MW; F6C3D3343AF27527 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IntAct; Q9VKU4; ...
Ensembl; CG13144; Drosophila melanogaster.
FlyBane; FBgn003226; CG13144,
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bystematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Biol. 3: RESEARCH0084.1-RESEARCH0084.20(2002)
                                                                                                                                            melanogaster euchromatic genome Bequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002)
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Hypothetical protein OSJNBa0026E05.20.
Name=OSJNBa0026E05.20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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112 TSTSPTPNASSSSTAAVA 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QEYXX1 ORYSA PRELIMINARY;
QEYXX1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 66.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                        genomics perspective.";
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                                                                                                                                                                                                                                                  SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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Q9U113 LEIMA PRELIMINARY;
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                                                                                                                                           Q68H99 PIG PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                    Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                 NCBI TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=L4830.01
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NON TER
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SEQUENCE
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Matches
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--- SUBCELLIULAR LOCATION: Inner membrane-associated (By similarity).
--- SIMILARITY: Belongs to the ABC transporter family.
EMBL; AAHD01000016; EAL/18994.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=2CP-C;
US DOB Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Anaeromyxobacter
dehalogenans 2CP-C.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP-binding; Inner membrane; Membrane; Nucleotide-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Larimer F., Land M.;
"Annotation of the draft genome assembly of Anaeromyxobacter dehalogenans SCP-C.";
Submitted (UNN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Bacteria; Proteobacteria; Daltaproteobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
NCBI_TaxID=290397;
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65.0%; Pred. No. 1.4e+02;
iive 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                         DB 2; Length 700;
                                                                                   Sasaki T., Matsumoto T., Katayose Y.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005647; BAD10533.1; -; Genomic_DNA.
Gramene; 96YXX1; -:
Hypochetical protein.
SEQUENCE 700 AA; 76230 MW; FA3A5DC8F7BEE6AA CRC64;
                                                                                                                                                                                                                                                                                                         Indels
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SEQUENCE 1430 AA; 152563 MW; 7CA816349DF383DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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PROSITE; PS50893; ABC_TRANSPORTER_2; 2.
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                                                                                                                                                                                                                                                      57.8%; Score 52; DB 66.7%; Pred. No. 69; ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=2CP-C;
US DOE Joint Genome Institute (JGI-ORNL);
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InterPro; IPR003439; ABC_transp_like.
Pfam; PP00005; ABC_tran; Z.
ProDom; PD000006; ABC_transporter; 1.
SMART; SM00382; AAA; Z.
                                                                                                                                                                                                                                                                                                                                                   2 ATEAQPSASSASTAAVAA 19
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NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABC transporter precursor.
ORFNames=AdehDRAFT 2109;
                                                                                                                                                                                                                                                                               Best Local Similarity 66.79
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q4NTX6_9DELT PRELIMINARY;
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Best Local Similarity
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Q4MTX6 9DELT
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Gaps
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: Contains 1 PH domain.
EMBL; AY690661; AAT99886.1; -; Genomic_DNA.
SMR; (OSH999; 1-254.
GO; GO:0005158; P:insulin receptor binding; IEA.
GO; GO:0004872; P:receptor activity; IEA.
InterPro; IPR002404; Insln_receptorS1.
Pfam; PF02174; IRS; 1.
Pfam; PF02174; IRS; 1.
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metāzoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
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1229 AA; 129798 MW; 8DF1FBC5900B042C CRC64;
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             25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Insulin receptor substrate-1 (Fragment).
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1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein L4830.01.
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PRT; 1229 AA.
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NUCLEOTIDE SEQUENCE.
STRAIN=Friedlin;
MEDLINE=98146435; PubMed=9477341;
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SMART; SM00233; PH; 1.
SMART; SM00310; PTBI; 1.
PROSITE; PS50003; PH_DOWAIN; 1.
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NUCLEOTIDE SEQUENCE
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PRT; 2193 AA.

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Q4PFYO_USTMA PRELIMINARY;
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A rroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
Bowyer P., Chen D., Collins M., Coulsen R., Davies R., Dyer P.S.,
Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
A Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.,
A Haash H., Harris D., Horiuchi H., Humphrey S., Jimenez J.,
Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,
Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,
A Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
A manuld M.A., Petrea M., Price C., Pritchard B.L., Quail M.A.,
Rabbinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,
Roming C.M., Rutter S., Salzberg S.L., Sanchez M.,
Sanchez-Perrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
Machida M., Hall N., Barrell B., Denning D.W.;
Machida M., Hall N., Barrell B., Denning D.W.;
Machida M., Hall N., Barrell B., Denning D.W.;
M. Accounty Sequence of the pathogenic and allergenic filamentous fungus
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Eukaryota; Fungi, Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=330879;
        Ivens A.C., Murphy L., Quail M., Harris D., Oliver K., Lawson D., Rajandream M.A., Barrell B.G.; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL139794; CAC22627.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 1312 AA; 136110 MW; 5093BEB91C885872 CRC64;

    -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is

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                                                                                                       Length 1312;
                                                                                            Score 51; DB 2; Length 1314
Pred. No. 1.86+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
SEQUENCE 1330 AA; 146261 MW; F7EECC4BC1C7D9CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aspergillus fumigatus.";
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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EMBL; AAHF01000012; EAL85569.1; -; Genomic_DNA.
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1046 TQVSPASAAAAAAAAA 1063
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                                                                                                         56.7%;
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13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
Hypothetical protein.
ORFNames=Afu6g04710;
                                                                                                                                                                                                                                                  Q4WDG9_ASPFU PRELIMINARY;
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                                                                                                                                    10; Conservative
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                                                                                                          Query Match
Best Local Similarity
     STRAIN=Friedlin;
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RC STRAIN-521;

RA AIL-SAHCH N., Allen T., An P., Anderson M., Anderson S., Arit-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S., Arit-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S., Arit-zahra M., Allen N., Allen T., Anderson S., Bartens E., Nusbaum T., Bly G., Baldwin J., Barry A., Barthonser J., Campor K., Chang J., Chanter J., Calixe N., Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixe N., Borowsky M., Boukhgalter B., Brunache A., Borter B., Cond. G., Cooke P., Colymore A., Considine T., Cook A., Cooke P., Corum B., Cond. Colymore A., Corisidine T., Cook A., Cooke P., Corum B., Chomo C., Ba David R., Dawee T., Degray S., Dodge S., Dooley K., Dagels R., Enckson J., Farina A., Faro S., Ferreira P., Fischer H., Anderson J., Farina A., Faro S., Farina J., Hulme W., Hulber R., Hafez N., Bricken J., Goyette A., Grandbois E., Galtres S., Anderson J., Farina A., Faro S., Farina J., Hatcher B., Hulme W., Husby E., Iliev I., Ander D., Onnes C., Kanal M., Kanat A., Kanar P., Kodira C., Kulbokas E., Labutti K., Rana D., Landers T., Leger J., Lewis D., Lewis T., Labutti K., Manning J., Marchell R., Maclean C., Mauceil E., Manning J., Marchella R., Machen P., Machen C., Mauceil E., Manning J., Marchella R., Machen P., Machen T., Mord W., Marchella R., Marcatthy M., Mcdonough S., Mcdher T., Machen C., Mauceil E., Marcatthy M., Mcdonough S., Mcdher T., Maclean T., Marchella R., Marcatthy M., Nodonnell P., Okoawo O., Oleary S., Omotosho B., Parker S., Parrin D., Phurkang V., Raymond C., Raneany V., Mihalev A., Mihova T., Marcell S., Rachupka T., Rameany W., Ramean W., Schupbach R., Staker S., Parrin D., Phurkang P., Rogers V., Ramean W., Schupbach R., Staker S., Theodore U., Mninson G., Settiguez J., Rohlukan B., Parker S., Theodore J., Morlukan B., Towys S., Tesmas Y., Thoulutean Y., Topham K., Towys S., Tesmas Y., Wallen D., Waller D., Waller D., Waller D., Waller D., Waller D., Waller D., Waller D., Waller D., Waller D., Waller D., Waller D., Waller D., Waller D., Waller D., Waller
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Submitted (FBB-2004) to the EMBL/Genbank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/Genbank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                               Eukaryota, Fungi, Basidiomycota, Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales, Ustilaginaceae; Ustilago.
NCBL_TaxID=237631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.7%; Score 51; DB 2; Length 2193; 55.0%; Pred. No. 3.1e+02; ive 3; Mismatches 6; Indels
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-1- SUBCELLULAR LOCATION: Nuclear (By similarity).
BEL; AACPO1000034; EAK81993.1; -; Genomic_DNA.
INTERFRO; IPRO01005; Myb_DNA_bd.
Pfam; PF00249; Myb_DNA-bInding; 2.
                                           Last sequence update)
Last annotation update)
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SEQUENCE 2193 AA; 233297 MW; 056AD432BE4CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1502 TLDEAKPGASSAPSAVLAGN 1521
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(TrEMBLrel. 31, C
(TrEMBLrel. 31, L
(TrEMBLrel. 31, L
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                                                                                                                       Hypothetical protein.
ORFNames=UM00983.1;
                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
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Best Local Similarity
                                                                                                                                                                                                       Ustilago maydis 521
                                               13-SEP-2005
                                                                               13-SEP-2005
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RESULT 14 Q4PFY0_USTMA

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TOTAL DATE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=DSS-3 / ATCC 700808 / DSM 15171;

Whoded=15602564; DOI=10.1038/nature0317;

Whoran M.A., Buchan A., Gonzalez J.M., Heidelberg J.F., Whitman W.B., M. Gonzalez J.M., Lewis M., Johris J., Weaver B., Puqua C., M., Lewis M., Johris S., Weaver B., Puqua C., Sheldon W.M., Ye W., Miller T.R., Carlton J., Rasko D.A., Paulsen I.T., Ren Q., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R., Walson W.C., Sullivan S.A., Rosovitz M.J., Martone neuricoment.", Ward N., Ward N.; Schengtu J., Ward N.; Schengtu J., Ward N.; Genome sequence of Silicibacter pomeroyi reveals adaptations to the Tarthe environment.";

Mature 432:910-913.2004).

EMBL; CP000031; AAV95416.1; -; Genomic_DNA.

InterPro; IPR006837; DUF610 Yibo.

Remi, PP04748; Polysacc_deac_2; 1.

Complete protecome; Hypothetical protein.

SEQUENCE 481 AA; 48634 MW; 983E8BCA07279DIA CRC64;
RESULT 15

QSIRIO SILPO

ID QSIRIO.

DGIRIO.

DT 01-FEB-2005 (TrEMBLrel. 29, Created)

DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)

DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)

DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)

DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)

DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)

CR Norderical protein:

CR Norderial Protecobacteria, Protecobacteria, Rhodobacterales;

CR Rhodobacteraceae; Silicibacter.

OX NCBI TAXID=89184;
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Search completed: January 25, 2006, 19:13:35 Job time: 71.3 secs |||:|||: ||| | | 175 TATDAQPAQESASVAEAPA 193

1 TATEAQPSASSASTAAVAA 19

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JOSEPH PARTICLE OF APPLICATION OF SEQUENCE 161, APPLICATION OF 6821519

J. GENERAL INFORMATION:

J. APPLICANT: Day, Craig H.

APPLICANT: Hosken, Nancy A.

JAPLICANT: Hosken, Oceph M.

JITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TITLE OF INVENTION: TREATMENT OF HERPES SIMPLEX VIRUS INFECTION

JITLE OF INVENTION: TREATMENT OF HERPES SIMPLEX VIRUS INFECTION

JITLE OF INVENTION: TREATMENT OF HERPES SIMPLEX VIRUS INFECTION

CURRENT APPLICATION NUMBER: US/10/237,551

CURRENT FILING DATE: 2002-06-06

NUMBER OF SEQ ID NOS: 254

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 161

LENGTH: 825
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1110
1411
148
155
1217
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851
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Sequence 23624, A
Sequence 32580, A
Sequence 31979, A
Sequence 47186, A
Sequence 24667, A
Sequence 24667, A
Sequence 2, Appli
Sequence 2, Appli
Sequence 46340, A
Sequence 46340, A
Sequence 32760, A
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Sequence 20152, A
Sequence 41733, A
Sequence 50, Appl
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                                                                            January 25, 2006, 18:50:05; Search time 16.6 Seconds (without alignments) 99.609 Million cell updates/sec
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Sequence 858; A
Sequence 424; A
Sequence 2, Apr
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1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

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5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-09-894-98A-47

US-09-344-529-4

US-09-252-91A-20152

US-09-562-737-51

US-09-562-737-58

US-09-70-767-41733

US-09-732-210-858

US-09-487-5588-424

US-09-487-5588-424

US-09-252-991A-32580

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US-09-252-991A-32580

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US-09-252-991A-32760
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Maximum Match 100%
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                                                       OM protein - protein search, using sw model
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Sequence 6, Appli
Sequence 12369, A
Sequence 23009, A
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Sequence 1137, A
Sequence 1039, Ap
Sequence 13, Appl
Sequence 13, Appl
Sequence 23804, A
Sequence 2465, Ap
Sequence 2473, A
Sequence 15, Appl
Sequence 2473, A
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Sequence 12443, A
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Sequence 1, Application US/10210428
; Patent No. 6814969
; GENERAL INFORMATION:
; APPLICANT: David M. Koelle
; APPLICANT: Nancy A. HOGHA
; TITLE OF INVENTION: IMMUNOLOGICALLY SIGNIFICANT HERPES
; TITLE OF INVENTION: SIMPLEX VIRUS ANTIGENS AND METHODS FOR USING SAME
; FILE REFERENCE: 30967-8-101
; CURRENT FILING DATE: 2002-07-31
; PRIOR FILING DATE: 2001-07-31
; RICHOR PLING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FRAESEQ for Windows Version 4.0
; SEQ ID NO
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Pred. No. 61;
2; Mismatches 5; Indels
US-09-793-708-1
US-09-105-537-31
US-09-105-537-31
US-09-902-540-12369
US-09-252-991A-25469
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US-09-252-991A-17115
US-09-270-767-31877
US-09-270-767-47094
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PCT-US96-02331-13
US-09-252-991A-23804
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Best Local Similarity 63.2%;
Matches 12; Conservative
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SEQ ID NO 20152
LENGTH: 84
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                                                                                                                                                                                                                                                                  Sequence 47, Application US/09894998A

Sequence 47, Application US/09894998A

Batent No. 6537555

GENERAL INFORMATION:

APPLICANT: Hosken, Nancy Ann
APPLICANT: Craig H. Day

APPLICANT: Bavin C. Dillon

APPLICANT: Sleath, Paul R.

TITLE OF INVENTION: TREATMENT OF HERPES SIMPLEX VIRUS INFECTION

TITLE OF INVENTION: TREATMENT OF HERPES SIMPLEX VIRUS INFECTION

TITLE OF INVENTION: 182011.538

CURRENT FILING DATE: 2001-06-28

NUMBER OF SEQ ID NOS: 64

SOFTWARE: PASSESQ for Windows Version 4.0

SEQ ID NO 47

LENGTH: 826
                                                                                                           Gaps
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Patent No. 6821519

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bosken, Nancy A.
APPLICANT: Hosken, Nancy A.
APPLICANT: Parsons, Joseph M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TITLE OF INVENTION: TREATMENT OF HERPES SIMPLEX VIRUS INFECTION FILE REFERENCE: 210121.538C3
CURRENT APPLICATION NUMBER: US/10/237,551
CURRENT APPLICATION NUMBER: US/10/237,551
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                                                                  Query Match 52.2%; Score 47; DB 2; Length 825; Best Local Similarity 63.2%; Pred. No. 61; Matches 12; Conservative 2; Mismatches 5; Indels
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Pred. No. 61;
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2; Mismatches
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2; Mismatches
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Best Local Similarity 63.2%;
Matches 12; Conservative
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Matches 12; Conservative
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US-10-237-551-47
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             , ORGANISM: HSV2
US-10-237-551-161
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US-09-894-998A-47
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TYPE: PRT
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Pacience 20152, Application US/09252991A

Pacent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS:
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                         GENERAL INFORMATION:
APPLICANT: Hew, Choy L.
APPLICANT: Hew, Choy L.
APPLICANT: Hew, Choy L.
APPLICANT: How, Coulpin-Type Autifreeze Polypeptides and Nucleic Acids
FILE REFERENCE: 016252-002620US
FILE REFERENCE: 016252-002620US
CURRENT PELING DATE: 1999-06-24
EARLIER APPLICATION NUMBER: US 60/090,794
EARLIER APPLICATION NUMBER: US 60/095,713
EARLIER PILING DATE: 1998-06-07
NUMBER OF SEQ ID NOS: 19
SEQ ID NOS: 19
SEQ ID NO 2
EDGTWARE: Patentin Ver. 2.0
SEQ ID NO 2
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; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;
; FILE REPERENCE: File Reference: 7326-094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 8.5;
5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 92;
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Pred. No. 6.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TATEAQPSASSASTAAVAAN 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Pseudomonas aeruginosa US-09-252-991A-20152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.
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US-09-344-529-2
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Best Local Similarity 50.0%;
Matches 10; Conservative !
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nes 10; Conservative
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US-09-252-991A-20152
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US-09-270-767-41733
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; TYPE: PRT
; ORGANISM: Puccinia graminis
US-09-732-210-858
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Silva, Jeff
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US-09-487-558B-424
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US-07-814-220-2
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APPLICANT:
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Sequence 858, Application US/09732210

Patent No. 6573361

GRNERAL INFORMATION:

APPLICANT: Bunkers, Greg J.

APPLICANT: Mittanck, Cindy A.

APPLICANT: Way Younie S.

TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use

FILE REFERENCE: 38-21(15.036)B

CURRENT APPLICATION NUMBER: US/09/732,210

CURRENT PILING DATE: 2000-12-07

PRIOR PAPLICATION NUMBER: US 60/169,513

PRIOR FILING DATE: 1999-12-07

PRIOR FILING DATE: 1999-12-07

PRIOR FILING DATE: 1999-12-07

NUMBER OF SEQ ID NOS: 1753

SEQ ID NO 858

LENGTH: 158
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US-09-562-737-50
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55.6%; Pred. No. 42;
ive 3; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 50, Application US/09562737;
Patent No. 6428967;
GENERAL INFORMATION:
APPLICANT: Herz, Joachim;
APPLICANT: Getchardt, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways;
TITLE OF INVENTION: LDL Receptor Signaling Pathways;
CURRENT APPLICATION NUMBER: US/09/562,737;
CURRENT FILING DATE: 2000-05-01;
NUMBER OF SEQ ID NOS: 132;
SOFTWARE: PatentIn Ver. 2.1;
SEQ ID NO 50
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Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                            FEATURE:
; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-41733
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 41733
LENGTH: 334
                                                                                                                               ORGANISM: Drosophila melanogaster
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167 ATAAPPTTSNAPTSAAA 184
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Matches 10; Conservative
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Best Local Similarity 52.9
Matches 9; Conservative
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US-09-562-737-50
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APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REPERENCE: 109272.130
CURRENT APPLICATION NUMBER: US/09/487,558B
CURRENT FILING DATE: 2000-01-19
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                                           Gaps
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Patent No. 5925540

GENERAL INFORMATION:

APPLICANT: Caccet, Thomas

APPLICANT: Toth, Thomas E.

APPLICANT: Szumanski, Maria B.W.

TITLE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND

TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSE: WHITHAM, CURTIS & WHITHAM

STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,

STREET: Suite 900
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Length 158;
                                         6; Indels
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Score 44; DB 2;
Pred. No. 25;
4; Mismatches
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Best Local Similarity 40.0%; Pred. No. 97;
Matches 8; Conservative 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/487,558
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 446
SEQ ID NO 424
LENGTH: 503
                                                                                                                                                                                                                                           Sequence 424, Application US/09487558B Patent No. 6949356 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Saccharomyces cerevisiae US-09-487-558B-424
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                                                                                     1 TATEAQPSASSASTAAVAA 19
                                                                                                              Query Match
Best Local Similarity 47.4%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Milne, Todd
No. 6949356man,
                                                                                                                                                                                                                                                                                                            APPLICANT: Busby, Robert
APPLICANT: Cali, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
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TELLEFAX: 703-391-9035
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
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                                                                                                                                                                 US-07-812-421-2
                                                                             LENGTH:
                                                                                                                                                                                                                  Query Match
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US-07-812-421-2

Sequence 2, Application US/07812421

Sequence 2, Application US/07812421

Patent No. 5932697

GENERAL INFORMATION:

APPLICANT: Caceci, Thomas

APPLICANT: Szumanski, Maria B.W.

TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION

TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: WHITHAM, CURTIS & WHITHAM

STREET: Reston

STREET: Reston

STREET: Suite 900

CITY: Reston

STREET: WA

COUNTRY: USA

COUNTRY: USA

COMPUTER: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

CLASSIFICATION: 435

FILING DATE: 23-DBC-1991

CLASSIFICATION: WUMBER: US 07/588,437

FILING DATE: 25-SEP-1990

ATTORNEY, AGENT INFORMATION:

NAME: Whitham: Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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47.8%; Score 43; DB 1; Length 98;
Best Local Similarity 55.6%; Pred. No. 20;
Matches 10; Conservative 4; Mismatches 4; Indels
COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: IEM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/814,220

FILING DATE: 23-DEC-1991

CLASSIFICATION DATA:

PRICH APPLICATION DATA:

PRICH APPLICATION NUMBER: US 07/588,437

PILING DATE: 25-SEP-1990

ATTORNEY/AGENT INFORMATION:

NAME: Whitham, Michael E.

REGISTRATION NUMBER: 32,635

REGISTRATION NUMBER: 32,635

REGISTRATION NUMBER: 32,635

TELEPHONE: 703-391-2510

TELEPHONE: 703-391-2510

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LUMBTH: 98 aming acids
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REFERENCE/DOCKET NUMBER: CIT.016
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 || || :|::|:|| || 13 ATAATAAAAAATAAA 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-814-220-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
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RESULT 13

US-09-252-991A-23624

i Sequence 23624, Application US/09252991A

i Sequence 23624, Application US/09252991A

i Sequence 23624, Application US/09252991A

i Patent No. 6551795

i GENERAL INFORMATION:

ITILE OF INVENTION: MCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

ITILE OF INVENTION: MCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

ITILE OF INVENTION: MCHEIC ACID AND AMINO ACID SEQUENCES

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INCORDATION:
APPLICANT: MARC J. RUDEHIGELD et al.
APPLICANT: MARC J. RUDEHIC ACID AND ANINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARCIGICA AND THERAPEUTICS
TITLE OF INVENTION: ARCIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: 107196,136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32580
LENGTH: 143
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Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 107;
                                                                                                                                             47.8%; Score 43; DB 1; Length 98; 55.6%; Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43; DB 2;
Pred. No. 23;
3; Mismatches
                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 32880, Application US/09252991A ; Patent No. 6551795
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23624
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13 ATAATAAAAAATAATAA 30
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Best Local Similarity 66.7%;
Matches 10; Conservative
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: 98 amino acids
amino acid
                                                                                                                                                                                               10; Conservative
                                           TOPOLOGY: linear
MOLECULE TYPE: protein
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RESULT 15
US-09-270-767-31979
is Sequence 31979, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
i APPLICANT: Homburger et al.
i TITLE OF INVENTION: NUCLeic acids and proteins of Drosophila melanogaster
i TITLE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; NUMBER OF SEQ ID NOS: 62517
; NUMBER OF SEQ ID NOS: 62517
; SEQ ID NO 31979
; LENGTH: 184
; TYPE: PRT

i ORGANISM: Drosophila melanogaster
US-09-270-767-31979
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  0; Gaps
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  6; Indels
4; Mismatches
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                                                             1 TATEAOPSASSASTAAVAAN 20
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166 ESSESSSAAAAAVAA 181
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10; Conservative
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Sequence 167322, Sequence 1844, App Sequence 123073, Sequence 151154, Sequence 151154, Sequence 1182, App Sequence 14409, A Sequence 161, App Sequence 17, App Sequence 47, Ap

684, App 1965, Ap 123073, 151154, 359994,

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Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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APPLICANT: Smith, Daniel J.
APPLICANT: Taubman, Martin A.
TITIE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens
FILE REFERENCE: 25669-020
CURRENT APPLICATION NUMBER: US/10/797,821
CURRENT FILING DATE: 2004-03-09
PRIOR FILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: 60/363,209
PRIOR FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: 60/402,483
PRIOR FILING DATE: 2002-08-08
PRIOR FILING DATE: 2002-08-08
PRIOR FILING DATE: 2002-08-08
                                                                                                                                                                                                                                                                                                    ## Sequence 3, Application US/10383930

| Sequence 3, Application US/10383930
| Publication No. US20040127400A1
| GABERAL INFORMATION:
| APPLICANT: Smith, Daniel J
| APPLICANT: Taubman, Martin A
| TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein FILE REFERENCE: 25669-018
| CURRENT APPLICATION NUMBER: US/10/383,930
| CURRENT FILING DATE: 2003-03-07
| PRIOR PILING DATE: 2002-08-08
| PRIOR PILING DATE: 2002-08-08
| PRIOR FILING DATE: 2002-08-08
| PRIOR FILING DATE: 2002-08-08
| NUMBER OF SEQ ID NOS: 41
| SOFTWARE: Patentin Version 3.2
| SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 90; DB 4; Length 20; Best Local Similarity 100.0%; Pred. No. 4.5e-06; Matches 20; Conservative 0; Mismatches 0; Indels
US-10-437-963-167322
US-10-925-297-684
US-10-264-237-1965
US-10-437-963-123073
US-10-437-963-151154
US-10-0425-115-359994
US-10-0425-115-3599994
US-10-0425-115-3599994
US-10-0425-1182
US-11-097-143-38100
US-11-097-143-38100
US-11-097-143-38100
US-11-097-143-38100
US-10-210-988-161
US-10-217-551-161
US-10-217-551-161
US-10-217-551-161
US-10-217-551-161
US-10-217-988-17
US-10-945-095-161
US-10-945-096-47
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Publication No. US20050031633A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT; ORGANISM: Streptococcus mutans US-10-383-930-3
  RESULT 2
US-10-797-821-3
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   LENGTH: 20
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Sequence 45050, A
Sequence 121603,
Sequence 331255,
Sequence 331259,
Sequence 262085,
Sequence 53395, A
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Sequence 196822,
Sequence 313230,
                                                                                             (without alignments)
139.276 Million cell updates/sec
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                                                                                  January 25, 2006, 19:13:51 ; Search time 60 Seconds
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(cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/USIO8_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/USIO8_PUBCOMB.pep:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd
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US-10-797-821-29

US-10-797-821-29

US-10-797-821-30

US-10-797-821-31

US-10-383-930-31

US-10-797-821-31

US-10-797-821-31

US-10-797-821-31

US-10-797-821-33

US-10-425-115-331255

US-10-425-115-31255

US-10-425-114-53955

US-10-425-114-53955

US-10-425-114-53955

US-10-425-114-71651
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Maximum Match 100%
Listing first 45 summaries
                                                           - protein search, using sw model
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90
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Match Length DB
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US-10-425-115-313230

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RESULT 5
US-10-797-821-29
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                         LENGTH: 431
SEQ ID NO 30
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Publication No. US20040127400A1

GENERAL INFORMATION:

APPLICANT: Taubman, Martin A

TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein

FILE REFERENCE: 25669-018

CURRENT FILING DATE: 2003-03-07

PRIOR APPLICATION NUMBER: 60/402,483

PRIOR FILING DATE: 2002-08-08

NUMBER OF FILING DATE: 2002-08-08

NUMBER OF FILING DATE: 2002-08-08

SOFTWARE: PALCATION NUMBER: 60/363,209

PRIOR FILING DATE: 2002-08-08

SOFTWARE: PALCATION VOWER: 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 29, Application US/10383930
; Bedience 29, Application US/10383930
; Publication No. US20040127400A1
; GRERAL INFORMATION:
; APPLICANT: Taubman, Martin A
; TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
; FILE REPREBRUE: 25669-018
; CURRENT PILING DATE: 2003-03-07
; PRIOR PILING DATE: 2002-08-08
; PRIOR FILING DATE: 2002-08-08
; PRIOR FILING DATE: 2002-03-07
; PRIOR FILING DATE: 2002-03-07
; RIOR APPLICATION NUMBER: 60/363,209
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 29
; LENGTH: 431
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100.0%; Score 90; DB 4; Length 431;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                         Length 20;
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Best Local Similarity 100.0%; Pred. No. 4.5e-06;
Matches 20; Conservative 0; Mismatches 0;
  PRIOR FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: 60/081,550
PRIOR PILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.2
SEQ ID NO 3
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  306 TATEAQPSASSASTAAVAAN 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TATEAQPSASSASTAAVAAN 20
                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: GpbB peptide US-10-797-821-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-10-383-930-29
                                                                                                                                                                                                                                               ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-383-930-30
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                                                                                                                                                                                                                                                                         FEATURE:
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Sequence 29, Application US/10797821
; Sequence 29, Application US/10797821
; Publication No. US20050031633A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Daniel J.
; APPLICANT: Taubman, Martin A.
; TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens
; FILE REFERENCE: 25669-020
; CURRENT FILING DATE: 2004-03-09
; PRIOR FILING DATE: 2003-03-07
; PRIOR PELICATION NUMBER: 60/402,483
; PRIOR FILING DATE: 2002-03-07
; PRIOR FILING DATE: 2002-03-07
; PRIOR PELICATION NUMBER: 60/402,483
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 60/402,483
; PRIOR FILING DATE: 1999-04-12
; PRIOR FILING DATE: 1999-04-12
; PRIOR PILING DATE: 1999-04-13
; PRIOR FILING DATE: 1999-04-13
; PRIOR PILING DATE: 1999-04-13
; PRIOR PILING DATE: 1999-01-08
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; Squence 30, Application US/10797821
; Bublication No. US2005003163341
; GENERAL INPORMATION:
    APPLICANT: Smith, Daniel J.
    APPLICANT: Taubman, Martin A.
    TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens
    FILE REFERENCE: 2569-020
; CURRENT APPLICATION NUMBER: US/10/797,821
CURRENT FILING DATE: 2004-03-09
; PRIOR FILING DATE: 2003-03-07
; PRIOR FILING DATE: 2003-03-07
; PRIOR FILING DATE: 2003-03-07
; PRIOR PLICATION NUMBER: 60/363,209
; PRIOR PLICATION NUMBER: 60/402,483
; PRIOR PLING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 09/290,049
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                                                                                                          100.0%; Score 90; DB 4; Length 431; 100.0%; Pred. No. 0.00012; tive 0; Mismatches 0; Indels
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100.0%; Score 90; DB 5; L
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 20; Conservative 0; Mismatches 0;
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US-10-797-821-29
TYPE: PRT; ORGANISM: Streptococcus mutans US-10-383-930-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.2
SEQ ID NO 29
                                                                                            Query Match
Best Local Similarity 100.0°
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Gaps

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sequence 31, Application US/10797821

Sequence 31, Application US/10797821

Sequence 31, Application No. US2050031633A1

GENERAL INFORMATION:

APPLICANT: Smith, Daniel J.

APPLICANT: Smith, Daniel J.

TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens

FILE REFERENCE: 25669-200

CURRENT FILING DATE: 2004-03-09

PRIOR APPLICATION NUMBER: US/10/797,821

CURRENT FILING DATE: 2003-03-07

PRIOR PLILNG DATE: 2003-03-07

PRIOR PLILNG DATE: 2002-08-08

PRIOR FILING DATE: 1999-04-12

PRIOR PELING DATE: 1999-04-12

PRIOR FILING DATE: 1999-04-13

PRIOR PELING DATE: 1999-04-13

PRIOR PILING DATE: 1999-04-13
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| Sequence 32, Application US/10797821
| Publication No. US20050031633A1
| Publication No. US20050031633A1
| REBERRAL INFORMATION:
| APPLICANT: Smith, Daniel J. |
| APPLICANT: Taubman, Martin A. |
| TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens |
| FILE REFERENCE: 25669-020 |
| CURRENT APPLICATION NUMBER: US/10/797,821 |
| CURRENT FILING DATE: 2004-03-09 |
| PRIOR FILING DATE: 2003-03-07 |
| PRIOR PLING DATE: 2003-03-07 |
| PRIOR PLING DATE: 2002-03-07 |
| PRIOR APPLICATION NUMBER: 60/402,483 |
| PRIOR PLING DATE: 1999-04-12 |
| PRIOR APPLICATION NUMBER: 60/402,483 |
| PRIOR APPLICATION NUMBER: 60/402,483 |
| PRIOR APPLICATION NUMBER: 60/402,483 |
| PRIOR APPLICATION NUMBER: 60/091,550 |
| PRIOR APPLICATION NUMBER: 60/091,550 |
| PRIOR APPLICATION NUMBER: 60/081,550 |
                                                                                                                                                                             Query Match 93.3%; Score 84; DB 4; Length 432; Best Local Similarity 95.0%; Pred. No. 0.0009; Matches 19; Conservative 0; Mismatches 1; Indels
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Best Local Similarity 95.0%; Pred. No. 0.0009;
Matches 19; Conservative 0; Mismatches 1; Indels
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                                                        ; ORGANISM: Streptococcus mutans US-10-383-930-32
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LENGTH: 432
                     TYPE: PRT
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### Sequence 31, Application US/10383930

### Publication No. US20040127400A1

### Sequence 31, Application US/10383930

### Sequence 31, Application NO. US20040127400A1

### APPLICANT: Smith, Daniel J

### APPLICANT: Taubman, Martin A

### TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein

### FILE REFERENCE: 25669-018

### CURRENT APPLICATION NUMBER: US/10/383,930

### CURRENT FILING DATE: 2002-03-07

### PRIOR PILING DATE: 2002-08-08

### PRIOR PILING DATE: 2002-08-08

### PRIOR PILING DATE: 2002-03-07

### NUMBER OF SEQ ID NOS: 41

### SOFTWARE: PatentIn version 3.2

### SOFTWARE: PATENTING NUMBER: OF SEQ ID NOS: 41

### CORGANT: ASS

### CORGANT: A
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; Sequence 32, Application US/10383930
; Publication No. US20040127400A1
; GRNERAL INFORMATION:
APPLICANT: Smith, Daniel J
APPLICANT: Taubman, Martin A
; TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
FILE REPERENCE: 25669-018
; CURRENT APPLICATION NUMBER: US/10/383,930
; CURRENT PILING DATE: 2003-03-07
; PRIOR FILING DATE: 2002-08-08
; PRIOR PLICATION NUMBER: 60/402,483
; PRIOR PLICATION NUMBER: 60/402,483
; PRIOR PLICATION NUMBER: 60/402,483
; PRIOR PLICATION NUMBER: 60/363,209
; PRIOR PLICATION NUMBER: 60/363,209
; RUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin version 3.2
; LENGTH: 432
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Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 20; Conservative 0; Mismatches 0;
PRIOR FILING DATE: 1999-04-12
PRIOR PLING DATE: 1998-04-13
PRIOR FILING DATE: 1998-04-13
PRIOR PILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.2
SEQ ID NO 30
LENGTH: 431
TYPE: PRI
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Best Local Similarity 95.04
Matches 19; Conservative
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US-10-383-930-32
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RESULT 13
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                                                                                                                                              TYPE: PRT
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CURRENT APPLICATION NUMBER: US/10/797,821
CURRENT FILING DATE: 2004-03-09
PRIOR APPLICATION NUMBER: US/383,930
PRIOR FILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: 60/363,209
PRIOR FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: 60/302,483
PRIOR FILING DATE: 2002-08-08
PRIOR FILING DATE: 2002-08-08
PRIOR FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: 60/402,483
PRIOR FILING DATE: 1999-04-12
PRIOR FILING DATE: 1999-04-12
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Publication No. US20040127400A1

GENERAL INFORMATION:
APPLICANT: Smith, Daniel J
APPLICANT: Taubman, Martin A
ITILE OF INVENTION: Immunogenicity of Glucan Binding Protein
FILE REFERENCE: 25669-018
CURRENT APPLICATION: NUMBER: US/10/383,930
CURRENT APPLICATION: NUMBER: 06/402,483
FRIOR APPLICATION NUMBER: 60/402,483
FRIOR APPLICATION NUMBER: 60/363,209
PRIOR FILING DATE: 2002-08-08
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.2
SEQ ID NO 33
LENGTH: 431
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PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION WUMBER: 60/115,142
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.2
SEQ ID NO 32
LENGTH: 432
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Publication No. US20050031633A1
GENERAL INFORMATION:
APPLICANT: Smith, Daniel J.
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US-10-383-930-33
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Sequence 18, Application US/10797821
; Sequence 18, Application US/10797821
; General INPORMATION:
; APPLICANT: Smith, Daniel J.
; APPLICANT: Taubman, Martin A.
; TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens
; TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens
; TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens
; FILE REFERENCE: 25669-020
; FILING DATE: 2004-03-09
; RIOR APPLICATION NUMBER: 60/402,483
; PRIOR FILING DATE: 2002-03-07
; PRIOR PILING DATE: 2002-03-07
; PRIOR PILING DATE: 2002-03-07
; PRIOR PILING DATE: 1999-04-12
; PRIOR PILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: 60/01,550
; PRIOR APPLICATION NUMBER: 60/01,550
; PRIOR APPLICATION NUMBER: 60/01,550
; PRIOR APPLICATION NUMBER: 60/01,550
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; Sequence 18, Application US/10383930
; Publication No. US20040127400A1
; GENERAL INFORMATION:
; APPLICANT: Smitch, Daniel J
; APPLICANT: Taubman, Martin A
; TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
; FILE REFERENCE: 25669-018
; CURRENT FILING DATE: 2003-03-07
; PRIOR PAPLICATION NUMBER: 60/402,483
; PRIOR APPLICATION NUMBER: 60/402,483
; PRIOR APPLICATION NUMBER: 60/363,209
; RIOR APPLICATION NUMBER: 60/363,209
; RIOR PILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 18
; LENGTH: 20
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Pred. No. 0.0086;
0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.2
SEQ ID NO 33
                                                                                                                                                                                                                                                                                                                                                                                                                                             306 TATEAQPSASSASTAVVTAN 325
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Best Local Similarity 100.0%; P.
Matches 15; Conservative 0;
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US-10-797-821-33
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## APPLICANT: venter, J. Clays
### APPLICANT: et al.
### TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
### TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
### TITLE OF INVENTION: DROSOPHILA GENES.
### TITLE OF INVENTION: DROSOPHILA GENES.
### TITLE OF INVENTION: DROSOPHILA GENES.
### TITLE OF INVENTION: DROSOPHILA GENES.
### TITLE OF INVENTION: DROSOPHILA GENES.
### CURRENT APPLICATION NUMBER: US/11/097,143
### CURRENT APPLICATION NUMBER: 60/167,832
### RRIOR FILING DATE: 1999-10-05
### PRIOR FILING DATE: 1999-10-19
### PRIOR FILING DATE: 1999-11-12
### PRIOR FILING DATE: 1999-11-12
### PRIOR FILING DATE: 1999-11-12
### PRIOR FILING DATE: 1999-11-12
### PRIOR FILING DATE: 1999-11-12
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### PRIOR FILING DATE: 1999-11-12
### PRIOR FILING DATE: 1999-11-12
### PRIOR FILING DATE: 2000-01-12
### PRIOR FILING DATE: 2000-01-12
### PRIOR FILING DATE: 2000-02-24
### PRIOR FILING DATE: 2000-03-23
### PRIOR FILING DATE: 2000-03-23
### NUMBER OF SEQ ID NOS: 43008
### SEQ ID NOS: 43008
### SEQ ID NOS: 43008
### SEQ ID NOS: 43008
### LENGTH: 291
### PRIOR PAPELS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 74.4%; Score 67; DB 5; Length 20; Best Local Similarity 100.0%; Pred. No. 0.0086; Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 30285, Application US/11097143; Publication No. US20050208558A1; GENERAL INFORMATION:
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112 TSTSPTPNASSSSTAAVA 129
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
I LENGTH: 20
TYPE: PRT
CORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                         CTHER INFORMATION: GbpB peptide US-10-797-821-18
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US-11-097-143-30285
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Search completed: January 25, 2006, 20:10:01 Job time : 60 Becs

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Best Local Similarity 100.
Matches 20; Conservative
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Sequence 1668, Ap
Sequence 77, Appl
Sequence 88, Appl
Sequence 70, Appl
Sequence 72, Appl
Sequence 72, Appl
Sequence 72, Appl
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Sequence 7150, Ap
Sequence 3, Appli
Sequence 6, Appli
Sequence 874, App
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150, App
6, Appli
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                                                                 January 25, 2006, 19:15:26; Search time 5.5 Seconds (without alignments) 39.378 Million cell updates/sec
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Sequence 208;
Sequence 50, A
Sequence 4476,
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Sequence 150,
Sequence 6, A
Sequence 32,
Sequence 77,
Sequence 127,
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1: /cgn2 6/ptodata/2/pubpaa/USOB NEW PUB.pep:*
2: /cgn2 6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*
3: /cgn2 6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*
4: /cgn2 6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*
5: /cgn2 6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*
6: /cgn2 6/ptodata/2/pubpaa/USO10 NEW PUB.pep:*
7: /cgn2 6/ptodata/2/pubpaa/USO10 NEW PUB.pep:*
8: /cgn2 6/ptodata/2/pubpaa/USO10 NEW PUB.pep:*
8: /cgn2 6/ptodata/2/pubpaa/USO0 NEW PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-10-821-234-1668

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US-11-156-084-72

US-11-156-084-136

US-11-156-084-136

US-11-156-084-136

US-11-156-084-136

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US-11-156-084-136

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26 38 42.2 357 6 US-10-821-234-1325 Sequence 1325, App 28 42.2 383 7 US-11-168-874-10 Sequence 10, Appl 29 38 42.2 477 7 US-11-168-874-12 Sequence 261, Appl 29 38 42.2 512 6 US-10-6517-939-261 Sequence 261, Appl 31 38 42.2 512 6 US-10-517-939-236 Sequence 236, Appl 32 38 42.2 579 6 US-10-131-826A-219 Sequence 236, Appl 33 38 42.2 1076 6 US-10-131-826A-219 Sequence 31, Appl 34 27.5 41.7 590 6 US-10-93-554A-83 Sequence 31, Appl 37.5 41.7 580 6 US-10-93-554A-83 Sequence 31, Appl 37.5 41.7 580 6 US-10-975-798 Sequence 31, Appl 37.5 41.7 580 6 US-10-975-798 Sequence 224, Appl 37 41.1 286 7 US-11-150-054A-5 Sequence 224, Appl 40 37 41.1 286 7 US-11-103-052-11 Sequence 11.08, Appl 42 37 41.1 319 6 US-10-30-30-21 Sequence 11, Appl 42 37 41.1 319 6 US-10-99-554A-193 Sequence 11, Appl 43 37 41.1 319 6 US-10-995-554A-193 Sequence 11, Appl 43 37 41.1 407 6 US-10-995-554A-193 Sequence 2, Appl 44 37 41.1 430 6 US-10-995-561-1014 Sequence 2, Appl 54 37 41.1 431 7 US-11-169-013-2 Sequence 2, Appl 54 37 41.1 431 7 US-11-169-013-2 Sequence 2, Appl 54 37 41.1 431 7 US-11-169-013-2 Sequence 2, Appl 54 37 41.1 431 7 US-11-169-013-2 Sequence 2, Appl 54 37 41.1 431 7 US-11-169-013-2 Sequence 2, Appl 54 37 41.1 431 7 US-11-169-013-2 Sequence 2, Appl 54 37 41.1 431 7 US-11-169-013-2 Sequence 2, Appl 54 37 41.1 431 7 US-11-169-013-2 Sequence 2, Appl 54 37 41.1 431 7 US-11-169-013-2 Sequence 2, Appl 54 37 41.1 431 7 US-11-169-013-2 Sequence 2, Appl 54 37 41.1 431 7 US-11-169-013-2 Sequence 2, Appl 54 37 41.1 431 7 US-11-169-013-2 Sequence 2, Appl 54 37 41.1 431 7 US-11-169-013-2 Sequence 2, Appl 54 37 41.1 431 7 US-11-169-013-2 Sequence 2, Appl 54 37 41.1 431 7 US-11-169-013-2 Sequence 2, Appl 54 37 41.1 431 7 US-11-169-013-2 Sequence 2, Appl 54 37 41.1 431 7 US-11-169-013-2 Sequence 2, Appl 54 37 41.1 431 7 US-11-169-013-2 Sequence 3, Appl 54 37 41.1 431 7 US-11-169-013-2 Sequence 3, Appl 54 37 41.1 431 7 US-11-169-013-2 Sequence 3, Appl 54 37 41.1 431 7 US-11-169-013-2 Sequence 3, Appl 54 37 41.1 431 7 US-11-169-013-2 Sequence 3, Appl
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ALIGNMENTS

RESULT 2
US-10-821-234-1668

i Sequence 1668

j Sequence 1668

s Cancer 1668

publication No. US20050255114A1

i GENERAL INFORMATION:

APPLICANT: Labat, Ivan

APPLICANT: Adarmani, Susan

APPLICANT: Tang, Y. Tom

APPLICANT: Tang, Y. Tom

APPLICANT: Application NUMBER: US/10/821,234

CURRENT APPLICATION NUMBER: US 60/462,047

PRIOR PILING DATE: 2003-04-07

NUMBER OF SEQ ID NOS: 1704

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Query Match
Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                    LENGTH: 150
TYPE: PRT
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1. Sequence 88. Application US/11156084

1. Sequence 88. Application US/11156084

2. Sequence 88. Application US/11156084

3. Sequence 88. Application No. US20060010515A1

3. GENERAL INFORMATION:

4. TITLE OF INVENTION:

5. TITLE OF INVENTION:

6. CHRENT APPLICATION NUMBER: US/11/156,084

7. CURRENT PILING DATE:

7. CURRENT PILING DATE:

7. NUMBER OF SEQ ID NOS: 364

7. SOFTWARE: Patentin version 3.2

7. SEQ ID NO 88

7. LENGTH: 139
                                                                                                                                                                                                                                                                                                       Sequence 77, Application US/11156084
Publication No. US20060010515A1
GENERAL INFORMATION:
TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads to TITLE OF INVENTION: agronomically interesting phenotypes
FILE REFERENCE: (38-21)
CURRENT FILING DATE: 2005-06-17
NUMBER OF SEQ ID NOS: 364
SEQ ID NO 77
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Pred. No. 1.3;
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Pred. No. 2.1;
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SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 1668
LENGTH: 441
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; ORGANISM: Zea mays subsp. mays
US-11-156-084-88
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2 AHPSAAAVSSTALAAN 17
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Best Local Similarity 84.6%;
Matches 11; Conservative
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Best Local Similarity 56.27
Conservative
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                                                   TYPE: PRT
ORGANISM: Homo sapiens
US-10-821-234-1668
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Best Local Similarity
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US-11-156-084-77
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RESULT 5

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NS-11-156-084-72

Sequence 72, Application US/11156084

Publication No. US20060010515A1

GENERAL INFORMATION:

APPLICANT: Monsanto Technology LLC

TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads to

TITLE OF INVENTION: OCONTROlled expression of cytokinin biosynthetic genes leads to

TITLE OF INVENTION: UNMBER: US/11/156,084

CURRENT APPLICATION WUMBER: US/11/156,084

CURRENT FILING DATE: 2005-06-17

NUMBER OF SEQ ID NOS: 364

SOFTWARE: Patentin version 3.2

SEQ ID NO 72

LENGTH: 168

TYPE: PRT

CREANISM: Zea mays subsp. mays

FEATURE:
Sequence 70. Application US/11156084

Publication No. US20060010515A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Monsanto Technology LLC
APPLICANT: Monsanto Technology LLC
TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads to
TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads to
TITLE OF INVENTION: Agronomically interesting phenotypes
TITLE APPLICATION NUMBER: US/11/156,084
CURRENT APPLICATION NUMBER: US/11/156,084
CURRENT FILING DATE: 2005-06-17
NUMBER OF SEQ ID NOS: 364
SOFTWARE: Patentin version 3.2
SEQ ID NO 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 75, Application US/11156084
Sequence 75, Application US/11156084
Publication No. US20060010515A1
GENERAL INFORMATION:
TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads to TITLE OF INVENTION: agronomically interesting phenotypes
FILE REFERENCE: (38-21)
CURRENT PILING DATE: 2005-06-17
NUMBER OF SEQ ID NOS: 364
SOFTWARE: Patentin version 3.2
SEQ ID NO 75.
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ilarity 56.2%; Pred. No. 1.8;
Conservative 4; Mismatches
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THILE MERERACKS: P3330RL2128

CURRENT APPLICATION NUMBER: 05/049911

PRIOR PELICATION NUMBER: 60/049911

PRIOR PELICATION NUMBER: 60/056974

PRIOR PELICATION NUMBER: 60/056974

PRIOR PELING DATE: 1997-08-18

PRIOR APPLICATION NUMBER: 60/059113

PRIOR PELING DATE: 1997-09-17

PRIOR PELING DATE: 1997-09-17

PRIOR PELING DATE: 1997-09-17

PRIOR PELING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059127

PRIOR APPLICATION NUMBER: 60/059127

PRIOR PELING DATE: 1997-09-17

PRIOR PELING DATE: 1997-09-18

PRIOR PELING DATE: 1997-09-19

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P330R1C128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gарв
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2; Mismatches
                                                                                                                                                                              Sequence 208, Application US/10131826A, Publication No. US20050245730A1, GENERAL INFORMATION:
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2 AHPSAAAVSSTALAAN 17
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Tumas, Daniel
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Matches 10; Conservative
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritgen, Mary E.
                                                                                                                                                                                                                                                      APPLICANT: Baker, Kevin P. APPLICANT: Beresini, Maureen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Watanabe, Colin K
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Sherwood, Steven
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                                                                                                                                                              US-10-131-826A-208
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US-10-467-657-50
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 135, Application US/11156084
Publication No. US20060010515A1
GENERAL INFORMATION:
APPLICANT: Monsento Technology LLC
TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads to TITLE OF INVENTION: agronomically interesting phenotypes
FILE REPRENCE: (38-21)
CURRENT APPLICATION NUMBER: US/11/156,084
CURRENT FILING DATE: 2005-06-17
NUMBER OF SEQ ID NOS: 364
SOUTHWARE: Patentin version 3.2
SEQ ID NO 136
LENGTH: 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Monsanto Technology LLC
TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads to
TITLE OF INVENTION: agronomically interesting phenotypes
FILE REFERENCE: (38-21)
CURRENT APPLICATION NUMBER: US/11/156,084
CURRENT PILING DATE: 2005-06-17
NUMBER OF SEQ ID NOS: 364
SOFTWARE: Patentin version 3.2
SEQ ID NO 135
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; NAME/KEY: misc feature
; LOCATION: (160)...(160)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid; FEATURE;
; NAME/KEY: misc feature
; LOCATION: (162)...(162)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid; US-11-156-084-72
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// InCATION: (195)...(195)

// OTHER INFORMATION: Xaa can be any naturally occurring amino acid

US-11-156-084-136
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Matches 9; Conservative
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Best Local Similarity 56.2
Matches 9; Conservative
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; ORGANISM: Zea mays
US-11-156-084-135
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US-11-156-084-135
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CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 7150
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Pred. No. 11;
1; Mismatches 1; Indels
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; Sequence 4476, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASTGNANI Vega
APPLICANT: MASTGNANI Vega
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
               APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
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CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 4476
LENGTH: 387
                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SEQWIN99, Version 1.04
SEQ ID NO 50
LENGTH: 387
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; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-50
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Best Local Similarity 83.3%;
Matches 10; Conservative
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Matches 10; Conservative
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GENERAL INFORMATION:
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US-10-467-657-7150
                                                                                                                                             FILE REFERENCE:
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APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNACI Bliabbetta
APPLICANT: MONACI Bliabbetta
IIILE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

Sequence 7150, Application US/10467657 Publication No. US20050260581A1 GENERAL INFORMATION:

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Sequence 3, Application US/11052554A

Sequence 3, Application US/11052554A

Sequence 3, Application No. US20050288866A1

GENERAL INFORMATION:
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
TITLE OF INVENTION: UNMBER: US/11/052,554A

CURRENT APPLICATION NUMBER: US 60/589,227

PRIOR PILING DATE: 2004-07-20

PRIOR FILING DATE: 2004-07-20

PRIOR FILING DATE: 2004-07-20

PRIOR FILING DATE: 2004-07-20

NUMBER OF SEQ ID NOS: 763

SEQ ID NOS: 763

SED ID NO 3.
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Publication No. US20060010518A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: FELDMANN, Kenneth A
APPLICANT: THEISS, Noah
TITLE OF INVENTION: NUCLECTIOE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL FOR
TITLE OF INVENTION: MODIFYING PLANT CHARACTERISTICS
TITLE OF INVENTION: MODIFYING PLANT CHARACTERISTICS
FILE REFERENCE: 2750-1597PUS2
CURRENT APPLICATION NUMBER: 006-05-27
CURRENT APPLICATION NUMBER: 60/575,183
PRIOR APPLICATION NUMBER: 60/575,183
PRIOR FILING DATE: 2004-05-27
NUMBER: OF SEQ ID NOS: 8
SOUTWARE: Patentin version 3.3
SEQ ID NO 6
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                                                                                              47.8%; Score 43; DB 6; Length 387; 83.3%; Pred. No. 11; animative 1; Mismatches 1; Indels
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TYPE: PRT
CRGANISM: Neisseria gonorrhoeae
US-10-467-657-7150
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Best Local Similarity 83...
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Matches 10; Conservative
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US-11-139-425-6
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; TYPE: PRT
; ORGANISM: Oryza sativa (japonica cultivar-group)
US-11-139-425-6
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^{0;} Gaps Query Match
45.6%; Score 41; DB 7; Length 406;
Best Local Similarity 42.1%; Pred. No. 22;
Matches 8; Conservative 7; Mismatches 4; Indels

¹ TATEAQPSASSASTAAVAA 19 |::||||::||| 73 TSSAPSPSASASASAA 91

Search completed: January 25, 2006, 20:11:07 Job time: 5.5 secs

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The present sequence is that of a peptide comprising amino acid residues 6-25 of the glucan binding protein-B (GbpB) of Streptococcus mutans strain SK13 ADD91649. The peptide binds to a major histocompatibility complex (MHC) class II protein. It was identified as a potential B cell epitope using a matrix-based algorithm for epitope prediction, which was used to search the primary amino acid sequence of GbpB for known MHC class II binding motifs. The peptide can be used in immunogenic compositions and subunit vaccines for dental caries. These comprise MHC class II protein-binding GbpB peptides covalently linked with peptide subunits (preferably from the catalytic domain) of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Diepitopic or multiepitopic polypeptides can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
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ADF06779
ADR06447
ADR66447
ADR66724
ADF67204
ADF0716
ABP0145
ABP01530
ABP01530
ABP45815
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Taubman MA;
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WO2003075845-A2
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  Smith DJ,
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Copyright (c) 1993 - 2006 Compugen Ltd.
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Database

Result No.

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RESULT 2

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ADD93649 standard; protein; 431 AA.
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08-AUG-2002; 2002US-0402483P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MfC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
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prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in passive immunisation.
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                                                                                                                                                                                                                                                                                                                            immunogenicity; immune stimulation; glucan binding protein-B; microparticle; major histocompatibility complex; tooth disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 85; DB 9; Length 20;
Pred. No. 4.7e-06;
; Mismatches 0; Indels
                                                                               ch 100.0%; Score 85; DB 7; Length 20; Similarity 100.0%; Pred. No. 4.7e-06; 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                      Streptococcus mutant glucan binding protein B peptide #4.
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                                                                                                                                                                                                                          ADX37247 standard; peptide; 20 AA
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08-JAN 1999; 99US-0115142P.
12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-0363209P.
08-AUG-2003; 2003US-0402483P.
07-MAR-2003; 2003US-00383930.
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(TAUB/) TAUBMAN M A.
                                                                                                                                                                                                                                                                                                                                                                    Streptococcus mutans
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Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
Streptococcus mutans glucan binding protein-B.
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WPI; 2003-845091/78

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The present sequence is the protein sequence of the glucan binding protein. B (GDpB) of Streptococcus mutans strain SK32. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions comprise major histocompatibility complex (WHC) class II protein-binding GbpB peptides, especially HLA-binding peptides, cowplently linked with peptide subunits of a glucosyltransferase. The antibody in a mammal. Dispitopic or multiepitopic polypeptides can be prepared synthetically or by recombinant bNA technology. Antibodies
                                                  Composition useful as vaccines for dental caries comprises a fragmefit of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
                                                                                                                                               Claim 6; Page 7; 49pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                           passive immunisation.
                   GENBANK; AY046410
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> 1 LSAVLVSGVTLSSATTLSAV 20 6 LSAVLVSGVTLSSATTLSAV Query Match
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ADD93650; RESULT 4 ADD93650

ADD93650 standard; protein; 431 AA. (first entry) 29-JAN-2004

Streptococcus mutans glucan binding protein-B.

Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunògen.

Streptococcus mutans

WO2003075845-A2

18-SEP-2003

07-MAR-2003; 2003WO-US006962

07-MAR-2002; 2002US-0363209P.

(FORS-) FORSYTH INST.

Taubman MA; Smith DJ,

GENBANK; AY046411.

WPI; 2003-845091/78.

Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein. Claim 5; Page 8; 49pp; English.

The The present sequence is the protein sequence of the glucan binding protein-B (GbpB) of Streptococcus mutans strain 3VR4. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes, includes immunogenic compositions and vaccines for dental novention provides immunogenic compositions

ö caries. The compositions comprise major histocompatibility complex (MHC) class II protein-binding GDpB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Dispitopic or multieptropic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GDpB can be used in Gaps ; 100.0%; Score 85; DB 7; Length 431; 100.0%; Pred. No. 0.00022; ive 0; Mismatches 0; Indels LSAVLVSGVTLSSATTLSAV 25 1 LSAVLVSGVTLSSATTLSAV 20 20; Conservative immunisation. Best Local Similarity Sequence 431 AA; Query Match passive Matches

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ADD93653 standard; protein; 431 AA 29-JAN-2004 (first entry) ADD93653; ADD93653 RESULT

Streptococcus mutans glucan binding protein-B.

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Gaps

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; Score 85; DB 7; I ; Pred. No. 0.00022; 0; Mismatches 0;

100.0%;

Length 431; Indels

Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen. Streptococcus mutans

WO2003075845-A2.

18-SEP-2003

07-MAR-2003; 2003WO-US006962.

07-MAR-2002; 2002US-0363209P.

(FORS-) FORSYTH INST.

Taubman MA; Smith DJ,

WPI; 2003-845091/78. GENBANK; AY046414

gment of complex dental caries comprises a fragment to a major histocompatibility compl Composition useful as vaccines for a glucan binding protein-B binding class II protein.

5; Page 8-9; 49pp; English. Claim The present sequence is the protein sequence of the glucan binding protein—B (GDpB) of Streptococcus mutans strain SSM3. The sequence includes a number of human leucocyta antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions comprise major histocompatibility complex (MHC) class II protein-binding GDpB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Dispitopic or multiphtopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GDpB can be used in immunisation. passive

Sequence 431 AA;

Score 85; DB 7; Length 431; Pred. No. 0.00022; 100.0%; Query Match Best Local Similarity us-10-797-821-4.rag

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The invention relates to a composition comprising a fragment of a glucan binding protein-B (GbpB) and a biocompatible microparticle, where the fragment binds to a major histocompatibility complex (MHC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds to a Streptococcus mutans GbpB protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
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microparticle; major histocompatibility complex; tooth disease.
                                                               immunogenicity, immune stimulation, glucan binding protein-B; microparticle; major histocompatibility complex; tooth disease.
                                 Streptococcus mutant glucan binding protein B variant #2.
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100.0%; Pred. No. 0.00022;
ive 0; Mismatches 0;
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12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-0363209P.
08-AUG-2002; 2002US-0402483P.
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21-APR-2005 (first entry)
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les 20; Conservative
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(TAUB/) TAUBMAN M A.
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microparticle; major histocompatibility complex; tooth disease
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08-JAN-1999; 99US-0115142P.
12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-0363209P.
08-AUG-2002; 2002US-0402483P.
07-MAR-2003; 2003US-00383930.
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Best Local Similarity 100،۰
Best Local Similarity 200،۰
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 Conservative
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(TAUB/) TAUBMAN M A.
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Gaps

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Indels

Length 431;

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The present invention relates to a computational method (MI) for identifying adhesin and adhesin-like proteins, by computing the sequence-based attributes of protein sequences using five attribute modules of a neural network software, training an artificial neural network software, training an artificial neural network software, training an artificial neural network (PRM) for each of the computed five attributes, and identifying the adhesin and adhesin and adhesin-like proteins as set of 274 annotated genes concoding adhesin and adhesin-like proteins, having 274 fully defined 162-concoding adhesin and adhesin-like proteins, having 105 hypothetical defined 306-18876 base pairs (SEQ ID NO: 385-58) sequences; a set of 105 hypothetical defined 306-18876 base pairs (SEQ ID NO: 1279); a set of 105 hypothetical adhesin and adhesin-like proteins, having 105 fully defined 53-3716 base pair (SEQ ID NO: 1-279); a set of 105 hypothetical adhesin and adhesin-like proteins, having 105 fully defined 106-5291 base pair (SEQ ID NO: 289-384) sequences; and a fully connected multilayer feed forward ANN (I) based on (MI). (MI) is useful for identifying and short-liketing proteins for further testing in development of new vaccine formulations concerns for identifying putative adhesins pathogenic organisms. (MI) is useful for identifying putative adhesins that are important in development of agastic ulcer and urinary tract infections. (MI) identifies adhesins from distantly related organisms, and from bacteria belonging to a wide continuacy proteins. (MI) is capable of predicting adhesive nature of phylogenetic spectrum. (MI) is capable of predicting adhesive nature of the phylogenetic spectrum. (MI) is capable of predicting adhesive nature of continuacy in the present sequence is a microbial pathogen adhesin
    Computational method for identifying adhesin and adhesin like molecules, comprises computing sequence-based attributes of protein sequences using neural network software and training an artificial neural network.
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Pred. No. 0.00022;
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GENBANK; AY046413.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a composition comprising a fragment of a glucan binding protein-B (GppB) and a biocompatible microparticle, where the fragment binds to a major histocompatibility complex (MHC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds to a Streptococcus mutans GbpB protein of the invention.
                                                                                                                                                                                                                                                                                                                                                   New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; SEQ ID NO 33; 73pp; English.
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99US-0115142P.
99US-00290049.
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20-JUL-2004; 2004US-0589227P
09-MAR-2004; 2004US-00797821
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Matches 20; Conservative
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TAUBMAN M A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 431 AA;
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                                      13-APR-1998;
08-JAN-1999;
12-APR-1999;
07-MAR-2002;
08-AUG-2002;
                                                                                                                                                      07-MAR-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-AUG-2005
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                                                                                                                                                                                             (SMIT/)
(TAUB/)
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The present sequence is the protein sequence of the glucan binding protein—B (GbpB) of Streptococcus mutans strain 38N1. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions comprise major histocompatibilty complex (MHC) class II protein-binding GbpB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The antibody in a mammal. Dispitopic or multipeltopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing
           Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunogenicity; immune stimulation; glucan binding protein-B;
microparticle; major histocompatibility complex; tooth disease.
                                                                                                                                                                                                                                                                                                                                  Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus mutant glucan binding protein B variant #4.
                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                  Score 85; DB 7; I
Pred. No. 0.00022;
                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADX37275 standard; protein; 432 AA
                                                                                                                                                                                                                                                                                                                                                                                              20
                                                                                                                                                                                                                                                                                                                                                                                                                          6 LSAVLVSGVTLSSATTLSAV 25
                                                                       5; Page 8; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                              LSAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mammals against dental caries
                                                                                                                                                                                                                                                                                                                                Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 20; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0115142P.
99US-00290049.
2002US-0363209P.
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2003US-00383930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SMIT/) SMITH D J.
(TAUB/) TAUBMAN M A.
                                                                                                                                                                                                                                                                      passive immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2005-151644/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus mutans
                                                                                                                                                                                                                                                                                                     Sequence 432 AA;
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12-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADX37275;
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                                                                     Claim
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The present sequence is the protein sequence of the glucan binding protein-B (GbpB) of Streptococcus mutans strain 15JP2. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The includes a number of numunogenic compositions and vaccines for dental caries. The compositions comprise major histocompatibility complex (MHC) class II protein-binding GbpB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Dispitopic or multiplicpic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in
The invention relates to a composition comprising a fragment of a glucan binding protein-B (GbpB) and a biocompatible microparticle, where the fragment binds to a major histocompatibility complex (MHC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds to a Streptococcus mutans GbpB protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
                                                                                                                                                                                          Gaps
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                                                                                                                                                          100.0%; Score 85; DB 9; Length 432; 100.0%; Pred. No. 0.00022;
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                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus mutans glucan binding protein-B.
                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                      ADD93651 standard; protein; 432 AA
                                                                                                                                                                                                                               1 LSAVLVSGVTLSSATTLSAV 20
                                                                                                                                                                                                                                                  Claim 5; Page 8; 49pp; English.
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                                                                                                                                                                                            20; Conservative
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Matches 19; Conserv
                                                                                                                                                                          Sest Local Similarity
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                                                                                                                       Sequence 432 AA;
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                                                                                                                                                           Query Match
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Claim 3; SEQ ID NO 32; 73pp; English.

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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus progenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory cativity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and activity antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used to recombinantly produce (I) and may be streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity
                                     Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antihflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
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                                                                                                                                                                                                                                                                                                                                                                                                           Fraser C;
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Pred. No. 0.11;
2; Mismatches
   Streptococcus polypeptide SEQ ID NO 1014.
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24-NOV-2000; 2000GB-00028727.
                                                                                                                                                                                                                                 29-OCT-2001; 2001WO-GB004789
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Hes 15; Conservative
                                                                                                                                                                                                                                                                                                                                               CHIRON SPA.
INST GENOMIC RES
                                                                                                                 Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus proteins
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Tettelin H;
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                                                                                                                                                                                                                                                                                                                                               (CHIR-)
                                                                                                                                                                                                                                                                                                                                                                   (GENO-)
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Matches
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   셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing
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0
                                                                                                                                                                                                                                                                                     immunogenicity; immune stimulation; glucan binding protein-B;
microparticle; major histocompatibility complex; tooth disease.
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                                                                                                                                                                                                                                                 Streptococcus mutant glucan binding protein B variant #3.
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                                                                                                                             ADX37274 standard; protein; 432 AA.
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                   LSAVLVSGVTLSSATTLSAI 25
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LSAVLVSGVTLSSATTLSAV
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990S-0115142P.
990S-00290049.
2002US-0363209P.
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                                                                                                                                                                                                                                                                                                                                               Streptococcus mutans
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TAUBMAN M A.
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08-JAN-1999;
12-APR-1999;
07-MAR-2002;
08-AUG-2002;
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                                                                                                                                                                     ADX37274;
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Matches
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This invention describes a novel nucleic acid molecule encoding a hyperimmune serum reactive antigen or its fragment from Streptococcus pyogenes. The nucleic acid molecule or hyperimmune serum-reactive antigen or its fragment are useful for the manufacture of a pharmaceutical preparation, especially a vaccine, against S. pyogenes infection. In addition, the hyperimmune serum reactive antigen or fragment is used for the isolation and/or purification and/or identification of an interaction partner of the hyperimmune serum reactive antigen or its fragment, for the generation of a peptide (e.g. anticalines) binding to the antigen or it fragment, or for the manufacture of a functional nucleic acid selected from aptamers and spiegelmers. The nucleic acid molecule may also be used for the manufacture of functional ribonucleic acids, such as ribozymes, pyogenes hyperimmune serum reactive antigens, fragments and the encoding polynucleotide described in the invention.
                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid molecules encoding hyperimmune serum-reactive antigens from Streptococcus pyogenes, useful for diagnosing, preventing and treating S. pyogenes infections.
                                                                                                                                                                                                                                                       Winkler B, Gelbmann D;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 14; SEQ ID NO 152; 145pp; English.
                                                                                                                                     02-MAR-2004; 2004WO-EP002087.
                                                                                                                                                                          04-MAR-2003; 2003EP-00450061
                    Streptococcus pyogenes.
                                                                                                                                                                                                                (INTE-) INTERCELL AG
                                                                                                                                                                                                                                                                                          WPI; 2004-653698/63.
N-PSDB; ADR83734.
                                                                                                                                                                                                                                                     Meinke A, Nagy E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 398 AA;
                                                       WO2004078907-A2
                                                                                              16-SEP-2004
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1 LSAVLVSGVTLSSATTLSA 19

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Gaps ; 0

78.8%; Score 67; DB 8; Length 398; 78.9%; Pred. No. 0.11; ive 2; Mismatches 2; Indels

Query Match
Best Local Similarity 78.99
Matches 15; Conservative

Search completed: January 25, 2006, 19:01:42 Job time : 69.2 secs

```
GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
```

OM protein - protein search, using sw model

January 25, 2006, 18:48:55; Search time 9.1 Seconds (without alignments) 211.465 Million cell updates/sec Run on:

1 LSAVLVSGVTLSSATTLSAV 20 US-10-797-821-4 85 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		de			SOMMALES	
Result		Query				
No.	Score	Match	Match Length	8	£	Description
1	48	56.5	306	7	AC0258	probable phage pro
7	48	56.5	456	N	E86903	hypothetical prote
м	47	55.3	461	7	7600NL	secreted 45K prote
4	46	54.1	192	7	AG0875	probable membrane
ហ	44	51.8	601	N	A84256	bacterio-opsin act
9	43	50.6	118	~	E97897	50S ribosomal prot
7	43	50.6	118	~	E95026	ribosomal protein
∞	43	50.6	120	~	D69696	ribosomal protein
O	43	50.6	320	~	A40660	outer membrane pro
10	43	50.6	366	N	G97305	100
11	43	50.6		~	G97912	etical
12	43	50.6	661	~	E95042	
	43	50.6		7	H71453	hypothetical prote
14	42	49.4		7	A87406	ribosomal protein
15	42	49.4		~	AB3628	transcription regu
16	42	49.4		~	S32908	hypothetical prote
17	42	49.4	363	~	A70636	probable fadE18 pr
18	42	49.4		~	F83602	hypothetical prote
19	42	49.4		~	A86503	pyruvate kinaße [i
20	42	49.4		~	A72119	pyruvate kinaße CP
21	42	49.4		~	S32171	hydroxyneurosporen
22	42	49.4		~	G64039	hypothetical prote
23	42	49.4	554	~	B82934	
24	42	49.4	699	~	F82258	DNA ligase VC0971
25	42	49.4	619	~	D64182	DNA ligase (NAD) (
56	42	49.4	737	~	S72442	
27	42	49.4	837	~	G82542	DNA ligase XF2556
28	41	48.2	120	~	AH2813	
29	41	48.2	120	~	D97592	50S ribosomal prot

probable transport	hypothetical prote	hypothetical prote	conserved hypothet	hypothetical prote	agrobacterium viru	hypothetical prote	chemotaxis MotB pr	conserved hypothet	hypothetical prote	gamma-glutamyltran	capsular polysacch	siderophore recept	RhtA Rhizobactin r	proline dehydrogen	proline dehydrogen
H91103	C85949	D64421	A87691	G75609	AH3180	G72730	AC0203	D69012	AC2195	T49441	B70036	T46821	A95420	C98219	AG3067
71	~	~	~	N	N	ď	N	N	N	N	~	~	N	0	6
192	192	228	231	272	336	369	427	470	576	586	598	746	746	1228	1228
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48.	48.	48.	48	48.	48	48.	48.2	48.	48	48	48.2	48	48	48.2	48
41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	RESULT 1
	AC0258
	probable phage protein YPO2116 [imported] - Yersinia pestis (strain CO92)
	C;Species: Yersinia pestis
	C;Date: 02-Nov-2001 #sequence revision 02-Nov-2001 #text change 09-Jul-2004
_	C;Accession: AC0258
_	R; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B
_	deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
	il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
_	Nature 413, 523-527, 2001

Aritle: Genome sequence of Yersinia pestis, the causative agent of plague.

A; Reference number: AB0001; MUD:21470413; PMID:11586360

A; Accession: AC0258

A; Residue: preliminary

A; Molecule type: DNA

A; Residues: 1-306 < KUR>

A; Crosser-references: UNIPROT: QBZEP4; UNIPARC: UPI00000DCC41; GB: AL590842; PIDN: CAC90927.1

C; Genetics:
A; Gene: YP02116

Gaps ö 56.5%; Score 48; DB 2; Length 306; 61.1%; Pred. No. 5.9; tive 3; Mismatches 4; Indels Query Match
Best Local Similarity 61.1[§]
Matches 11, Conservative

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221 AVPVTGVTLNKTTTILAV 238 3 AVLVSGVTLSSATTLSAV 20 g ò

hypothetical protein usp45 [imported] - Lactococcus lactis subsp. lactis (strain IL1403 C, Species: Lactococcus lactis subsp. lactis C, Species: Lactococcus lactis subsp. lactis C, Species: Lactococcus lactis subsp. lactis C, Species: Lactococcus lactis subsp. lactis C, Species: Lactococcus lactis subsp. lactis C, Species: Lactococcus lactis c, Mincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrl R, Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrl A, Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s A, Reference number: A86625; MUD:21235186; PMID:11337471
A, Accession: E86903
A, Residues: L456 <STO>
A, Residues: L456 <STO>
A, Residues: L456 <STO>
A, Experimental source: strain IL1403
C, Genetics: A, Gene: usp45

Gaps ö Query Match 56.5%; Score 48; DB 2; Length 456; Best Local Similarity 55.0%; Pred. No. 8.9; Matches 11; Conservative 4; Mismatches 5; Indels

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A;Accession: A04256
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-601 <STO>
A;Cross-references: UNIPROT:Q9HQU9; UNIPARC:UPI00000637AA; GB:AE004437; NID:g10580551; I
C;Genetics:
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Streptococus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
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C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: B97897
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; I
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; N.
F.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, S709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Reference number: A97872; MUID:21429245; PMID:11544234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-118 <KUR>
A;Cross-references: UNIPROT:Q97SUG; UNIPROT:Q8CWV2; UNIPARC:UPI0000051357; GB:AE007317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:Q978U6; UNIPROT:Q8CWV2; UNIPARC:UPI0000051357; GB:AE005672; A;Experimental source: strain TIGR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50S ribosomal protein L18 [imported] - Streptococcus pneumoniae (strain R6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ribosomal protein L18 [imported] - Streptococcus pneumoniae (strain TIGR4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.6%; Score 43; DB 2; Length 118;
A; Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Genetics:
A;Gene: SP0226
C;Superfamily: Escherichia coli ribosomal protein L18
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C,Superfamily: Escherichia coli ribosomal protein L18
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Pred. No. 14;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  .;
3
                                                                                                                                                                                                                                                                                                                                                                                                                  DB
49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206 SAVLAAGDALSDASTRGAV 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 SAVLVSGVTLSSATTLSAV 20
                                                                                                                                                                                                                                                                                                                                                                                                                  51.8%;
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Best Local Similarity 75.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Conservative
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48 VAGVTLASASTL 59
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A; Residues: 1-118 < KUR>
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Matches 11; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
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C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Datession: A84256
R;NG, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.
Fing, W.V.; Kennedy, S.P.; Mahairas, T.
Fung, K.H.; Alam, M.; Freitas, T.
Froc. Natl. Acad. Sci. Us.A. 37, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C; Accession: AG0875
R; Parkhill, J; Dougan, G; James, K.D; Thomson, N.R.; Pickard, D.; Wair, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
Nature 413, 848-852, 2001
A; Anthors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Athors: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A; Reference number: AB0502; MUD:21534947; PMID:11677608
A; A; Accession: AG0875
A; A; Accession: AG0875
A; A; Accession: AG0875
A; A; Accession: Ag0875
A; A; Accession: Ag0875
A; A; Accession: Ag0875
A; A; Accession: Ag0875
A; A; Accession: A; Accessi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable membrane protein STY3230 [imported] - Salmonella enterica subsp. enterica serov
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AG0875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                           secreted 45K protein precursor - Lactococcus lactis
C;Species: Lactococcus lactis
C;Species: Lactococcus lactis
C;Date: 16-Uul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: JN0097
R;Van Asseldonk, M.; Rutten, G.; Oteman, M.; Siezen, R.J.; de Vos, W.M.; Simons, G.
Gene 95, 155-160, 1990
A;Title: Cloning of usp45, a gene encoding a secreted protein from Lactococcus lactis & A;Reference number: JN0097; MUID:91071599; PMID:2123812
A;Accession: JN0097
A;Residues: L461 <VAN>
A;Residues: 1-461 <VAN>
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Pred. No. 13;
4; Mismatches 5; Indels
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3; Mismatches
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6 ISAILMSTVILSAAAPLSGV 25
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Best Local Similarity 55.0
Matches 11; Conservative
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Give germination protein GerKB, membrane protein [imported] - Clostridium acetobutylic Cispecies: Clostridium acetobutylicum (Cispecies: Clostridium acetobutylicum (Cispecies: Clostridium acetobutylicum (Cispecies: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004 (Cispecies) (Cispecies: 16-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004 (Cispecies) (Cispecies: Not in Daly, M.J.; Braton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee J. Bacteriol. 183, 4823-4838, 2001 A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Classification: G97305 A; Reference number: A96900; MUD:21359325, PMID:21359325 A; Status; preliminary
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R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; S., P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:2142245; PMID:11544234
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C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C;Accession: E95042
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heison, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
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C,Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
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Pred. No. 77;
4; Mismatches
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Best Local Similarity 64.3%;
Matches 9; Conservative
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Best Local Similarity 52.55,
Conservative
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8 ALLILAVALSSAASLSA
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9 LAGVTLLAATTLAA 22
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R;Kunst, R: Ogasawara, N: Moszer, I:; Albertini, A.M.; Alloni, G:; Azevedo, V:; Berter C; Bron, S:; Brouillet, S:; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwod, C.R.; Henarut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koeter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Latiduois, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauchois, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Sarro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolla, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Senzor, A;Authors: Yoshikawa, H.F.; Zumatein, E.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Voshida, R.; Aittle: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A;Accession: D65056

A;Status: prellminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-120 <a href="https://docs.org/10.104">https://docs.org/10.104</a>; GB: NUD:
A;Residues: 1-120 <a href="https://docs.org/10.104">https://docs.org/10.104</a>; GB: NUD:
A;Residues: The complete genome sequence not shown; translation not shown
A;Residues: 1-120 <a href="https://docs.org/10.104">https://docs.org/10.104</a>; GB: NUD:
A;Residues: The complete genome sequence not shown; translation not shown
A;Residues: 1-120 <a href="https://docs.org/10.104">https://docs.org/10.104</a>; GB: NUD:
A;Residues: The complete genome sequence not shown; translation not shown
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R; Haake, D.A.; Champion, C.I.; Martinich, C.; Shang, B.S.; Blanco, D.R.; Miller, J.N.; I. Dacteriol. 175, 42224-4234, 1993
A; Title: Molecular cloning and sequence analysis of the gene encoding OmpLl, a transmemb A; Reference number: A40660; MUID: 93308103; PMID: 8320237
A; Accession: A40660
A; Asaccession: A40660
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                                                                                                                                                                                                                                                                                                                                                             ribosomal protein 118 rplR - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
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Date: 21-Jan-1994 #sequence_revision 25-Apr-1997 #text_change 20-Sep-1999
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A;Cross-references: UNIPARC:UP100000B7892
A;Note: sequence extracted from NCBI backbone (NCBIN:134517, NCBIP:134519)
C;Superfamily: Leptospira alstoni outer membrane protein OmpL1
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                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  outer membrane protein OmpLi - Leptospira alstoni
   Pred. No. 14;
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Similarity 75.0%;
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 58.8°
Matches 10, Conservative
                                                                                                                                                  |:||||:|||
48 VAGVTLASASTL 59
                                                                                                            6 VSGVTLSSATTL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 VSGVTLSSATTL 17
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VNGVTLASASTL 59
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   Best Local
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                                     Matches
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completed: January 25, 2006, 19:15:16
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Job time: 10.1 secs
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A; Map position: II
            Best Local
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AB3628
                                           Matches
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R; Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2011
A; Pitc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2011
A; Pitc. Complete Genome Sequence of Caulobacter crescentus.
A; Reference number: A87249; MUD:21173698; PMID:11259647
A; Status: preliminary
A; Status: preliminary
A; Residues: 1-116 <STOO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M.; Sawadbayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekir M.; Ohituku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi DNA Res. 5, 55-76, 1998
A; Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a A; Reference number: A71000; MUID:98344137; PMID:9679194
A; Reference number: A71000; MUID:98344137; PMID:9679194
A; Racession: H71453
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
A; Residues: 1-787 < KMA>
A; Residues: 1-787 < KMA>
A; Residues: 1-787 < KMA>
A; Residues: UNIPROT:058025; UNIPARC:UPI0000062D86; GB:AP000001; NID:93236128; PI
A; Experimental source: strain OT3
A; Mote: this accession replaces an interim accession for a sequence replaced by GenBank C; Genetics:
A; Gene: PH0287
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A;Reference number: A95000; MUD:21357209; PMID:11463916
A;Accession: B95042
A;Status: preliminary
A;Rolecule type: DNA
A;Residues: 1-661 <KUR>
A;Residues: 1-661 <KUR>
A;Access-references: UNIPARC:UPI0000165A8D; GB:AE005672; PIDN:AAK74534.1; PID:g14971835; A;Coss-reference: strain TIGR4
C;Genetics:
A;Gene: SP0366
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C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C;Accession: H71453
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.: Hino. Y.: Vamamot
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C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                      Score 43; DB 2; Length 661;
Pred. No. 77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
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Local Similarity 64.3%;
nes 9; Conservative .
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10 LAGVTLLAATTLAA 23
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Matches
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transcription regulator, crp family BMBI10947 [imported] - Brucella melitensis (strain 1. C;Species: Brucella melitensis
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession. AB3628
R;DelYecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Mazur, M.; Goltsman, E.; Selkov, B.; Blzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess; Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens: A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q8YBF3; UNIPARC:UPI0000586A0; GB:AE008918; PIDN:AAL54189.1;
A;Experimental source: strain 16M
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Pred. No. 19;
2; Mismatches
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Pred. No.
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  75.0%;
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Similarity 75.0 9; Conservative
                                                                                              49 GVTLASASTLEA 60
                                                                  8 GVTLSSATTLSA 19
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: AB3628
A;Status: preliminary
A;Molecule type: DNA
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wolbachia p gloeobacter photorhabdu

burkholderi

anopheles g wolbachia s gluconobact clostridium

063qy8 062h95 062h95 062h95 07nczl 07nczl 07nczl 07nczl 07nczl 05cq37 05cq37 05g8x4 05g8x4 05gws7 05qws7 05dxy2 05

idiomarina burkholderi halobacteri

xanthomonas

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STRAIN=5SM3;
MEDLINE=21481971; PubMed=11598068;
DOI=10.1128/IAI.69.11.6931-6941.2001;
Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 85; DB 2; Length 211; Pred. No. 4.9e-05; Mismatches 0; Indels
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STRAIN-GS-5 Kuramitsu;
Peruzzi F., Piggot P.J., Daneo-Moore L.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U78607; AAD00288.1; -; Genomic_DNA.
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Last annotation update)
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Last annotation update)
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AAPJ RHILV

Q63QFB BURPS

062H95 BURMA

RL18 WOLPH

Q7NCZI GLOVI

MIAA PHOLL

G5TQ37 AWOLTR

G5TQ37 AWOLTR

G5TQ48 WOLTR

G5TQ48 G1DLO

G6HVZ 9CLOT

G6HVZ 9CLOT

G6HVZ 9CLOT

G9HQU9 HALSA

G9HQU9 HALSA
                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
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01-OCT-2002 (TrEMBLrel. 22, Last ann
Putative secreted protein (Fragment)
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Q938VO;
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Q9ZAS7;
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    341
109
1109
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    NCBI_TaxID=1309;
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      SEQUENCE
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Best Local
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Q938V0_STRMU
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Q9ZAS7_ST
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Copyright (c) 1993 - 2006 Compugen Ltd.
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Duncan M.J.;
"Cloning of the Streptococcus mutans gene encoding glucan binding
protein B and analysis of genetic diversity and protein production in
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Chia J.S., Lee Y.Y., Huang P.T., Chen J.Y.;
"Identification of stress-responsive genes in Streptococcus mutans by
differential display reverse transcription-PCR.";
Infect. Immun. 69:2493-2501(2001).
                                                                                                                                                                                                                                                                                                                                                     STRAIN=GS-5;
MEDLINE=21461,977; PubMed=11598074;
MEDLINE=21461,971; PubMed=115980.2001;
Chia J.S., Chang L.Y., Shun C.T., Chang Y.Y., Chen J.Y.;
"A 60-kilodalton immunodominant glycoprotein is essential for cell wall integrity and the maintenance of cell shape in Streptococcus
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Immunodominant glycoprotein IDG-60 (Glucan-binding protein B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 85; DB 2; Length 431;
100.0%; Pred. No. 0.0001;
.ive 0; Mismatches 0; Indels
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                                                                          Streptococcus mutans.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=GS-5; Chang L.-Y., Lee Y.-Y., Chen J.-Y.; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=3VP4;
Jin S., Duncan M.J., Taubman M.A., Smith D.J.;
"Cloning of the gbpB gene from Streptococcus mutans.";
J. Dent. Res. 79:224-224(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44592 MW; 3EBE21FC5E47232E CRC64;
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Infect. Immun. 69:6931-6941(2001).
EMBL, AP338445, AAK08104.1; -; Genomic_DNA.
EMBL, AY046411; AAK94501.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
Pfam; PF05257; CHAP; 1.
PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
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MEDLINE=21481971; PubMed=11598068;
                                                                                                                                                                                                       MEDLINE=21153617; PubMed=11254612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Infect. Immun. 69:6987-6998(2001).
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ID QBDWM3 STRMU PRELIMINARY;
AC Q8DWM3;
DT 01-MAR-2003 (TrEMBLrel. 23, 0
DT 01-MAR-2003 (TrEMBLrel. 23, 3)
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NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE,
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Best Local Similarity
                                                                                                                                  NCBI_TaxID=1309;
                                                                                                               Streptococcus.
                                                                                                                                                                                          STRAIN=GS-5;
                                                           Name=sagA;
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 Duncan M.J.;
"Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates.";
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Pred. No. 0.0001;
; Mismatches 0; Indels
                                                                                                                                                                                                                                               Length 431;
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Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
                                                                                                                                                                                                                                             Score 85; DB 2; Length 43; Pred. No. 0.0001; O. Mismatches 0; Indels
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Linfect. Immun. 69:6931-6941(2001).
EMBL; AYO46410; AAKO94500.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
Fram; PP05257; CHAP; 1.
PRINTS; PR01852; STBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
SEQUENCE 431 AA; 44620 MW; 464FE3B563FB7E51 CRC64;
                                                                                                                                                 Pfam; PF05257; CHAP; 1.
PRINTS; PRO1852; SIBARPOTEIN.
PROSTIE; PSS0911; CHAP; 1.
SEQUENCE 431 AA; 44650 MW; 05D38DBDBBC4609F CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Glucan-binding protein B.
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EMBL; AX046414; AAK94504.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
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20; Conservative 0
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Best Local Similarity
Matches 20; Conserv
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NUCLEOTIDE SEQUENCE.
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10 9938 AC 9938
AC 9938 BC 10-D
DT 01-D

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"Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates.";
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                                                                                                                                                                                                                                                                                                                                         "Genome sequence of Streptococcus mutans UA159, a cariogenic dental
                                                                                                                                                                                           STRAIN-UALSS / ATC 700610 / Serotype c; MEDLINE-22295063; PubMed=12397186; DOI=10.1073/pnas.172501299; Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J., Ajdic D.J., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P., Qian Y., Li S., Zhu H., Najar F.Z., Lai H., White J., Roe B.A.,
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Putative secreted antigen GbpB/SagA; putative peptidoglycan
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100.0%; Pred. No. 0.0001;
Mismatches 0; Indels
                                                                                     Streptococcus mutans.
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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Jin S., Duncan M.J., Taubman M.A., Smith D.J.;
"Cloning of the gbpB gene from Streptococcus mutans.";
J. Dent. Res. 79:224-224 (2000).
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BmBi, ABO14855, AANS7811.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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EMBL; AY046413; AAK94503.1; -; Genomic_DNA.
InterPro; IPR007921; CHAR.
InterPro; IPR09148; SibA.
Pfam; PF05257; CHAR; 1.
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DOI=10.1128/IAI.69.11.6931-6941.2001;
                                             hydrolase.
Name=gbpB; OrderedLocusNames=SMU.22;
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PRINTS; PROINS; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
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PROSITE; PS50911; CHAP; 1.
SEQUENCE 432 AA; 44652 MW;
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Q938V1;
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Best Local Similarity
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NCBI_TaxID=1309;
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"Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates.";
Infect. Immun. 69:6931-6941(2001).
EMBL; AY046412; AAK94502.1; -; Genomic_DNA.
InterPro; IPR009148; SibA.
PF05257; CHAP.
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Score 85; DB 2; Length 432;
Pred. No. 0.0001;
Mismatches 0; Indels
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DOI=10.1128/IAI.69.11.6931-6941.2001;
Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
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Pred. No. 0.00014;
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                      432 AA
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Query Match
100.0%; Score 85; DB
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 20; Conservative 0; Mismatches
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PubMed=15272401; DOI=10.1086/422697;
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                                                                                                                                    6 LSAVLVSGVTLSSATTLSAV 25
                                                                                                 1 LSAVLVSGVTLSSATTLSAV 20
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PROSITE; PS50911; CHAP; 1.
SEQUENCE 432 AA; 44648 MW;
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STRAIN=SF370 / ArCC 700294 / Serotype M1;
STRAIN=SF370 / ArCC 700294 / Serotype M1;
MEDLINE=21192649; PubMed=11296296; DOI=10.1073/pnas.071559399;
MEDLINE=21192649; PubMed=11296296; DOI=10.1073/pnas.071559399;
Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.E.;
"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
Banks D.J., Porcella S.F., Barbian K.D., Beres S.B., Philips L.B., Voyich J.M., DeLeo F.R., Martin J.M., Somerville G.A., Musser J.M.; "Progress toward characterization of the group A Streptococcus metagenome: complete genome sequence of a macrolide-resistant serotype M6 strain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fagan P.K., Reinscheid D., Gottschalk B., Chhatwal G.S.; "Identification and characterization of a novel secreted protein from
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Pred. No. 0.062;
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AE006474; AAK33158.1; -; Genomic_DNA.
EMBL; AF319999; AAL73135.1; -; Genomic_DNA.
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                                                                                                                                J. Infect. Dis. 190:727-738(2004).
EMBL; CP000003; AAT86152.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
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PROSITE; PS50911; CHAP; 1.
Complete proteome; Signal.
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PROSITE; PS50911; CHAP; 1.
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InterPro; IPR009148; SibA.
Pfam; PF05257; CHAP; 1.
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SEQUENCE 398 AA;
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MEDLINE-22683278; PubMed=12799345; DOI=10.1101/gr.1096703;
Makagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
Nakagawa I., Kwabata S., Yamazaki K., Shiba T., Yasunaga T.,
Hayashi H., Hattori M., Hamada S.,
"Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
large-scale genomic rearrangement in invasive strains and new insights
into phage evolution.";
Genome Res. 13:1042-1055(2003).
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MBDLNE=2213808; Pubmed=1212206; DOI=10.1073/pnas.152298499;
Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
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NUCLEOTIDE SEQUENCE.

MEDLINE-21927593; PubMed=11917108; DOI=10.1073/pnas.062526099;

MEDLINE-21927593; PubMed=11917108; DOI=10.1073/pnas.062526099;

Smoot J.C., Barbian K.D., Van Gompol J.J., Smoot L.M., Chaussee M.S.

Salva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,

Parkins L.D., Berses S.B., Campbell D.S., Smith T.M., Zhang Q.,

Kapur V., Daly J.A., Veasy L.G., Musser J.M.;

"Genome sequence and comparative microarray analysis of serotype M18
group A Streptococcus strains associated with acute rheumatic fever
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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01-0cr-2002 (TrEMBLrel. 22, Last sequence update)
13.SEP-2005 (TrEMBLrel. 31, Last annotation update)
Putative secreted protein.
OrderedLocusNames=SP80015, SpyM3_0014;
                                                                                                       05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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EMBL; AE009955; AAL96849.1; -; Genomic_DNA.

InterPro; IPR007921; CHAP.

InterPro; IPR009148; SlbA.
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tive 2; Mismatches
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PROSITE; PS50911; CHAP; 1.
Complete proteome.
SEQUENCE 398 AA; 42028 MW;
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Q8P318; Q7CFL7;
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Q7CNQ7;
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6 LSAVLVSGVTLSAAASVHA 24
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"Ges., a Chimeric and Variable Gene, Bncodes an Extracellular Protein Involved in Cellular Segregation in Streptococcus thermophilus.";

J. Bacteriol. 187:2737-2746(2005).

EMBL; CP0000023; AAVS9752.1; -; Genomic DNA.

EMBL; AY30643; AAW82375.1; -; Genomic_DNA.

InterPro; IPR009148; SibA.
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Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M., Schlievert P.M., Musser J.M.; "Genome sequence of a serotype M3 strain of group A Streptococcus: phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete sequence and comparative genome analysis of the dairy bacterium Streptococcus thermophilus.";
Nat. Biotechnol. 22:1554-1558 (2004).
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PubMed=15543133, DOI=10.1038/nbt1034,
Bolotin A., Quinquis B., Renault P., Sorokin A., Ehrlich S.D.,
Kulakauskas S., Lapidus A., Goltsman E., Mazur M., Pusch G.D.,
Fonstein M., Overbeek R., Kyprides N., Purnelle B., Prozzi D.,
Ngui K., Masuy D., Hancy F., Burteau S., Boutry M., Delcour J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streprococcus thermophilus (strain ATCC BAA-250 / LMG 18311).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.8%; Score 61; DB 2; Length 474; 73.7%; Pred. No. 0.64; 2; Indels :ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             78.8%; Score 67; DB 2; Length 398; 78.9%; Pred. No. 0.062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                         398 AA; 42028 MW; SDCEDA78CB863B60 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
OSM6K4_STRT2
LD GSM6K4_STRT2 PRELIMINARY; PRT; 474 AA.
AC GSM6K4;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Glucan binding protein (PosB).
GN Name-pcsB; OrderedLocusNames=stu0022;
                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083 (2002) EMBL; BA000034; BAC63110.1; -; Genomic_DNA. EMBL; AE014136; AAM78621.1; -; Genomic_DNA. InterPro; IPR007921; CHAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LSAVLVSGVTLSSATTLSA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 LSAVLVSGVTLGAATTVGA 24
                                                                                                                                                                                                                                                                                       PRINTS; PRO1852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
Complete proteome.
SEQUENCE 398 AA; 42028 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF05257; CHAP; 1.
PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
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Best Local Similarity 73.74
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 78.9:
Matches 15; Conservative
                                                                                                                                                                                                                                                                 Pfam; PF05257; CHAP; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=264199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=LMG 18311;
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J. Bacteriol. 183:1175-1183 (2001).
EMBL; A277729. CAC2B144.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                   "Complete sequence and comparative genome analysis of the dairy bacterium Streptococcus thermophilus.";
Nat. Biotechnol. 22:1554-1558(2004).
EMBL: CD000024; AAV61641.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
Pfam; PF05257; CHAP: 1.
                                                                                                                                                                                                                                             NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
PubMed=1554313; DOI=10.1038/nbt1034;
Bolotin A., Quinquis B., Renault P., Sorokin A., Ehrlich S.D.,
Kulakauskas S., Lapidus A., Goltsman E., Mazur M., Pusch G.D.,
Fonstein M., Overbeek R., Kyprides N., Purnelle B., Prozzi D.,
Ngui K., Masuy D., Hancy F., Burteau S., Boutry M., Delcour J.,
Goffeau A., Hols P.,
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DOI=10.1128/JB.183.4.1175-1183.2001;
Reinscheid D.J., Gottschalk B., Schubert A., Eikmanns B.J.,
Chhatwal G.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 61; DB 2; Length 485;
Pred. No. 0.66;
                                                                                                   Glucan binding protein.
Name=pcsB; OrderedLocusNames=str0022;
Streptococcus thermophilus (strain CNRZ 1066).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   485 AA; 49165 MW; 8665E4B1FC6CF7CA CRC64;
                                      01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
        485 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
      PRT;
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PROSITE; PS50911; CHAP; 1.
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QSM212_STRT1 PRELIMINARY;
QSM212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9AKA4 STRAG PRELIMINARY;
Q9AKA4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PosB protein precursor.
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Best Local Similarity
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                                                                                                                                                                                                           NCBI TaxID=299768;
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                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genome sequence and comparative genomic analysis of an emerging human pathogen, serotype V Streptococcus agalactiae."; proc. Natl. Acad. Sci. U.S.A. 99:12391-12396 (2002).
EMBL; AE014192; AAM98925.1; -; Genomic_DNA.
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                                                                                                                                       1;
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                                                                                                   Query Match 62.9%; Score 53.5; DB 2; Length 447; Best Local Similarity 70.0%; Pred. No. 9.1; Matches 14; Conservative 4; Mismatches 1; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                          PCSB protein.
Name-pscB; OrderedLocusNames=SAG0017;
Streptococcus agalactiae (serotype V).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
Pfam; PF05257; CHAP; 1.
PRINTS; PR01852; SIBAPROTEIN.
PROSTTE; PS0911; CHAP; 1.
Complete proteome.
SEQUENCE 447 AA; 46681 MW; F4DB14B0A5F962C8 CRC64;
                               25 Potential.
447 PCBB protein.
46681 MW; F4DB14B0A5F962C8 CRC64;
                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                    447 AA
                                                                                                                                                                                                                                                                                                    PRT;
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PROSITE; PS50911; CHAP; 1.
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QÜEZH1 STRAS PRELIMINARY;
QBEZH1;
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26 4
447 AA;
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NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus.
NCBI_TaxID=216466;
                                                                   SEQUENCE
                  Signal.
SIGNAL
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Search completed: January 25, 2006, 19:13:37 Job time: 72.3 secs

Sequence 2, Appli Sequence 2, Appli Sequence 6, Appli Sequence 2, Appli Sequence 4, Appli Sequence 6, Appli Sequence 6135, A Sequence 3022, Ap Sequence 31328, A Sequence 31328, A Sequence 361, App Sequence 43368, A Sequence 45809, A Sequence 5990, Ap Sequence 5990, Ap

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; OTHER INFORMATION: Leader Sequence of Usp45 in Lactococcus lactis; Patent No. 6605286
US-09-060-878-3
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09060878A

Patent No. 6605286

GENERAL INFORMATION:
APPLICANT: Steidler. Lothar
APPLICANT: Remaut, Erik
APPLICANT: Wells, Jeremy Mark
APPLICANT: Le Page, Richard William Falla
TITLE OF INVENTION: Delivery of Biologically Active
TITLE OF INVENTION: Delivery of Biologically Active
TITLE OF INVENTION: Delivery of Siologically Active
TITLE OF INVENTION: 1998-04-16
GURRENT APPLICATION NUMBER: US/09/060,878A
CURRENT PILING DATE: 1998-04-16
EARLIER APPLICATION NUMBER: GB9521568.7
EARLIER FILING DATE: 1995-10-20
NUMBER OF SEQ ID NOS: 6

SOFTWARE: PagtSEQ for Windows Version 3.0
US-09-171-387-2
US-09-653-499-4
US-09-653-499-4
US-09-653-499-4
US-10-135-988-2
US-10-135-988-4
US-10-135-988-4
US-10-135-988-4
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US-09-2770-767-4368
US-09-2770-767-4368
US-09-2770-767-4368
US-09-2770-767-4368
US-09-770-170-6
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Pred. No. 0.48;
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                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Suit, Bruno
APPLICANT: Schmitz, Albert
TITLE OF INVENTION: Bacterial Vectors
INVERSPONDENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08186222
Patent No. 5559007
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 55.0
Matches 11; Conservative
   RESULT 2
US-08-186-222-4
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     SEQ ID NO 3
LENGIH: 27
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                                                                                                                   January 25, 2006, 18:50:05; Search time 16.6 Seconds (without alignments) 99.609 Million cell updates/sec
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Sequence 4, A
Sequence 6, A
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/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd
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US-09-252-991A-31813
US-09-270-76-45727
US-09-134-000C-3742
US-08-873-479-42
US-09-252-991A-32329
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US-09-621-976-7132
US-09-533-110-625
US-09-732-210-655
US-09-107-433-8060
US-09-107-433-3472
US-08-362-739-2
US-08-36-739-2
US-08-36-739-2
US-09-533-110-3976
US-09-533-110-622-064-2
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US-09-198-452A-114
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US-08-475-886-6
US-08-397-232-2
US-08-397-232-4
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Maximum Match 100%
Listing first 45 summaries
                                                                                    OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                          seq length: 0 seq length: 2000000000
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Match Length DB
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85
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Maximum DB
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Database :

Result

Sequence:

Run on:

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Gaps

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Length 27; Indels

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NAME/KEY: UNSURE
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US-09-621-976-7132
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Sequence 2, Application US/08186222

Patent No. 5559007

GENERAL INFORMATION:
APPLICANT: Schmitz, Albert
TITLE OF INVENTION: Bacterial Vectors
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZTATE: New York
COUNTRY: USA
ZTATE: HO532

COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Batentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RILING NATE: RECENTIN RELEASE
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: EN PC compatible
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Flam PC compatible
COMPUTER: Flam PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/186,222
FILING DATE: CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/672,205
FILING DATE: 19-MAR-1991
APPLICATION NUMBER: US 906400.7
FILING DATE: 22-MAR-1990
ATTORNEY/AGENT INPORMATION:
NAME: Villamizar. Johann
REGISTRATION NUMBER: 30,598
REFERENCE/DOCKET NUMBER: 30,598
REFERENCE/DOCKET NUMBER: 4-17994/A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 30,598
REFERENCE CHARACTERISTICS:
TELEPAK: (914)347-5769
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LEMOTH: 92 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 47; DB
Pred. No. 2.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
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CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/672,205
FILING DATE: 19-MAR-1991
APPLICATION NUMBER: GB 9006400.7
FILING DATE: 22-MAR-1990
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 30,598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 55.0%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-186-222-2
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GENERAL INCORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR PILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NOS: 8344
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Pred. No. 16;
4; Mismatches 5; Indels
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Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 713.2 Application US/09621976

Patent No. 6639063

GENERAL INFORMATION:
APPLICANT: Johnsh Mine Edwards, J.B.
APPLICANT: Johnst, S. Y.
TITLE OF INVENTION:
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SEQ ID NO 7132

LENGTH: 73

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 70
OTHER INFORMATION: Xaa = * , Cys, Phe, Leu, Ser, Trp, Tyr
NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 7064, Application US/09543681A ; Patent No. 6605709
                                                                                                                                                                                                                                                                                                                                    1 LSAVLVSGVTLSSATTLSAV 20
                                                                                                                                                                                                                                                                                                                                                               6 ISAILMSTVILSAAAPLSGV 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914)785-7121
TELEPHONE: (914)785-7121
TELEPAX: (914)347-5769
INFORMATION FOR SEQ ID NO: 2:
SEQUINCE CHARACTERISTICS:
LENGTH: 461 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-186-222-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LSAVLVSGVTLSSATTLSA 19
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Best Local Similarity 52.6%;
Matches 10; Conservative
                                                                                                                                                                                                                                            Query Match
Best Local Similarity 55.0%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT; ORGANISM: Proteus mirabilis
US-09-543-681A-7064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                         ô
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                                                                                                                                                                                                                                  Score 43; DB 2; Length 120;
Pred. No. 13;
3; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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PRIOR APPLICATION DATA:
RILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: ArindliO, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: misc_feature
; LOCATION: (B) LÖCATION 1...127
; SEQUENCE DESCRIPTION: SEQ ID NO: 5060:
US-09-107-532A-5060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Enterococcus faecium
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: US 60/169,340
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 1753
LENGTH: 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5060, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
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OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INPORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5060:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 127 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                       50.6%;
                                                                                                                                           ; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-09-732-210-655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                  Query Match
Best Local Similarity 75.0
Matches 9; Conservative
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Best Local Similarity 75.0
Matches 9; Conservative
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48 VNGVTLASASTL 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-107-532A-5060
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CURRENT APPLICATION NUMBER: US/09/583,110

CURRENT FILING DATE: 1998-06-30

PRIOR FILING DATE: 1998-06-30

PRIOR FILING DATE: 1998-05-12

PRIOR FILING DATE: 1998-05-12

PRIOR FILING DATE: 1998-05-12

RIOR APPLICATION NUMBER: US 60/051,553

READ ID NOS: 5322
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Patent No. 6573361

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bunkers, Greg J.
APPLICANT: Mitanck, Cindy A.
APPLICANT: Mitanck, Cindy A.
APPLICANT: Wu, Yonnie S.
TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use PILE REFERENCE: 39-21 (15036) B
CURRENT APPLICATION NUMBER: US/09/732,210
CURRENT FILING DATE: 2000-12-07
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                                                                                                                                                                                                                                                                                                                                                                             Query Match 51.8%; Score 44; DB 2; Length 73; Best Local Similarity 69.2%; Pred. No. 5; Matches 9; Conservative 3; Mismatches 1; Indels
                                                                LOCATION: 6
OTHER INFORMATION: Xaa = Cys,Gly
NAME/KEY: UNSURE
LOCATION: 72
OTHER INFORMATION: Xaa = Cys,Tyr
NAME/KEY: UNSURE
LOCATION: 69
OTHER INFORMATION: Xaa = Ile,Lys,Arg,Thr
NAME/KEY: UNSURE
                           * , Lys, Gln, Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/169,513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4129, Application US/09583110
Patent No. 6699703
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                 ; LOCATION: 71
; OTHER INFORMATION: Xaa = Leu, Met, Val
US-09-621-976-7132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Streptococcus pneumoniae US-09-583-110-4129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 LESVLVSGITVSS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LSAVLVSGVTLSS 13
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                        OTHER INFORMATION: Xaa =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 9; Conserv
                                               NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-583-110-4129
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| Sequence 2. Application US/08914350A |
| Patent No. 6685945
| GENERAL INFORMATION: |
| APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA |
| APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA |
| APPLICANT: THANKE, David A. |
| APPLICANT: CHAMPION, Cheryl I. |
| APPLICANT: LOVETY, Michael A. |
| APPLICANT: MILLER, James N. |
| TILL OF INVENTION: CLONED LEPTOSPIRA OUTER MEMBRANE PROTEIN |
| FILE REFERENCE: UCLA140-2 |
| CURRENT PAPLICATION NUMBER: US/08/914,350A |
| CURRENT APPLICATION NUMBER: US 08/362,739 |
| PRIOR FILING DATE: 1994-12-20 |
| PRIOR FILING DATE: 1994-12-20 |
| PRIOR FILING DATE: 1994-03-31 |
| NUMBER OF SEQ ID NOS: 7 |
| SOFTWARE PATENTIN VERSION 3.1 |
| SEO ID NO? 7 |
| SOFTWARE PATENTIN VERSION 3.1 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                     CLONED Leptospira OUTER MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ore 43; DB 1; Length 320;
ed. No. 45;
Mismatches 4; Indels
                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,739
FILING DATE:
APPLICANT: Champion, Cheryl I.
APPLICANT: Lovett, Michael A.
APPLICANT: Lovett, Michael A.
APPLICANT: Miller, James N.
TITLE OF INVENTION: CLONED Leptospira OUTER ME
NUMBER OF SEQUENCES: 7
CORRESPONDENCES: 7
CORRESPONDENCES: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/040,747
FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.D., John R.,
REGISTRATION NUMBER: 31,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PI
TELECOMMUNICATION INFORMATION
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 AVLVSGVTLSSATTLSA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 ALLILAVALSSAASLSA 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 58.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-362-739-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                            ZIP: 90067
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LENGTH: 320
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                                                                                                                                                                   Sequence 3472, Application US/09107433
Patent No. 6800744
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
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                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: «Unknown»
OPERATING SYSTEM: «Unknown»
SOFTWARE: «Unknown»
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: JULY 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature;
LOCATION: (B) LOCATION 1...140;
SEQUENCE DESCRIPTION: SEQ ID NO: 3472:
US-09-107-433-3472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
TELECOMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                               THERAPEUTICS
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Patent No. 5658757
GENBRAL INFORMATION:
APPLICANT: Haake, David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 140 amino acids TYPE: amino acid
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STATE: Massachusetts
COUNTRY: USA
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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57 VAGVTLASASTL 68
         VSGVTLSSATTL 17
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GENERAL INFORMATION:
APPLICANT: Griffais, R.
APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev TITLE OF INVENTION: and treatment of infection
FILE REPERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
                                                                              Sequence 12623, Application US/09902540

Sequence 12623, Application US/09902540

Sequence 12623, Application US/09902540

Sequence 12623, Application US/09902540

Sequence 12623, Application US/09902540

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

FILE REPRENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR PILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 12623
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Pred. No. 1.1e+02;
4; Mismatches 5; Indels
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Pred. No. 1.1e+02;
4; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 114, Application US/09198452A
; Patent No. 6559294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-114
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Best Local Similarity 52.6%;
Matches 10; Conservative 4
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Best Local Similarity 53.3%;
Matches 8; Conservative
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TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
FILE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: PATHO0-079
CURRENT APPLICATION NUMBER: US/09/583,110
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR PILING DATE: 1998-06-30
PRIOR PILING DATE: 1998-06-30
PRIOR PILING DATE: 1998-05-12
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
SEQ ID NO 3976
LENGTH: 660
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APPLICANT: Bachmann, Martin F

APPLICANT: Maurer, Patrik F

TITLE OF INVENTION: Hapten-Carrier Conjugates and Uses Thereof

FILE REFERENCE: 1700.0300001

CURRENT APPLICATION NUMBER: US/10/622,064

CURRENT FILING DATE: 2003-07-18

PRIOR APPLICATION NUMBER: US 60/396,575

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin version 3.2
                                                                      Query Match 50.6%; Score 43; DB 2; Length 320; Best Local Similarity 58.8%; Pred. No. 45; Matches 10; Conservative 3; Mismatches 4; Indels
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Pred. No. 32;
6; Mismatches 4; Indels
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Pred. No. 1.1e+02;
4; Mismatches 1;
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; Sequence 3976, Application US/09583110
; Settent No. 6699703
; GENERAL INFORMATION:
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6 LAIVVLSALSLSSTTALAA 24
; ORGANISM: Leptospira kirschneri
US-08-914-350A-2
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8 ALLILAVALSSAASLSA 24
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Best Local Similarity 47.4%;
Matches 9; Conservative (
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US-10-622-064-2
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Best Local Similarity 64.3
Matches 9; Conservative
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(cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
        GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-10-797-821-4
US-10-383-930-29
US-10-383-930-39
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US-10-797-821-29
US-10-797-821-39
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US-10-425-114-47654
US-10-425-115-251444
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Maximum Match 100%
Listing first 45 summaries
                                            OM protein - protein search, using sw model
                                                                                                                    1 LSAVLVSGVTLSSATTLSAV 20
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Gapop 10.0 , Gapext 0.5
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APPLICANT: Smith, Daniel J.
APPLICANT: Smith, Daniel J.
APPLICANT: Taubman, Martin A.
TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens
FILE REFERENCE: 25669-020
CURRENT APPLICATION NUMBER: US/10/797,821
CURRENT FILING DATE: 2004-03-09
PRIOR APPLICATION NUMBER: 10/383,930
PRIOR PILING DATE: 2003-03-07
PRIOR PILING DATE: 2002-03-07
PRIOR PILING DATE: 2002-03-07
PRIOR PILING DATE: 2002-03-07
PRIOR PILING DATE: 2002-08-08
PRIOR FILING DATE: 2002-08-08
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| Sequence 4, Application US/10383930
| Publication No. US20040127400A1
| GENERAL INFORMATION:
| APPLICANT: Smith, Daniel J
| APPLICANT: Taubman, Martin A
| TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
| FILE REFERENCE: 25669-018
| CURRENT APPLICATION NUMBER: US/10/383,930
| CURRENT FILING DATE: 2003-03-07
| PRIOR PILING DATE: 2002-08-08
| PRIOR FILING DATE: 2002-08-08
| PRIOR FILING DATE: 2002-08-08
| PRIOR FILING DATE: 2002-08-07
| NUMBER OF SEQ ID NOS: 41
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US-09-815-242-13572
US-10-617-320-3472
US-10-617-320-3473
US-10-282-122A-74812
US-10-425-115-28596
US-10-914-350-2
US-10-914-350-2
US-10-32-391-5
US-10-330-5
US-10-330-5
US-10-381-391-5
US-10-381-391-5
US-09-916-230-8
US-10-289-454-8
US-10-289-456-8
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US-10-289-456-8
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US-10-289-456-8
US-10-289-456-8
US-10-289-456-8
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Publication No. US20050031633A1
GENERAL INFORMATION:
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; ORGANISM: Streptococcus mutans
US-10-383-930-4
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Best Local Similarity 100.
Matches 20; Conservative
     RESULT 2
US-10-797-821-4
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        LENGTH: 20
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608, App 268, App

Sequence Sequence Sequence Sequence

74331,

US-10-282-122A-73739 US-10-282-122A-74331

Sequence Sequence Sequence Sequence

13214, A

US-09-815-242-13214 S-10-474-776-608 S-10-472-928-268 S-10-501-282-390

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; Sequence 29, Application US/10383930
; Publication No. US20040127400A1
; GENERAL INFORMATION:
    APPLICANT: Smitch, Daniel J
    APPLICANT: Taubman, Martin A
    TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
; FILE REPERENCE: 25669-018
; CURRENT APPLICATION NUMBER: US/10/383,930
; CURRENT FILING DATE: 2003-03-07
; PRIOR PILING DATE: 2002-08-08
; PRIOR PILING DATE: 2002-08-08
; PRIOR PILING DATE: 2002-09-07
; RIOR RELING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 431
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; Sequence 30, Application US/10383930
; Publication No. US20040127400A1
; GENERAL INFORMATION:
APPLICANT: Smith, Daniel J
; APPLICANT: Taubman, Martin A
; TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
FILE REFERENCE: 25669-018
CURRENT APPLICATION NUMBER: US/10/383,930
; CURRENT APPLICATION NUMBER: 60/402,483
PRIOR PILING DATE: 2003-00-08
; PRIOR FILING DATE: 2002-08-08
; PRIOR FILING DATE: 2002-09-08
; NUMBER OF FILING APPLICATION NUMBER: 60/363,209
; NUMBER OF SEQ 1D NOS: 41
; SOFTWARE: Patentin version 3.2
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                                                                                                                                                                                                                                                                                                                                                                       Length 20;
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Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 20; Conservative 0; Mismatches 0; Indels
PRIOR FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: 60/081,550
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.2
SEQ ID NO 4
LENGTH: 20
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US-10-797-821-4
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; ORGANISM: Streptococcus mutans
US-10-383-930-29
                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial
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US-10-383-930-30
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US-10-383-930-29
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Sequence 29, Application US/10797821
| Caguance 29, Application US/10797821
| Publication No. US20050031633A1
| GENERAL INCOFMATION:
| APPLICANT: Smith, Daniel J. |
| APPLICANT: Smith, Daniel J. |
| TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens |
| TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens |
| TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens |
| TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens |
| TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens |
| TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens |
| PRIOR PILING DATE: 2069-03-09 |
| PRIOR PILING DATE: 2002-03-07 |
| PRIOR PILING DATE: 2002-03-07 |
| PRIOR PILING DATE: 1999-04-12 |
| PRIOR PILING DATE: 1999-04-12 |
| PRIOR PILING DATE: 1999-04-13 |
| PRIOR PILING DATE: 1999-01-08 |
| PRIOR PILING DATE: 1999-01-08 |
| PRIOR PILING DATE: 1999-01-08 |
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publication No. US20040127400A1

publication No. US20040127400A1

publication No. US20040127400A1

publication No. US20040127400A1

publication No. US20040127400A1

publication No. US20040127400A1

publication No. US2004012 No. US200400A1

publication No. US200400A1

publication No. US20040A1

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                                                                                                                                                                                                                                                                                                           Length 431;
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100.0%; Score 85; DB
Best Local Similarity 100.0%; Pred. No. 8.8
Matches 20; Conservative 0; Mismatches
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; ORGANISM: Streptococcus mutans
US-10-383-930-33
LENGTH: 431
TYPE: PRT
ORGANISM: Streptococcus mutans
US-10-383-930-30
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 29
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Best Local Similarity
Matches 20; Conserv
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US-10-797-821-29
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US-10-383-930-33
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RESULT 10
US-10-797-821-32
; Sequence 32, Application US/10797821
; Publication No. US20050031633A1
; Publication No. US20050031633A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Daniel J.
; APPLICANT: Smith, Daniel J.
; APPLICANT: Taubman, Martin A.
; TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens
; FILE REFERENCE: 2569-020
; CURRENT APPLICATION NUMBER: US/10/797,821
; CURRENT FILING DATE: 2004-03-09
; PRIOR PLING DATE: 2003-03-07
; PRIOR PPLICATION NUMBER: 60/402,483
; PRIOR APPLICATION NUMBER: 60/402,483
; PRIOR APPLICATION NUMBER: 09/290,049
; PRIOR PLING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: 60/081,550
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US-10-383-30.32
sequence 32, Application US/10383930
sequence 32, Application US/10383930
sequence 32, Application US/10383930
sequence 32, Application US/10383930
sequence 32, Application US/10383930
sequence 32, Application US/10/383930
sequence 32, 2669-018
sequence 32, 2669-018
sequence 32, 2669-018
sequence 32, 2003-03-07
sequence 32, 2003-03-07
sequence 32, 2003-03-07
sequence 32, 2003-03-07
sequence 32, 2003-03-07
sequence 32, 2003-03-07
sequence 32, 2003-03-07
sequence 33, 2003-03-07
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Best Local Similarity 100.0%; Pred. No. 8.9e-05;
Matches 20; Conservative 0; Mismatches 0;
       PRIOR APPLICATION NUMBER: 60/081,550
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR FILING DATE: 1999-01-08
NUMBER: OF ED IN NOS: 45
SOFFWARE: Patentin version 3.2
SEQ ID NO 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSAVLVSGVTLSSATTLSAV 25
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                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Streptococcus mutans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *** APPLICANT: Smith, Daniel J. APPLICANT: Smith, Daniel J. APPLICANT: Smith, Daniel J. APPLICANT: Smith, Daniel J. APPLICANT: Smith, Daniel J. APPLICANT: Taubman, Martin A. TITLE OF INVENTION Glucan Binding Protein and Glycosyltransferase Immunogens; FILE OF INVENTION Glucan Binding Protein and Glycosyltransferase ITLE OF INVENTION SIZES 2069-020; CURRENT FILING DATE: 2004-03-09; PRIOR APPLICATION NUMBER: 60/363,209 PRIOR APPLICATION NUMBER: 60/363,209 PRIOR FILING DATE: 2002-08-08

**PRIOR FILING DATE: 2002-08-08

**PRIOR FILING DATE: 1999-04-12

**PRIOR FILING DATE: 1999-04-13

**PRIOR FILING DATE: 1999-01-08

**NUMBER OF SEQ ID NOS: 45

**SCO ID NO SEQ ID NOS: 45

**SCO ID NO SEQ ID NOS: 45

**SCO ID NO SEQ ID NOS: 45
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APPLICANT: Taubman, Martin A.
TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens FILE REFERENCE: 25669-020
CURRENT APPLICATION NUMBER: US/10/797,821
CURRENT FILING DATE: 2004-03-09
PRIOR APPLICATION NUMBER: 60/363,209
PRIOR FILING DATE: 2002-03-07
PRIOR FILING DATE: 2002-03-07
PRIOR FILING DATE: 2002-03-07
PRIOR FILING DATE: 2002-03-07
PRIOR FILING DATE: 2002-04-08-08
PRIOR FILING DATE: 1999-04-12
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                                                                                                                                                                    Query Match 100.0%; Score 85; DB 5; Length 431; Best Local Similarity 100.0%; Pred. No. 8.8e-05; Matches 20; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 8.8e-05;
ive 0; Mismatches 0; Indels
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Publication No. US20050031633A1
GENERAL INFORMATION:
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Publication No. US20050031633A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                   1 LSAVLVSGVTLSSATTLSAV 20
                                                                                                                                                                                                                                                                                                                                                            6 LSAVLVSGVTLSSATTLSAV 25
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; LENGTH: 431
; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-10-797-821-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Streptococcus mutans
US-10-797-821-30
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Best Local Similarity 100.09
Matches 20; Conservative
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APPLICANT: Lau, Jingdong
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Green, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 47654
LENGTH: 177
TYPP:
TYPP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 600, Application US/10474792
; Sequence 600, Application US/10474792
; Publication No. US20040236072A1
; GENERAL INFORMATION:
APPLICANT: Cagureky, Robert
; APPLICANT: Minter, Louise
; APPLICANT: Winter, Louise
; TITLE OF INVENTION SURFACE PROTEINS OF STREPTOCOCCUS PYOGENES
; TITLE OF INVENTION SURFACE PROTEINS OF STREPTOCOCCUS
; CURRENT PILLING DATE: 2003-10-14
; CURRENT PRILING DATE: 2003-10-14
; SEQID NOS 600
; SEQ ID NOS 600
; SEQ ID NOS 600
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US-10-425-114-47654
                                                                                                                                                                                                                        Score 84; DB 5; 1 Pred. No. 0.00013;
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Pred. No. 0.052;
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                                                                                                                                                                                                                                                                     1; Mismatches
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.2
SEQ ID NO 31
LENGTH: 432
                                                                                                                                                                                                                                                                                                                 1 LSAVLVSGVTLSSATTLSAV 20
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; ORGANISM: Streptococcus pyogenes
US-10-474-792-600
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; ORGANISM: Streptococcus mutans
US-10-797-821-31
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Best Local Similarity 78.9%;
Matches 15; Conservative ;
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11 Similarity 95.0%;
19; Conservative 1
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ORGANISM: Glycine max
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Best Local Similarity
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US-10-474-792-600
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Sequence 31, Application US/10797821

Publication No. US20050031633A1

APPLICANT: Smith, Daniel J.

APPLICANT: Smith, Daniel J.

TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens

TITLE OF INVENTION WIMBER: US/10/797,821

CURRENT APPLICATION NUMBER: US/383,930

PRIOR PILING DATE: 2003-03-07

PRIOR PLING DATE: 2002-03-07

PRIOR PLING DATE: 2002-03-07

PRIOR PLING DATE: 2002-03-07

PRIOR PLING DATE: 2002-03-07

PRIOR PLING DATE: 1909-04-12

PRIOR PLING DATE: 1999-04-12

PRIOR PLING DATE: 1999-04-13
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Pred. No. 8.9e-05;
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98.8%; Score 84; DB 4; I
Best Local Similarity 95.0%; Pred. No. 0.00013;
Matches 19; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                      0; Mismatches
           PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.2
SEQ ID NO 32
LENGTH: 432
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US-10-797-821-32
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20; Conservative
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Best Local 9
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Query Match 56.5%; Score 48; DB 4; Length 177; Best Local Similarity 60.0%; Pred. No. 18; Matches 12; Conservative 1; Mismatches 7; Indels
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Best Local Similarity 55.0%; Pred. No. 2.9;
Matches 11; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                       RESULT 15
US-060-678-3
; Sequence 3, Application US/09060878A
; Sequence 3, Application US/09060878A
; Patent No. US20010006642A1
; GENERAL INFORMATION:
; APPLICANT: Steidler, Lothar
APPLICANT: Remaut, Erik
; APPLICANT: Le Page, Richard William Falla
; TITLE OF INVENTION: Dell'very of Biologically Active
; TITLE OF INVENTION: Dell'very of Biologically Active
; TITLE OF INVENTION: Polypeptides
; TITLE OF INVENTION: Polypeptides
; TITLE REFERENCE: 8865-009-99
; CURRENT APPLICATION NUMBER: US/09/060, 878A
; CURRENT FILING DATE: 1998-04-16
; EARLIER FILING DATE: 1995-10-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FASTESEQ for Windows Version 3.0
; LENGTH: 27
; TVDE: non.
                                                                                        1 LSAVLVSGVTLSSATTLSAV 20
                                                                                                                          80 LSATLVAAVTLKERRTASAV 99
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ORGANISM: Artificial Sequence
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Search completed: January 25, 2006, 20:10:02 Job time : 61 secs

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2526, Ap
2526, Ap
25, Appl
181, App
28, Appl
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352, Appl
2, Appli
833, App
218; App
333, App
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806, App
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75, Appl
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                                                       January 25, 2006, 19:15:26; Search time 5.5 Seconds (without alignments) 39.378 Million cell updates/sec
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                                                                                                                                                                                                                                                                            Published Applications AA New:*

1: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
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6: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-11-155-084-352
US-11-125-402-2
US-11-053-076-218
US-11-052-554A-333
US-10-793-626-2126
US-10-793-626-2126
US-10-793-626-806
US-10-793-626-806
US-10-793-626-806
US-11-052-554A-181
US-11-052-554A-181
US-11-052-554A-181
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US-10-763-712A-75
US-10-517-939-84
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                                                                                                                                                                    75621 seqs, 10829074 residues
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 GenCore version
Copyright (c) 1993 - 2006
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Maximum Match 100%
Listing first 45 summaries
                                     OM protein - protein search, using sw model
                                                                                                                  1 LSAVLVSGVTLSSATTLSAV 20
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length: 2000000000
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Match Length DB
                                                                                             US-10-797-821-4
85
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26 35 41.2 141 7 US-11-103-957-51 Sequence 51, Appl 27 35 41.2 297 6 US-10-453-372-70 Sequence 70, Appl 29 35 41.2 297 6 US-10-6389-96 Sequence 70, Appl 29 35 41.2 297 6 US-10-513-639-17 Sequence 70, Appl 30 35 41.2 550 6 US-10-513-639-17 Sequence 76, Appl 31 35 41.2 550 6 US-10-6453-372-66 Sequence 61, Appl 32 41.2 578 6 US-10-6453-372-66 Sequence 61, Appl 32 41.2 600 6 US-10-878-556A-43 Sequence 61, Appl 35 41.2 660 7 US-11-033-039-385 Sequence 91, Appl 36 41.2 661 7 US-11-19-502-1 Sequence 1, Appl 36 41.2 661 7 US-11-19-502-1 Sequence 2, Appl 36 41.2 1016 7 US-11-109-51A-22 Sequence 2, Appl 36 41.2 1016 7 US-11-103-957-41 Sequence 41, Appl 41 35 41.2 1016 7 US-11-103-957-41 Sequence 3, Appl 41 35 41.2 1016 7 US-11-03-957-41 Sequence 3, Appl 41 35 41.2 141 103-957-41 Sequence 2, Appl 41 35 41.2 141 103-957-41 Sequence 2, Appl 56 US-10-451-375-3 Sequence 1262, Appl 56 US-10-811-35-284-283 Sequence 1262, Appl 57 US-11-03-554A-283 Sequence 1262, Appl 57 US-11-052-554A-283 Sequence 1262, Appl 57 US-11-052-554A-141 Sequence 72, Appl 57 US-11-129-143-72 Sequence 72, Appl 57 US-11-129-143-72 Sequence 72, Appl 57 US-11-129-143-72 Sequence 72, Appl 57 US-11-129-143-72 Sequence 72, Appl 57 US-11-129-143-72 Sequence 72, Appl 57 US-11-129-143-72 Sequence 72, Appl 58 US-11-129-143-72 Sequence 72, Appl 74 US-11-129-143-72 Sequence 72, Appl 74 US-11-129-143-72 Sequence 72, Appl 74 US-11-129-143-72 Sequence 72, Appl 74 US-11-129-143-72 Sequence 72, Appl 74 US-11-129-143-72 Sequence 72, Appl 74 US-11-129-143-72 Sequence 72, Appl 74 US-11-129-143-72 Sequence 72, Appl 74 US-11-129-143-72 Sequence 72, Appl 74 US-11-129-143-72 Sequence 72, Appl 74 US-11-129-143-72 Sequence 72, Appl 74 US-11-129-143-72 Sequence 72, Appl 74 US-11-129-143-72 Sequence 72, Appl 74 US-11-129-143-72 Sequence 72, Appl 74 US-11-129-143-72 Sequence 72, Appl 74 US-11-129-143-72 Sequence 72, Appl 74 US-11-129-143-72 Sequence 72, Appl 74 US-11-129-143-72 Sequence 72, Appl 74 US-11-129-143-72 Sequence 72, Appl 74 US-11-129-143-72 Sequence 72, Appl 74 US-11-129
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Sequence 833, Application US/10485788A

Publication No. US20050282743A1

GENERAL INFORMATION:

APPLICANT: Lu. Peter S.

APPLICANT: Schweizer, Johanne B.

APPLICANT: Schweizer, Johanne Marie

APPLICANT: Arbor Vita Corporation

TITLE OF INVENTION: Molecular Interactions in Cells

FILE REFERENCE: 20054-003320US

CURRENT APPLICATION WOMBER: US/10/485,788A

CURRENT APPLICATION NUMBER: US 60/309,841

PRIOR APPLICATION NUMBER: US 60/30,061

PRIOR FILING DATE: 2001-08-03

PRIOR PILING DATE: 2002-02-25

PRIOR PILING DATE: 2002-02-25

PRIOR PILING DATE: 2002-02-05

PRIOR PILING DATE: 2002-08-02

NUMBER OF SEQ ID NOS: 841

SOFTWARE: PATCHIN VETSION 3.1
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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US-10-485-788A-833
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TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads to
TITLE OF INVENTION: agronomically interesting phenotypes
FILE REPRENCE: (38-21)
CURRENT APPLICATION NUMBER: US/11/156,084
CURRENT PLING DATE: 2005-06-17
SUMBER OF SEQ ID ANOS: 364
SOFTWARE: Patent In version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NS-11-021-441-46

Sequence 46, Application US/11021441

Publication No. US20050249748A1

Sequence 46, Application WS/11021441

Publication No. US20050249748A1

APPLICANT: DUBENSKY, Thomas W., Jr.

APPLICANT: DUBENSKY, Thomas W., Jr.

APPLICANT: COCK, David N.

TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE

TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION WUMBER: US 60/616,750

PRIOR FILING DATE: 2004-10-01

PRIOR FILING DATE: 2004-00-05

PRIOR FILING DATE: 2004-00-30

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                                                                                                                                                                                                                                                Score 67; DB 7; Length 398;
Pred. No. 0.002;
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                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                               ; TYPE: PRT
; ORGANISM: Streptococcus pyogenes MGAS8232
US-11-052-554A-252
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                                                                                                                                                                                                                                                                                                                                                                                            1 LSAVLVSGVTLSSATTLSA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin version 3.3 SEQ ID NO 252
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1 Similarity 78.9%;
15; Conservative
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                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 15; Conserva
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US-11-156-084-352
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APPLICANT: Maurer, Patrik F
APPLICANT: Maurer, Patrik F
TITLE OF INVENTION: Hapten-Carrier Conjugates and Uses Thereof
TITLE OF INVENTION: Hapten-Carrier
CURRENT APPLICATION NUMBER: US/11/125,402
CURRENT FILING DATE: 2005-05-10
FRIOR APPLICATION NUMBER: US/10/622,064
FRIOR APPLICATION NUMBER: US 60/396,575
FRIOR APPLICATION NUMBER: US 60/396,575
FRIOR APPLICATION NUMBER: US 60/396,575
FRIOR FILING DATE: 2002-07-18
SOFTWARE: Patentin Version 3.2
SOFTWARE: Patentin Version 3.2
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                                                                                                                                    Length 313;
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; SEQ ID NO 352
; LENGTH: 313
; TYPE: PT TYPE: PROTOTHADGUS luminescens subsp. laumondii TTO1
US-11-156-084-352
                                                                                                                                    52.9%; Score 45; DB 7; 55.6%; Pred. No. 3.8; tive 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/11125402
Publication No. US20050281845A1
GENERAL INFORMATION:
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6 LAIVVLSALSLSSTTALAA 24
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172 LEVFLISGKTLTELTTLS 189
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                                                                                                                             Query Match
Best Local Similarity 55.69
Matches 10; Conservative
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ORGANISM: Escherichia coli
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WS-10-793-626-2126

WS-10-793-626-2126

Bublication No. US2050255478A1

Bublication No. US2050255478A1

GENDRAL INFORMATION:

APPLICANT: KIMMERLY, WILLIAM JOHN

TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

FILER REFERENCE: PU3-480US

CURRENT APPLICATION NUMBER: US/10/793,626

CURRENT FILING DATE: 1999-11-09

PRIOR APPLICATION NUMBER: 60/164,258

PRIOR APPLICATION NUMBER: 60/164,258

NUMBER OF SEQ ID NOS: 4472

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2126

LENGTH: 200
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JEQUENCE 806, Application US/10793626

Publication No. US20050255478A1

SEQUENCE 806, Application US/10793626

Publication No. US20050255478A1

APPLICANT: KIMMERLY, WILLIAM JOHN

TITLE OF INVENTION: STAPPLICACCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

TITLE OF INVENTION NUMBER: US/10/793,626

CURRENT APPLICATION NUMBER: US/10/793,626

CURRENT PILING DATE: 1999-11-09

PRIOR FILING DATE: 1999-11-09

NUMBER OF SEQ ID NOS: 4472

SEQ ID NOS: 4472

SEQ ID NOS: 4472

SEQ ID NOS: 4472
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; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
0S-10-793-626-2126
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                                                                                                                                                                                                                                                                                                                                                                            45.9%; Score 39; DB 7; Length 124; 50.0%; Pred. No. 11; ive 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                    ORGANISM: Mycobacterium tuberculosis H37Rv
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR FILING DATE: 2004-07-20
PRIOR PLING DATE: 2004-07-20
PRIOR PLING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
SSCTWARE: PatentIn version 3.3
LENGTH: 124
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47 VVVTGVTLSSENPPASV 63
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12 AVAVAGVATAAATTVT 27
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                     US-11-052-554A-333
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Publication No. US20050288866A1
GENERAL INFORMATION
GENERAL INFORMATION
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAFEUTIC POTENTIAL
FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
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APPLICANT: Lu, Peter S.
APPLICANT: Schweizer, Johannes
APPLICANT: Schweizer, Johannes
APPLICANT: Schweizer, Johannes
APPLICANT: Schweizer, Johannes
APPLICANT: Schweizer, Johannes
APPLICANT: Belmares, Michael P.
TITLE OF INVENTION: METHODS OF DIAGNOSING CERVICAL CANCER
FILE REFERENCE: VITA-OSCIP
CURRENT PILING DATE: 2005-02-07
PRIOR PILING DATE: 2003-09-09
PRIOR PILING DATE: 2003-07-29
PRIOR APPLICATION NUMBER: 60/490,094
PRIOR PILING DATE: 2003-07-29
PRIOR PILING DATE: 2003-07-29
PRIOR PILING DATE: 2003-07-29
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PRIOR PILING DATE: 2002-08-03
PRIOR PILING DATE: 2002-08-03
PRIOR PILING DATE: 2002-08-03
PRIOR PILING DATE: 2002-08-03
PRIOR PILING DATE: 2002-08-03
PRIOR APPLICATION NUMBER: 60/309,841
PRIOR PILING DATE: 2002-08-03
PRIOR PILING DATE: 2002-08-03
PRIOR PILING DATE: 2002-08-03
PRIOR PILING DATE: 2002-08-03
PRIOR PILING DATE: 2002-02-28
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                                                                 DB 6; Length 106;
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45.9%; Score 39; DB 3
Best Local Similarity 41.2%; Pred. No. 9.2;
Matches 7; Conservative 7; Mismatches
                                                                                                                     7; Mismatches
                                                          Query Match 45.9%; Score 39; Best Local Similarity 41.2%; Pred. No. 9 Matches 7; Mismatch
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SORTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 218
LENGTH: 106
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 218, Application US/11053076 Publication No. US20050255460A1 GENERAL INFORMATION:
                                                                                                                                                                                   4 VLVSGVTLSSATTLSAV 20
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60 VMVNGVSMENATSAFAI 76
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; ORGANISM: Homo sapiens
US-11-053-076-218
US-10-485-788A-833
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US-11-094-519A-41
; Sequence 41, Application US/11094519A
; Publication No. US20050281810A1
; GENERAL INFORMATION:
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LAIVVLSALSLSSTAALAA 24
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Best Local Similarity 56.2%;
Matches 9; Conservative
                                              352 LOPVFVGGVTVTNAT 366
1 LSAVLVSGVTLSSAT 15
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US-11-052-554A-25
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Publication No. US20050260581A1

GENERAL INFORMATION:

APPLICANT: CHIRON SpA

APPLICANT: FONTANA Maria Rita

APPLICANT: FONTANA Maria Rita

APPLICANT: PIZZA Mariagrazia

APPLICANT: MASIGRANI Vega

CURRENT APPLICATION NUMBER: US/10/467,657

CURRENT FILIAG DATE: 2003-08-11

FRICA APPLICATION NUMBER: GB-0103424.8

PRIOR APPLICATION NUMBER: GB-0103424.8

PRIOR APPLICATION NUMBER: 2001-02-12

NUMBER OF SEQ ID NOS: 9218

SOFTWARE: SEQ ID NOS: 9218

SEQ ID NO 2526

LENGTH: 823
                                                                                                                                                                                                                                                                                                                                        Sequence 5762, Application US/10467657

publication No. US20050260581A1

GENERAL INFORMATION:
APPLICANT: CHIRON SpA

APPLICANT: FONTAM Maria Rita
APPLICANT: FONTAM Maria Rita
APPLICANT: FONTAM Maria Rita
APPLICANT: MASIGNANI Vega

TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657

CURRENT PILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8

PRIOR PILING DATE: 20001-02-12

NUMBER OF SEQ ID NOS: 9218

SOFTWARE: SEGWIN99, version 1.04

SEQ ID NOS: 9218

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44.7%; Score 38; DB 6; Length 823;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
Matches 8; Conservative 3; Mismatches 4; Indels
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                                                                      Query Match 44.7%; Score 38; DB 6; Length 414; Best Local Similarity 52.9%; Pred. No. 64; Matches 9; Conservative 4; Mismatches 4; Indels
; OTHER INFORMATION: amino acid sequence US-10-793-626-806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Neisseria gonorrhoeae US-10-467-657-2526
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US-10-467-657-5762
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US-10-467-657-2526
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US-10-467-657-5762
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Sequence 25, Application US/11052554A

Sequence 25, Application US/11052554A

Sequence 25, Application No. US20050288866A1

GENERAL INFORMATION:
APPLICANT: Sachdeva.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
TITLE OF INVENTION: WINDER: US/11/052,554A

CURRENT APPLICATION NUMBER: US 60/589,227

PRIOR FILING DATE: 2004-07-20

FRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR FILING DATE: 2004-02-06

PRIOR FILING DATE: 2004-07-06

NUMBER OF SEQ ID NOS: 763

SOFTWARE: PatentIn version 3.3

SEQ ID NO 25

LENGTH: 182
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APPLICANT: BERNSTEIN, Jeanne
APPLICANT: LEVINE, Zurit
TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
FILE REFERENCE: 2786-0140P
CURRENT APPLICATION NUMBER: US/11/094,519A
CURRENT APPLICATION NUMBER: US/09/695,293
PRIOR FILING DATE: 2000-10-25
PRIOR FILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PATCHIN VET. 2.1
SEQ ID NO 41
LENGTH: 865
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Pred. No. 1.5e+02;
3; Mismatches 4;
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GENERAL INPORMATION:

APPLICANT: Sacindeva, et al.

TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN-LIKE

TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL

FILE REFERENCE: 30653/40359A

CURRENT APPLICATION NUMBER: US/11/052,554A

CURRENT APPLICATION NUMBER: US/05-007

PRIOR PILING DATE: 2004-07-20

PRIOR PELING DATE: 2004-02-06

NUMBER OF SEQ ID NOS: 763

SOOTWARE: Patentin version 3.3

SEQ ID NO 181

LENGTH: 182

TYPE: PRT

ORGANISM: Shigella flexneri 2a str. 2457T

US-11-052-554A-181
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Best Local Similarity 44.4%; Pred. No. 35;
Matches 8; Conservative 6; Mismatches 4; Indels
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Aag39522 Aag39521

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ADD31624
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ALIGNMENTS

Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen. Streptococcus mutans glucan binding protein-B peptide fragment. ADD93625 standard; peptide; 20 AA. (first entry) 29-JAN-2004 ADD93625; ADD93625 RESULT CCCCCCCCCCX8X4F4F4X8X8X8X8X8X8X8X8X8X8X8X8X8X8X8X

07-MAR-2003; 2003WO-US006962. WO2003075845-A2 18-SEP-2003.

Streptococcus mutans.

07-MAR-2002; 2002US-0363209P. (FORS-) FORSYTH INST.

Taubman MA; Smith DJ, WPI; 2003-845091/78.

Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.

Claim 11; Page 10; 49pp; English.

The present sequence is that of a peptide comprising amino acid residues 16-35 of the glucan binding protein-B (GbpB) of Streptococcus mutans strain SK32 ADD93649. The peptide binds to a major histocompatibility complex (MHC) class II protein. It was identified as a potential B cell epitope using a matrix-based algorithm for epitope prediction, which was used to search the primary amino acid sequence of GbpB for known MHC class II binding motifs. The peptide can be used in immunogenic compositions and subunit vaccines for dental caries. These comprise MHC class II protein-binding GbpB peptides covalently linked with peptide subunits (preferably from the catalytic domain) of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Diepitopic or multiepitopic polypeptides can be

Description ,		Adn20492 Bacterial
SUMMARIES	ADD93625 ADX37248 ADX93650 ADD93653 ADX37272 ADX37272 ADX37272 ADX37276 ADX37276 ADX37276 ADX37276 ADX37276 ADX37276 ADX37276 ADX37276 ADX37276 ADX37276 ADX37276 ADX37276 ADX37276 ADX37276 ADX37276 ADX3286	ADN20492
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Minimum DB seq Maximum DB seq	length: length:	2000000000	000	0			
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Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
                                                                                                  Streptococcus mutans glucan binding protein-B.
                                         ADD93649 standard; protein; 431 AA.
                                                                              29-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New composition comprising a fragment of a glucan binding protein-B (dpbB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
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prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in passive immunisation.
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                                                                                                                                                                                                                                                   immunogenicity; immune stimulation; glucan binding protein-B;
microparticle; major histocompatibility complex; tooth disease.
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                                                           Score 92; DB 7; Length 20;
Pred. No. 2.4e-08;
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                                                                                                                                                                      ADX37248 standard; peptide; 20 AA
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08-JAN-1999; 99US-0115142P.
12-APR-1999; 99US-0015090049.
07-MAR-2002; 2002US-0363209P.
08-AUG-2002; 2003US-0402483P.
07-MAR-2003; 2003US-00383930.
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Matches 20; Conservative
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Matches 20; Conservative
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(TAUB/) TAUBMAN M A.
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Streptococcus mutans.
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Gaps

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0; Indels

0; Mismatches

20; Conservative

(first entry)

29-JAN-2004

07-MAR-2003; 2003WO-US006962.

WO2003075845-A2.

18-SEP-2003

Taubman MA;

Smith DJ,

(FORS-) FORSYTH INST

100.0%; Score 92; DB 7; Length 431; 100.0%; Pred. No. 1e-06;

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caries. The compositions comprise major histocompatibility complex (MHC) class II protein-binding GDpB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Dispitopic or multiepitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GDpB can be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus mutans glucan binding protein-B.
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                                                                                                                       passive immunisation.
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                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                          Sequence 431 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                        ADD93653;
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                                                                                                                                                 The present sequence is the protein sequence of the glucan binding protein—B (GDpB) of Streptococcus mutans strain SK32. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental carles. The compositions comprise major histocompatibility complex (WHC) class II protein-binding GbpB peptides, especially HLA-binding peptides, cowpositions are used in a claimed method of eliciting production of an antibody in a mammal. Dispitopic or multiepitopic polypeptides can be prepared synthetically or by recombinant bNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in
                                                  Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 92; DB 7; Length 431; Best Local Similarity 100.0%; Pred. No. 1e-06; Matches 20; Conservative 0; Mismatches 0; Indels
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                                                                                                                     Claim 6; Page 7; 49pp; English
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                                                                                                                                                                                                                                                                                                                                                   passive immunisation.
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 2003-845091/78.
                   GENBANK; AY046410.
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 431 AA;
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protein-B (GDPB) of Streptococcus mutans strain 55M3. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions comprise major histocompatibility complex (MHC) class II protein-binding GDPB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Diepitopic or multiepitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GDpB can be used in Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein. The present sequence is the protein sequence of the glucan binding Length 431; Score 92; DB 7; Pred. No. 1e-06; 5; Page 8-9; 49pp; English. 100.0%; immunisation. WPI; 2003-845091/78. Best Local Similarity GENBANK; AY046414 Sequence 431 AA; Query Match passive Claim

Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.

07-MAR-2003; 2003WO-US006962. 07-MAR-2002; 2002US-0363209P.

WO2003075845-A2 18-SEP-2003 Taubman MA;

Smith DJ,

WPI; 2003-845091/78.

GENBANK; AY046411.

(FORS-) FORSYTH INST.

Claim 5; Page 8; 49pp; English.

The

The present sequence is the protein sequence of the glucan binding protein-B (GbpB) of Streptococcus mutans strain 3VR4. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. Invention provides immunogenic compositions and vaccines for dental invention

Matches

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The invention relates to a composition comprising a fragment of a glucan binding protein-B (GbpB) and a biocompatible microparticle, where the fragment binds to a major histocompatibility complex (MHC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds to a Streptococcus mutans GbpB protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
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microparticle; major histocompatibility complex; tooth disease.
                                                                     immunogenicity; immune stimulation; glucan binding protein-B; microparticle; major histocompatibility complex; tooth disease.
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                                      Streptococcus mutant glucan binding protein B variant #2.
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12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-0363209P.
08-AUG-2002; 2002US-04024399.
07-MAR-2003; 2003US-00383930.
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21-APR-2005 (first entry)
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                                                                                                                                  Streptococcus mutans
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08-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
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                                                                                                                                                                                                                                                                                                                   immunogenicity; immune stimulation; glucan binding protein-B;
microparticle; major histocompatibility complex; tooth disease.
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Pred. No. 1e-06;
Mismatches 0; Indels
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     0; Mismatches
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08-JAN-1999; 99US-0115142P.
12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-0363209P.
08-AUG-2002; 2002US-0402483P.
07-MAR-2003; 2003US-00383930.
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Les 20; Conservative
   Conservative
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TAUBMAN M A.
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Gaps

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10-FEB-2005

ADX37273;

RESULT 7

Best Loc Matches

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The present invention relates to a computational method (M1) for identifying adhesin and adhesin-like proteins, by computing the sequence-based attributes of protein sequences using five attribute modules of a contraining an artificial network (MNN) for each of the computed five attributes, and identifying the adhesin and adhesin-like proteins an artificial network (Pad) as capes of a diesin-like proteins probability of being an adhesin and adhesin-like proteins, having 274 fully defined 162 encoding adhesin and adhesin-like proteins, having 274 fully defined 162 genes encoding adhesin and adhesin-like proteins, having 105 hypothetical defined 306-18976 base pairs (SEQ ID NO: 385-658) sequences; a set of 105 hypothetical defined 306-18976 base pairs (SEQ ID NO: 12-79); a set of 279 annotated adhesin and adhesin-like proteins, having 105 fully defined 106-5291 base pair (SEQ ID NO: 12-79); a set of 105 hypothetical adhesin-like proteins, having 105 fully defined 106-5291 base pair (SEQ ID NO: 280-384) sequences; and a fully connected multilayer feed forward ANN (1) based on (M1). (M1) is useful for identifying and shesin and adhesin-like proteins for further testing in development of new vaccine forwulations conteins for therapeutic potential. And identifying and short-listing cueful for identifying putative adhesins that are important in discovery and preventing therapeuties for whooping cough, pneumonia, cueful for identifying putative adhesins that are important in discomminations culcar and uninary tract infections. (M1) is capable of predicting adhesin pathogen adhesin culcar and uninary tract infections. (M1) is capable of predicting adhesin and entered for manual pathogenetic spectrum. (M1) is capable of predicting adhesive nature of the proteins. The present sequence is a microbial pathogen adhesin
    Computational method for identifying adhesin and adhesin like molecules, comprises computing sequence-based attributes of protein sequences using neural network software and training an artificial neural network.
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                                                                                             16; SEQ ID NO 210; 402pp; English.
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bordetella pertussis infection; antibacterial; pneumonia;
antiinflammatory; respiratory-gen.; gastric ulcer; antiulcer;
gastrointestinal-gen.; urinary tract infection; antimicrobial; uropathic.
                                                                                                                                                                                                                                                                                                                                                                        New composition comprising a fragment of a glucan binding protein-B (dpbB) that binds to MrC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
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                                        980S-0081550P.
990S-0115142P.
990S-00290049.
2002US-0363209P.
09-MAR-2004; 2004US-00797821
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Matches 20; Conservative
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                                                                                                                                                                                                       SMITH D J.
TAUBMAN M A.
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                                                                                                                                                                                                                                                                                                                             WPI; 2005-151644/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 431 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2005076010-A2.
                                        13-APR-1998;
08-JAN-1999;
12-APR-1999;
07-MAR-2002;
08-AUG-2002;
                                                                                                                                                              07-MAR-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-AUG-2005.
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(TAUB/)
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Gaps

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Local Similarity 100.
nes 20; Conservative
                                                                                                                                      Streptococcus mutans
                                                             Sequence 432 AA;
                                                                                                                                            US2005031633-A1
                                                                                                                                                                                   (SMIT/) SMITH
                                                                                                                                                             13-APR-1998;
08-JAN-1999;
12-APR-1999;
07-MAR-2002;
08-AUG-2002;
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                                                                         Matches
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The invention relates to a composition comprising a fragment of a glucan binding protein-B (GbpB) and a biocompatible microparticle, where the fragment binds to a major histocompatibilty complex (MRIC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds to a Streptococcus mutans GbpB protein of the invention. Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen. 100.0%; Score 92; DB 9; Length 432; 100.0%; Pred. No. 1e-06; ive 0; Mismatches 0; Indels Streptococcus mutans glucan binding protein-B. ADD93651 standard; protein; 432 AA. 1 LSSATTLSAVKADDFDAQIA 20 Claim 5; Page 8; 49pp; English 07-MAR-2002; 2002US-0363209P. 07-MAR-2003; 2003WO-US006962 29-JAN-2004 (first entry) 20; Conservative Smith DJ, Taubman MA; passive immunisation. (FORS-) FORSYTH INST. Streptococcus mutans. WPI; 2003-845091/78. Query Match Best Local Similarity Matches 20; Conserv GENBANK; AY046412 Sequence 432 AA; Sequence 432 AA; WO2003075845-A2. 18-SEP-2003. ADD93651; 16 RESULT 8888888888 ð 8 ö The present sequence is the protein sequence of the glucan binding protein-B (GbpB) of Streptococcus mutans strain 3SNI. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The includes a number of human leucocyte antigen (HLA)-binding epitopes. The caries. The compositions comprise major histocompatibility complex (MHC) class II protein-binding GbpB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Dispitopic or multispitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against WHC class II binding fragments of GbpB can be used in passive immunisation. composition comprising a fragment of a glucan binding protein-B DB) that binds to MHC class II protein, and a biocompatible oparticle, useful for producing an antibody (claimed) for immunizing Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein. Gaps .; 0 immunogenicity; immune stimulation; glucan binding protein-B; microparticle; major histocompatibility complex; tooth disease 100.0%; Score 92; DB 7; Length 432; 100.0%; Pred. No. 1e-06; ive 0; Mismatches 0; Indels Streptococcus mutant glucan binding protein B variant #4. 100.0%; Prec. ... Claim 3; SEQ ID NO 32; 73pp; English. ADX37275 standard; protein; 432 AA 1 LSSATTLSAVKADDFDAQIA 20 16 LSSATTLSAVKADDFDAQIA 35 990S-0115142P. 99US-00290049. 2002US-0363209P. 2002US-0402483P. 2003US-00383930. Claim 5; Page 8; 49pp; English. mammals against dental caries 09-MAR-2004; 2004US-00797821 (first entry) Smith DJ, Taubman MA; microparticle, useful SMITH D J. TAUBMAN M A. WPI; 2005-151644/16.

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                                                                                                                                                                                                                                                        The present sequence is the protein sequence of the glucan binding protein. B (GppB) of Streptococcus mutans strain 15JP2. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions compositions and vaccines for dental class in protein-binding GbpB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The antibody in a mammal. Diepitopic or multiepitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in
Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
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Best Local Similarity 95.0
Matches 19; Conservative
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GppB)

RESULT 13

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invention is
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                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                       developmental biology; cell signalling; insecticide;
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   Drosophila melanogaster polypeptide SEQ ID NO 38595.
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11-JUL-2000; 2000US-00614150.
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499 TLPSPIRADDFDAQ 512
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                                                                                            Drosophila melanogaster.
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Matches 9; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 694 AA;
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                                                           pharmaceutical
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                                         Drosophila;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gapie
                                                                                                                                                                                                                                                                                 immunogenicity; immune stimulation; glucan binding protein-B;
microparticle; major histocompatibility complex; tooth disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98.9%; Score 91; DB 9; Length 432; 95.0%; Pred. No. 1.5e-06; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                              Streptococcus mutant glucan binding protein B variant #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; SEQ ID NO 31; 73pp; English.
                                                                                                                             ADX37274 standard; protein; 432 AA.
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LSSATTLSAVKADDFDAQIA 20
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08-JAN-1999; 99US-0115142P.
12-APR-1999; 99US-00150409.
07-MAR-2002; 2002US-0363209P.
07-MAR-2003; 2003US-0402483P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mammals against dental caries.
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                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Taubman MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SMIT/) SMITH D J.
(TAUB/) TAUBMAN M A.
                                                                                                                                                                                                                                                                                                                                          Streptococcus mutans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2005-151644/16.
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                                                                                                                                                                                                        21-APR-2005
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                                                                                                                                                                   ADX37274;
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Best Loc Matches

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RESULT 14
ABB70601
ID ABB70
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AC ABB70
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57377-ABR3072072). The sequence data for this patent did not form part of printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 41619; 21pp + Sequence Listing; English.
                                                                                                                                                                              Li PWD, Myers EW;
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                   Venter JC, Adams M,
                                                                                                                                                                                                                                                               WPI; 2001-656860/75.
N-PSDB; ABL15712.
                                                                                     (PEKE ) PE CORP NY
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Query Match 50.0%; Score 46; DB 4; Length 4643; Best Local Similarity 61.1%; Pred. No. 1.1e+03; Matches 11; Conservative 1; Mismatches 6; Indels Sequence 4643 AA;

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Gaps ;

Search completed: January 25, 2006, 19:01:43 Job time : 69.2 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

January 25, 2006, 18:48:55; Search time 9.1 Seconds (without alignments) 211.465 Million cell updates/sec

US-10-797-821-5 92 Title: Perfect score:

1 LSSATTLSAVKADDFDAQIA 20 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir 80:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	•
Result No.	Score	Query Match	Length	DB	ID	Description
	47	51.1	428	7	F85485	flavoprotein, elec
7	47	51.1	428	~	F90634	
m	47	51.1	428	0	C64725	
4	45	48.9	428	7	AG0511	FixC protein [impo
2	43	46.7	398	N	E87403	hetical
9	43	46.7	1196	7	A29130	beta-amylase (EC 3
7	42	45.7	427	7	H90728	probable pectinest
æ	42	45.7	427	N	A85580	probable pectinest
60	42	45.7	427	~	D64813	ybhc protein precu
10	42	45.7	837	7	H87638	TonB-dependent rec
11	42	45.7	840	7	A87639	TonB-dependent rec
12	42	45.7	868	~	A40114	fasciclin II precu
13	42	45.7	2422	7	T12687	ALR protein homolo
14	41	44.6	167	7	AI1167	hypothetical prote
15	41	44.6	167	~	AD1526	hypothetical prote
16	41	44.6	310	٦	S37695	calcium-binding pr
17	41	44.6	507	~	S05542	hypothetical prote
18	41	44.6	883	~	T37208	-
19	41	44.6	2514	Н	MINWVN2	겉
20	40	43.5	198	N	S60923	hypothetical prote
21	40	43.5	218	Н	B41316	flagellin Bl precu
22	40	•	254	~	T15938	hypothetical prote
23	40	43.5	290	N	F84839	hypothetical prote
24	40	43.5	611	~	A53418	calmegin precursor
25	40	43.5	815	0	T00538	probable serine pr
56	40	43.5	816	7	T08978	oteir
27	40	43.5	2492	н	A44213	
28	40	43.5	2492	-	C44213	nonstructural poly
29	40	43.5	2492	Н	MNWVTD	

nonstructural poly	nonstructural poly	nonstructural poly	hypothetical prote	hypothetical prote	probable ribonucle	hypothetical prote	probable proteinas	proteinase (import	regulatory protein	succinoglycan bios	succinoglycan bios	malate dehydrogena	anthranilate synth	anthranilate synth
872349	MINWVS	MNWV82	E95225	Н98089	S77813	875357	H98220	AH3065	F64750	AG3055	F98230	T41286	JQ1685	827752
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2493	2512	2514	86	86	114	153	186	186	297	329	337	341	621	621
43.5	43.5	43.5	42.4	42.4	42.4	42.4	42.4	42.4	42.4	42.4	42.4	42.4	42.4	42.4
0.4	40	40	39	39	39	39	39	39	39	39	39	39	39	39
30	35	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

C;Species: Escherichia coli C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 C;Accession: F85485 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayheriller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001 A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7. A;Reference number: A85480; MUD:21074935; PMID:11206551 A;Accession: F85485 A;Residuas; preliminary A;Molecule type: DNA A;Residuas: 1-428 <5TO. A;Eschus: preliminary A;Residuas: 1-428 <5TO. A;Eschus: preliminary A;Residuas: 1-428 <5TO. A;Eschus: preliminary A;Residuas: 1-428 <5TO. A;Eschus: preliminary A;Eschus: Dray A;Eschus: DNA A;Eschus: Dray A;Eschus: DNA A;Eschus: Dray A;Eschus: DNA A;Experimental source: strain O157:H7, substrain EDL933 flavoprotein, electron transport [imported] - Escherichia coli (strain 0157:H7, substra

C, Genetics:

C; Superfamily: fixC protein

Gaps ö 51.1%; Score 47; DB 2; Length 428; 52.9%; Pred. No..4.8; tive 4; Mismatches 4; Indels Conservative Best Local Similarity Matches 9; Conserv Query Match

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2 SSATTLSAVKADDFDAQ 18 ઠે

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Cipactein [imported] - Escherichia coli (strain 0157:H7, substrain RIMD 0509952)
Cispecies: Escherichia coli
Cipate: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
Cipate: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
Cipate: 18-Jul-2001
RiHayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and gen. A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Status: preliminary

A; Molecule type: DNA

A;Residues: 1-428 <HAY>
A;Cross-references: UNIPROT:Q8XA26; UNIPARC:UPI0000D075B; GB:BA000007; PIDN:BAB33469.1
A;Experimental source: strain O157:H7, substrain RIMD 0509952

A,Gene: EC80046 C,Superfamily: fixC protein

51.1%; Score 47; DB 2; Length 428; Query Match

Gaps

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C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Accession: E4403
C;Accession: E4403
R;Mierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n. J.; Ermolaeva, M.; White, O.; Salzaberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. US.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: UNIPROT: Q9A8V7; UNIPARC: UPI00000C730A; GB: AE005673; NID: 913422573; P. C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Bacillus polymyxa
C;Species: Ds-Oct-1987 #sequence revision 03-Mar-1994 #text_change 09-Jul-2004
C;Accession: A29130; B29130; A32251; A29108
C;Accession: A29130; B29130; A32251; A29108
R;Kawazu, T.; Nakanishi, Y.; Uozumi, N.; Sasaki, T.; Yamagata, H.; Tsukagoshi, N.; Udak-
J. Bacteriol. 169, 1564-1570, 1987
A;Title: Cloning and nucleotide sequence of the gene coding for enzymatically active fr
A;Reference number: A29130; MUID:87165765; PMID:2435707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPARC:UP1000017ACA0
R;Uozumi, N.; Sakurai, K.; Sasaki, T.; Takekawa, S.; Yamagata, H.; Tsukagoshi, N.; Udak.
C Bacteriol. 171, 375-382, 198
A;Title: A single gene directs synthesis of a precursor protein with beta- and alpha-am;
A;Reference number: A32251; MUID:89123046; PMID:2464578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              beta-amylase (EC 3.2.1.2) / alpha-amylase (EC 3.2.1.1) precursor - Bacillus polymyxa
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A;Residues: 1-936 <KAW>
A;Cross-references: UNIPROT:P21543; UNIPARC:UPI000017AC9F; GB:M15817
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Nucleic Acids Res. 15, 3934, 1987
A;Tille: Sequence of an active fragment of B. polymyxa beta amylase.
A;Actesesion: A29108; MUID:87231094; PMID:2438660
A;Accession: A29108
                                                                                                                                                                                                                                                                                                                                                                            - Caulobacter crescentus
Length 428;
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                                                                  Indels
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A, Status: not compared with conceptual translation
   Score 45; DB 3
Pred. No. 10;
3; Mismatches
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Pred. No.
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A)Cross-references: UNIPARC:UPIO00017ACA1
A;Experimental source: strain 72
                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein CC1244 [imported]
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144 LASRRAMAAVLSDGFDAYLA 163
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   48.9%;
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                                                                                                                                        2 SSATTLSAVKADDFDAQ
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Best Local Similarity 45.0
Matches 9; Conservative
                                                                      9; Conservative
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                                      Similarity
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   Query Match
Best Local S:
Matches 9
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                                                                                                                                                                                                                                                                                                                                  fixC protein - Bscherichia coli (strain K-12)

(5) FixC protein - Bscherichia coli (strain K-12)

N; Contains: probable quinone reductase (EC 1.6.5.-)

C; Species: Bscherichia coli

C; Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004

C; Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004

C; Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004

R; Blattner, Fx.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.A.; Rose, D.J.; Mau, B.; Shao, Y.

A; Rose, D.J.; Mau, B.; Shao, Y.

A; Rose complete genome sequence of Escherichia coli K-12.

A; Reference number: A64720; MUD:97426617; PMID:9278503

A; Reference number: A64720; MUD:97426617; PMID:9278503

A; Reference number: A64720; MUD:97426617; PMID:9278503

A; Residues: 1-428 *Subar.

A; Residues: preliminary

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A;Status: Dreliminary
A;Molecule type: DNA
A;Residues: 1-428 <PAR>
A;Cross-references: UNIPARC:UPI00000599AE; GB:AL513382; PIDN:CAD01231.1; PID:g16501360;
C;Genetics:
A;Gene: STY0087
C;Superfamily: fixC protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reaidues: 1-279,'IM',282-309,'F',311-428 <YUR>
A;Cross-references: UNIPARC:UPI000016EDD3; EMBL:D10483; NID:g216434; PIDN:BAA01319.1;
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C;Keywords: FAD; flavoprotein; oxidoreductase; transmembrane protein
F;8-24/Domain: transmembrane #status predicted <TVM>
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Pred. No. 4.8;
4; Mismatches
              Pred. No. 4.8;
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327 AAKTVLSAMKSDDFSKQ 343
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          52.9%;
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              Best Local Similarity 52.9
Matches 9; Conservative
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Best Local Similarity
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C; Superfamily: pectinesterase pemB

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C;Accession: D64813
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C. A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
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A;Cross-references: UNIPROT:P46130; UNIPARC:UPI000013A348; GB:AE000180; GB:U00096; NID:
A;Experimental source: strain K-12, substrain MG1655
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A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
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C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
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C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
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Pred. No. 34;
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                                                                           Length 427
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                                                                           Score 42; DB 2;
Pred. No. 34;
                                                    45.7%; Scor.
58.8%; Pred. No. 53,
2; Mismatches
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58.8%; Pred. No. 5.,
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LDSATSTSALRASEFE
                                                                       Query Match
Best Local Similarity 58.8<sup>3</sup>
Matches 10; Conservative
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nes 10; Conserv
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A;Molecule type: DNA
A;Residues: 1-837 <STO>
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Probable pectinesterase [imported] - Escherichia coli (strain O157:H7, substrain RIMD 05 C; Species: Escherichia coli
C; Species: Escherichia coli
C; Species: Escherichia coli
C; Species: Escherichia coli
C; Species: Bscherichia coli
C; Species: Bscherichia coli
C; Spacession: H99728
R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. Gasawara, N.; Yasunaga, T.; Ruhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A; Tille: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genca A; Reference number: A99629; MUID:21156231; PMID:11258796
A; Accession: H90728
A; Molecule type: DNA
A; Residues: 1-427 cHAY>
A; Cross-references: UNIPROT:Q8X891; UNIPARC:UPIO00000097C; GB:BA000007; PIDN:BAB34223.1;
A; Experimental source: strain O157:H7, substrain RIMD 0509952
C; Genetics:
A; Coperfamily: pectinesterase pemB
A;Residues: 'MIGL',2-66,'S',68-99,'D',101-153,'N',155-176,'Q',178-226,'KS',229-329,'S',3',737-740,'S',742-757,'N',759-776 <RHO>
A;Cross-references: UNIPARC:UP10000170CFF
A;Experimental source: ATCC 8523
C;Genetics:
C;Genetics:
A;Start codon: TTG
C;Punction:
A;Description: catalyzes both the hydrolysis of internal 1,4-alpha-D-glucosidic bonds (a b,8 tarm to non-reducing end (beta-amylase activity)
A;Pathway: glycosidase; hydrolase; polysaccharide degradation
C;Keywords: alycosidase; hydrolase; polysaccharide degradation
C;Keywords: signal sequence #status predicted <MAT>
F;0-1136/Porduct: beta-amylase core homology <AMY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probable pectinesterase ybhC [imported] - Escherichia coli (strain 0157:H7, substrain ED C.Species: Escherichia coli (C.Species: I6-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 (C.Species: I6-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 (C.Species: N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Roke, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamous1s, K.; Apodaca, A.Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.

A.Reference number: A85480; MUID:21074935; PMID:11206551

A.Scension: A85580
A.Status: preliminary
A.Molecule type: DNA
A.Residues: L-427 cSTO>
A.Cross-references: UNIPROT:QBX891; UNIPARC:UPI000000097C; GB:AE005174; NID:g12513707; FA;Experimental source: strain 0157:H7, substrain EDL933
A.Genetics:
A.Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
46.7%; Score 43; DB
Best Local Similarity 50.0%; Pred. No. 69;
Matches 9; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ed. No. 34;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.
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nes 10; Conservative
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C;Species: Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: All67
C;Accession: All167
C;Accession: All167
C;Accession: All67
C;Accession: Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
C; Dominguez-Bernal, G; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
C; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mc
Occ.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Fitle: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Cross-references: UNIPROT:Q8Y8Z7; UNIPARC:UP10000054D52; GB:NC_003210; PIDN:CAC98823...
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R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke:
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M.
A;Authors: Kreft, J.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-167 <GLA>
A;Cross-references: UNIPROT:Q92DRS; UNIPARC:UP10000CC338; GB:AL592022; PIDN:CAC95980.1
A;Experimental source: strain Clip11262
                                     A, Accession: T12687
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Residues: 1-2422 < PER>
A, Residues: 1-2422 < PER>
A, Residues: 1-2422 < PER>
A, Residues: 1-2422 < PER>
C, Cross-references: UNIPROT: O46083; UNIPARC: UPI000007FBE8; EMBL: AL021106; NID: e1371406; A, Experimental source: clone cosmid 63B12
C, Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein lin0748 [imported] - Listeria innocua (strain Clip11262)
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C.Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
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Pred. No. 18;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42; DB 2; Length 246. Pred. No. 2.2e+02; Sred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                           A,Cross-references: FlyBase:FBgn0000117
A,Introns: 462/2; 1914/3; 2089/3; 2288/2; 2331/3; 2392/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: strain EGD-e
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124 SGTEMGAIKAEDADKQ 139
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Best Local Similarity 50.0%;
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A;Accession: T12687
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Best Local Similarity
Matches 8; Conserv
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                        Tonbe-dependent receptor [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: O-Apr-2001 #text_change 09-Jul-2004
C;Accession: A87639
R;Nierman, W.C; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Bisen, J.; Heidelberg, J.
B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Exmolaeva, M.; Mite, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S. 98, 4136-4414, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUD:21173698; PMID:11259647
A;Accession: A87639
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-840 <STO>
A;Cross-references: UNIPROT:Q9A3Q5; UNIPARC:UP100000C798C; GB:AE005673; NID:g13424815; F
C;Genetics:
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fasciclin II precursor - American bird grasshopper C;Species: Schistocerca americana (American bird grasshopper)
C;Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 09-Jul-2004
C;Accession: A40114; B181817
R;Harrelson, A.L.; Goodman, C.S.
Science 242, 700-708, 1988
A;Title: Growth cone guidance in insects: fasciclin II is a member of the immunoglobulin A;Reference number: A40114; MUID:89043938; PMID:3187519
A;Accession: A40114
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-898 cHAR>
A;Cross-references: UNIPROT:P22648; UNIPARC:UPI000012A542
A;Cross-references: UNIPROT:P22648; UNIPARC:UPI000012A542
B;Cross-references: UNIPROT:P22648; UNIPARC:UPI000012A542
B;Cross-references: UNIPROT:P22648; UNIPARC:UPI000012A542
B;Cross-reference number: A94202; MUD:88276943; PMID:2839842
A;Reference number: A94202; MUD:88276943; PMID:2839842
A;Accession: B31817
A;Accession: B31817
A;Accession: B31817
A;Accession: B31817
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N;Alternate names: protein 63B12.3
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T12687
E;Ferrax, C; Yidal, S; Brun, C; Bucheton, A; Demaille, J.G.
submitted to the EMBL Data Library, January 1998
A;Description: Sequencing the distal X chromosome of Drosophila melanogaster.
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C;Genetics: A;Gene: lin0748

Query Match 44.6%; Score 41; DB 2; Length 167; Best Local Similarity 66.7%; Pred. No. 18; Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps

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NUCLECTIDE SEQUENCE.
STRAIN=SSM3;
MEDLINE=21481971; PubMed=11598068;
DOI=10.1128/IAI.69.11.6931-6941.2001;
Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
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Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
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Peruzzi F., Piggot P.J., Daneo-Moore L.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U78607; AAD00288.1; -; Genomic_DNA.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
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Glucan-binding protein B.
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DOI=10.1128/IA1.69.4.2493-2501.2001,
Chia J.S., Lee Y.Y., Huang P.T., Chen J.Y.;
"Identification of stress-responsive genes in Streptococcus mutans by
differential display reverse transcription-PCR.";
Infect. Immun. 69:2493-2501(2001).
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"cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production iclinical isolates.";

Infect. Immun. 69:6931-6941(2001).

EMBL; AY046411; AAK08104.1; -; Genomic_DNA.

EMBL; AY046411; AAK94501.1; -; Genomic_DNA.

InterPro; IPR007921; CHAP.

InterPro; IPR001921; CHAP.

Fam; PP05227; CHAP:

PRINTS; PR01952; BIAPPROTEIN.

PROSITE; PS50911; CHAP:

SRQUENCE 431 AA; 44592 MW; 3BBE21FC5E47232E CRC64;
                                                                                                                                                                                                                                                                                                                                                            MEDLINE-21481977; PubMed-11598074; DOI-10.1128/IAI.69.11.6987-6998.2001; DOI-10.1128/IAI.69.11.6987-6998.2001; Chia J.S., Chang L.Y., Shun C.T., Chorn J.Y.; Chang L.Y., Shun C.T., Chornor is essential for cell "A 60-kilodalton immunodominant glycoprocein is essential for cell wall integrity and the maintenance of cell shape in Streptococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Immunodominant glycoprotein IDG-60 (Glucan-binding protein
                                                                                          Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=GS-5, Chiang L.-Y., Lee Y.-Y., Chen J.-Y.; Chia J.-S., Chang L.-Y., Lee EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jin S., Duncan M.J., Taubman M.A., Smith D.J.; "Cloning of the gbpB gene from Streptococcus mutans."; J. Dent. Res. 79:224-224 (2000).
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QBDWM3 STRMU
ID QBDWM3 STRMU PRELIMINARY; PRT; 431 AA.
AC QBDWM3 STRMU PRELIMINARY; PRT; 431 AA.
DT 01-WAR-2003 (TrEMBLrel. 23, Created)
DT 01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
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Best Local Similarity 100.0%; Pred. No. 1.0.
Matches 20; Conservative 0; Mismatches
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                                                                                                                                                                                                 MEDLINE=21153617; PubMed=11254612;
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                                                                         Streptococcus mutans.
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"Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates.";
Infect. Immun. 69.6931-6941(2001).
EMBL: AV046410, AAX94500.1; -; Genomic_DNA.
InterPro; IPR007921; GIAP.
InterPro; IPR009148; SibA.
     Duncan M.J.;
"Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates.";
Infect. Immun. 69:6931-6941(2001).
EMBL, ANO46441, ANO46441; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
PRINTS; PR01852; SIBAPROTEIN.
PRINTS; PR01852; SIBAPROTEIN.
BROSITE; PS50911; CHAP; 1.
SEQUENCE 431 AA; 44650 MW; 05D38DBDBBC4609F CRC64;
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Pred. No. 1.6e-06;
Mismatches 0; Indels
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Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
                                                                                                                                                                                                                                    100.0%; Score 92; DB 2; Length 43
100.0%; Pred. No. 1.6e-06;
tive 0; Mismatches 0; Indels
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PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 44620 MW; 464FE3B563FB7E51 CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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MEDLINE=21481971; PubMed=11598068;
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NCBI_TaxID=1309;
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Q9AG98 STRMU PRELIMINARY; PRT; Q9AG98; 11-JUN-2001 (TrEMBLrel. 17, Created)

Q9AG98 STRMU

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NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE.
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                            Query Match
Best Local Similarity
Matches 20; Conserv
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1093872 ST

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Duncan M.J.;
Duncan M.J.;
Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates.";
Infect. Immun. 69:6931-6941(2001).
EMBL; AY046413; AX0454503.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR007921; CHAP.
InterPro; IPR007921; CHAP.
InterPro; IPR007921; CHAP.
SPGONSTS; PR01825; SIBAPROTEIN.
PROSTTS; PR01825; SIBAPROTEIN.
SROUGENCE 432 AA; 44652 NW; 3F88ECB9A1F3BE4F CRC64;
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                                                                                                                                                                                                             STRAIN=UAIS9 / ATCC 700610 / Serotype c;
MEDLINE=22295063; PubMed=12397186; DOI=10.1073/pnas.172501299;
Ağdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Carson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P.,
Qian Y., Li S., Zhu H., Najar P.Z., Lai H., White J., Roe B.A.,
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Putative secreted antigen GbpB/SagA; putative peptidoglycan
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                                                                                      Streptococcus mutans.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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STRAIN=3SN1;
Jin S., Duncan M.J., Taubman M.A., Smith D.J.;
"Cloning of the gbpB gene from Streptococcus mutans.";
J. Dent. Res. 79:224-224 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                431 AA; 44620 MW; 2D1CA685248CCD3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                 pathogen.";
Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
EMBL; AE014855; AANS7811.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Glucan-binding protein B.
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Pred. No. 1.6e-06;
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ilarity 100.0%; Pred. No. 1.6
Conservative 0; Mismatches
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DOI=10.1128/IAI.69.11.6931-6941.2001;
                                                hydrolase.
Name=gbpB; OrderedLocusNames=SMU.22;
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PROSITE; PS50911; CHAP; 1.
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Q938V1;
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nes 20; Conserv
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NCBI_TaxID=1309;
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Duncan M.J.;

Cloning of the Streptococcus mutans gene encoding glucan binding profining of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates.;

Infect. Immun. 69:6931-6941(2001).

EMBL; AV046412; AAV94502.1; -; Genomic_DNA.

InterPro; IRR007921; GHAP.

InterPro; IRR009148; SibA.

Ffam; PF05257; CHAP; InterPro;
                                                                 Gaps
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                   Score 92; DB 2; Length 432; Pred. No. 1.6e-06;
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Bradyrhizobiaceae; Rhodopseudomonas.
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DOI=10.1128/IAI.69.11.6931-6941.2001;
Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
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100.0%; Scc...
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                            432 AA
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05-JUL-2004 (TEMBLrel. 27, Last seq
05-JUL-2004 (TEMBLrel. 27, Last ann
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PubMed=14704707; DOI=10.1038/nbt923;
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                                                                                                                                                16 LSSATTLSAVKADDFDAQIA 35
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PROSITE; PSS0911; CHAP; 1.
SEQUENCE 432 AA; 44648 MW;
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95.0%;
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Best Local Similarity 95.04,
-1-6 19; Conservative
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QENA84;
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                                                                 20; Conservative
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01-FEB-2005
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Larimer R.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L. Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R., Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C., "Complete genome sequence of the metabolically versatile photosynthetic bacterium Rhodopseudomonas palustris.";

Nat. Biotechnol. 22:55-61(2004).

BMBL, BK572597; CAR26744.1; -; Genomic_DNA.

HSSP, O59413; 1G21.

GO; GO:0008233; Fibeptidase activity, acting on glycosyl bonds; IEA.
GO; GO:0008233; Fipeptidase activity; IEA.

InterPro; IPR002848; PhilJ/PfpI.
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NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

NUCLEOTIDE S., DOI=10.1038/nbt1034.

Bolotin A., Quinquis B., Renault P., Sorokin A., Ehrlich S.D.,

Kulakauskas S., Lapidus A., Goltsman E., Mazur M., Pusch G.D.,

Konstein M., Overbeek R., Kyprides N., Purnelle B., Prozzi D.,

Ngui K., Masuy D., Hancy F., Burteau S., Boutry M., Delcour J.,

Goffeau A., Hols P.,

Goffeau A., Hols P.,
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.3%; Score 50; DB 2; Length 187; 90.9%; Pred. No. 6.3;
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SEQUENCE 187 AA; 20279 MW; 3DAC3649ACC1257C CRC64;
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01-PEB-2005 (TrEMBLrel. 29, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
61ucab binding protein (PesB).
Name=pcsB; OrderedLocusNames=stu0022;
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EMBL; AY730643; AAW82375.1; -; Genomic_DNA.
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PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
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TIGRFAMs; TIGR01382; PfpI; 1.
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InterPro; IPR009148; SibA.
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Q5M6K4 STRT2 PRELIMINARY;
Q5M6K4;
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nes 10; Conservative
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SEOUENCE 474 AA:
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STRAIN=521;
STRAIN=521;
Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
Birren B., Nusbaum C., Abebe A., Abouelleil A., Anderson M.,
Arit-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,
Bayul T., Blitshsteyn B., Bloom T., Blye J., Boguslavskiy L.,
Bayul T., Blitshsteyn B., Bloom T., Blye J., Boguslavskiy L.,
Calwosky M., Boukhgalter B., Brunache A., Butler J., Calixte N.,
Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroon M.,
Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
David R., Davoe T., Dogges S., Dooley K., Dorrie P.,
Dorjee K., Dorris L., Duffey N., Duppes A., Elkins T., Engels R.,
Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

PUDMed=15543133; DOI=10.1038/nbt1034;

Bolotin A., Quinquis B., Renault P., Sorokin A., Ehrlich S.D.,

Kulakauskas S., Lapidus A., Goltsman E., Mazur M., Pusch G.D.,

Kulakauskas S., Lapidus R., Kyprides N., Purnelle B., Prozzi D.,

Rulakauskas S., Lapidus P., Burteau S., Boutry M., Delcour J.,

Agui K., Masuy D., Hancy F., Burteau S., Boutry M., Delcour J.,

Rooplete sequence and comparative genome analysis of the dairy

acceptual Streptococcus thermophilus.";

Nat. Biotechnol. 22.1554-1558(2004).

InterPro; IPR007148; SibA.

RINGERPOSST; CHAP.

RINGERPOSST; CHAP.

RRINTS; PR01852; SIBARROTEIN.

RRINTS; PR01852; SIBARROTEIN.

RROORITE; PS05011; CHAP; 1.

RROORITE; PS05011; CHAP; 1.

RROORITE; PS05011; CHAP; 1.
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Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.8%; Score 49.5; DB 2; Length 485; 56.5%; Pred. No. 21; ive 3; Mismatches 4; Indels 3
                                                                                                                                                                                                                                                                                                                      Glucan binding protein.
Name-pcsB; OrderedLocusNames=str0022;
Streptococcus thermophilus (strain CNRZ 1066).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                                                                                                                                                                                         01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
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                                                                                                                                                                                           PRT;
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1 LSSATTLSA---VKADDFDAQIA 20
                         10 LVSGVTLSAAASVHAEDYDSQIA 32
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QSM212;
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tes 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=299768;
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RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S., Ra Hagorian D., Hador A., Grandbois E., Gyaltsen K., Hafez M., Hagorian D., Hagors B., Hall J., Hatcher B., Haller A., Higgins H., Honan T., Horn A., Houden N., Hughes L., Hulme W., Husby E., Iliev I., Honan T., Jones C., Kamal M., Kamat A., Kamvysselis M., Karlsson E., Kalle C., Kieu A., Kisner P., Kodira C., Kilbokse E., Lewis T., Lewis T., Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T., Laman D., Landers T., Lokyitsang Y., Lokyitsang Y., Lokyitsang Y., Lokyitsang Y., Lokyitsang Y., Morien O., Lui A., Ma L.J., Marabella R., Marut K., Matthews C., Mauceli E., Manning J., Marabella R., Marut K., Matthews C., Maulor J., Marabella R., Marut K., Matthews C., Mauceli E., Mocarthy M., Mcdonough S., Mcghee T., Michael C., Mayer C., Mayer C., Mayer D., Mihalev A., Mihova T., Micol R., Nielsen T., Micol B., Mortosko D., Piqani B., Norbu C., Multain L., Macol R., Nielsen C., Nizzari M., Norbu C., Stonges C., Radriguez J., Rogers J., Ropor P., Ramesamy U., Rameau R., Stonges C., Stone C., Stone S., Stubbs M., Talamas J., Tchuing P., Stenger E., Stone C., Stone S., Stubbs M., Talamas J., Topham K., Towey S., Tsamla T., Tsomo N., Vallee C., Wang S., Wangchuk T., Wenkataraman V., Vinson J., Wo A., Wade C., Wang S., Wangch T., Wang S., Yang S., Wang C., Waller M. Harler C., Wang S., Wan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peacock C.S., Murphy L., Ivens A.C., Berriman M., Blackwell J., Smith D., Collins M., Fosker N., Harris D., Oliver K., O'Neil S., Saunders D., Seeger K., Warren T., Rajandream M., and Barrell B.G.; Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.

EMBL, CT005272; CAJ09636.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.2%; Score 48; DB 2; Length 462; 53.3%; Pred. No. 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 462 AA; 50701 MW; EB83795F497CBAC5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324 AA; 35283 MW; 3D4C39950E516140 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preliminary data.
EMBL; AACP01000192; EAK86611.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            324 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
Hypothetical protein.
ORFNames=LmjF36.6560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 SSATTLSAVKADDFD 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q4Q099 LEIMA PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=5664;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Q4Q099 LEIMA
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MEDLINE=21156211; PubWed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiha T., Hattori M., Shinagawa H., Complete genome sequence of enterchemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Res. 8:11-22(2001).
-!- FUNCTION: Could be part of an electron transfer system required for anaerobic carnitine reduction (By similarity).
-!- COFACTOR: FAD (Potenial).
-!- SIMILARITY: Belongs to the ETF-QO/fixC family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
Nature 409:529-533(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli O157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=01571H7 / EDL933 / ATCC 700927 / EHBC;
MEDLINE-21074935; PubMed=11206551; DOI=10.1038/35054089;
BERDIA N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Welch R.A., Blattner F.R.;
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Complete proteome; Blectron transport; FAD; Flavoprotein;
Oxidoreductase; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [Potential].
64B034F30D61DCF1 CRC64;
                                                                                                                                                                                                                                                                                                                                               01-FEB-2005 (Rel. 46, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=fixC; OrderedLocusNames=z0049, ECs0046;
Escherichia coli 0157:H7.
                                                                                                                                                                                                                                         428 AA
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EMBL; BA000007; BAB33469.1; -; Genomic_DNA.
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InterPro; IPR001327; FAD_Dyr_redox.
InterPro; IPR001005; NAD_BS.
InterPro; IPR001100; Pyr_redox.
InterPro; IPR003042; Rng_hydrolase.
                                    ||::|||:|||:
172 SSSKLSAAEMDDWDADV 189
2 SSATTLSAVKADDFDAQI 19
                                                                                                                                                                                                                                     FIXC ECO57 STANDARD;
Q7AHT0; Q8XA26;
01-FEB-2005 (Rel. 46, Created)
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PRINTS; PR00411; PNDRDT
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PIR; F90634; F90634.
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                                                                                                                                                                                                                                                                                                                                                                                                                            FixC protein.
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                                                                                                                                                                                                                                                                             "Systematic sequencing of the Escherichia coli genome: analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Walt A., Kahn M.L.;
"The fixA and fixB genes are necessary for anaerobic carnitine reduction in Bscherichia coli.";
-1. Bacteriol. 184:4044-4047(2002).
-1. FUNCTION: Could be part of an electron transfer system required for anerobic carnitine reduction.
-1. COFACTOR: FAD (Potential).
-1. SIMILARITY: Belongs to the ETF-QO/fixC family.
                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                    Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N.,
Isono K., Mizobuchi K., Nakata A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=044:K74;
MEDLINE=96066354; PubMed=7473063;
BioLhler K., Buchet A., Bourgis F., Kleber H.-P.,
Mandrand-Berthelot M.-A.;
"The fix Escherichia coli region contains four genes related carnitine metabolism.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FAD or NAD or NADP (ADP part)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome; Electron transport; FAD; Flavoprotein; Oxidoreductase; Transport.

NP_BIND 12 28 FAD or NAD or NADP (ADP part)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                         NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA)
13-SEP-2005 (Rel. 48, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D10483; BAB96611.1; -; Genomic_DNA.

EMBL; U00096; AAC73154.1; -; Genomic_DNA.

EMBL; X71977; CAAS0799.1; -; Genomic_DNA.

EMPL; CG4725; CG4725.

EchoBASE; EB1525; -.

EcoGene; EG11564; fixC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=K12 / BW25113;
MEDLINE=22077276; PubMed=12081978;
DOI=10.1128/JB.184.14.4044-4047.2002;
                                                                                                                                                                                                                                                                                                           0-2.4 min region.";
Nucleic Acids Res. 20:3305-3308(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IRR00137; Fad oxred.
InterPro; IRR00137; FAD pyr_redox.
InterPro; IRR001100; NAD BS.
InterPro; IRR001100; Pyr_redox.
InterPro; IRR001100; Pyr_redox.
InterPro; IRR003042; Rng_hydrolase.
Pfam; PR01266; DAO; 1.
PRINTS; PR00368; FADPNR.
PRINTS; PR00411; PNDRDTABEI.
PRINTS; PR00410; RNGMNOXGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Basic Microbiol. 35:217-227(1995)
                      FixC protein.
Name=fixC; OrderedLocusNames=b0043;
                                                                                                                                                                                                                  MEDLINE=92334977; PubMed=1630901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLECTIDE SEQUENCE OF 1-188.
                                                                                                                                                                                                                                                                                                                                                                                                MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROBABLE FUNCTION
                                                                Escherichia coli
                                                                                                                             NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=K12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                removed
This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=06:HI 7 CFT073 / ArCC 700928 / UPEC; MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799; MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799; Welch R.A., Burkles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D., MayNew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.; "Extensive mosaic structure revealed by the complete genome sequence
    Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of uropathogenic Bacherichia coli.";

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).

-!- FUNCTION: Could be part of an electron transfer system required for anserobic carnine reduction (By similarity).

-!- COPACTOR: FAD (Potential).
                                                                                                                                                                                                                                                                                                                                                         Escherichia coli 06.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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    IndelB
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428 AA; 45703 MW; 4D089EE9A30C7FBC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Belongs to the BTF-QO/fixC family.
    4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                             FIXC_ECOL6 STANDARD; PRT; 428 AA. P68645; P31575; P76626; 01-JUL-1993 (Rel. 26, Created) 01-JUL-1997 (Rel. 35, Last sequence update) 13-SEP-2005 (Rel. 48, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       428 AA
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    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR006076; Fad oxred, InterPro; IPR001327; FAD pyr_redox. InterPro; IPR001327; FAD pyr_redox. InterPro; IPR001100; Pyr_redox. InterPro; IPR003042; Rng_hydrolase. Pfam; PF01266; DAO; I. PRINTS; PR00418; PADPNR. PRINTS; PR00411; PNDRDTASEI. PRINTS; PR00420; RNGMNOXGNASE.
                                                                                                                                                                                                                                                                                                             PixC protein.
Name=fixC; OrderedLocusNames=c0053;
    4;
                                                                                                                                                                                                                                                                                                                                                                                                  Enterobacteriaceae; Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          327 AAKTVLSAMKSDDFSKQ 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE016755; AAN78549.1; -;
                                                                    327 AAKTVLSAMKSDDFSKQ 343
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                                                2 SSATTLSAVKADDFDAQ
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Best Local Similarity 52.9
Matches 9; Conservative
    9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=217992;
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                                                                                                                                                      RESULT 14
FIXC_ECOL6
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RESULT 15

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to

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(Potential).

MSB -> MT (in Ref. 3).

64 64 D -> E (in Ref. 1).

280 281 VV -> IM (in Ref. 1).

310 310 L -> F (in Ref. 1).

428 AA; 45703 MW; 4D089EB9A30C7FBC CRC64;
            CONFLICT
CONFLICT
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SEQUENCE
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Query Match Best Local Similarity 52.9%; Pred. No. 48; Matches 9; Conservative 4; Mismatches 4; Indels ò

0;

0; Gaps

Search completed: January 25, 2006, 19:13:38 Job time : 71.3 secs

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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Appli
Sequence 5, Appli
Sequence 2793, Ap
Sequence 3661, Ap
Sequence 32585, A
Sequence 21513, A
Sequence 19326, A
Sequence 19326, A
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                                                                                                   January 25, 2006, 18:50:05; Search time 16.6 Seconds (without alignments) 99.609 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgm2_6/prodata/1/iaa/5_COMB.pep:*
/cgm2_6/prodata/1/iaa/6_COMB.pep:*
/cgm2_6/prodata/1/iaa/H_COMB.pep:*
/cgm2_6/prodata/1/iaa/PcTuS_COMB.pep:*
/cgm2_6/prodata/1/iaa/RE_COMB.pep:*
/cgm2_6/prodata/1/iaa/RE_COMB.pep:*
5.1.6
Compugen Ltd
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US-09-901-572A-4

US-09-902-540-14436

US-09-28-35-6123

US-09-602-787A-92

US-09-28-991A-29343

US-09-291A-29343

US-09-991-28-3

US-09-991-28-3

US-09-991-28-3

US-09-991-28-3

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US-09-367-764-2

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US-09-270-767-32585
US-09-248-796A-21513
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US-09-902-540-12815
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                                                                                                                                                                                                                                                                                                                   572060 segs, 82675679 residues
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GenCore version (c) 1993 - 2006
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Maximum Match 100%
Listing first 45 summaries
                                                                      - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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92
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Maximum DB seq
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No.
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RESULT 2
10S-03-522-6746

1 Sequence 6746, Application US/09328352

2 Sequence 6746, Application US/09328352

3 Requence 6746, Application US/09328352

3 GENERAL INFORMATION:

4 APPLICANT: Gary L. Breton et al.

5 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

7 TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

7 TITLE OF THEREFERENCE: GTC99-03PA

7 CURRENT APPLICANTON NUMBER: US/09/328,352

7 CURRENT PILING DATE: 1999-06-04

7 NUMBER OF SEQ ID NOS: 8252

7 SEQ ID NO 6746

7 ENGTH: 1260
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                         Sequence 594, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 15, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 29, Appli
Sequence 919, App
Sequence 6765, Ap
Sequence 6765, Ap
                                                                                                                                                                                                                                                                                                                              Sequence 41866, Application US/09270767

Sequence 41866, Application US/09270767

Patent No. 6703491

GRNERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094

CURRENT PELLING NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 41866

LENGTH: 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 107;
US-09-602-777A-8
US-09-792-024-83
US-09-328-352-5924
US-08-604-789B-4
US-09-312-721A-4
US-09-313-300-4
US-09-318-721A-4
US-09-138-45-648-2
US-09-138-45-648-2
US-09-18-45-15-0
US-09-18-185A-15
US-09-18-85-6
US-09-97-132A-28
US-09-97-132A-28
US-09-543-681A-6765
US-09-543-681A-6765
US-09-583-110-5219
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Pred. No. 5.8;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Xaa means any amino acid
                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 53.3%;
Matches 8; Conservative
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RESULT 6
US-09-328-352-6123
US-09-328-352-6123
US-09-328-352-6123
Sequence 6123, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: GAIY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS
TITLE OF INVENTION TOWNERS: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
IENGTH: 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: STATE, Gregory J.
APPLICANT: Stater, Steven C.
APPLICANT: Stater, Steven C.
APPLICANT: Stater, Steven C.
APPLICANT: Stater, Steven C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT FPLING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 05/09/202,540
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 14436
LENGTH: 675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 42; DB 2; Length 675; Pred. No. 1.2e+02; 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                      Query Match 46.7%; Score 43; DB 2; Length 122
Best Local Similarity 52.9%; Pred. No. 1.7e+02;
Matches 9; Conservative 2; Mismatches 6; Indels
                                                                                                                                                                                                                        FEATURE: OTHER INFORMATION: MGC3 encoded by mgc3 gene
FILE REFERENCE: J209
CURRENT PEDLICATION NUMBER: US/09/901,572A
CURRENT FILING DATE: 2003-03-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 4
LENGTH: 1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 14436, Application US/09902540; Patent No. 683347; GENERAL INFORMATION: APPLICANT: Goldman, Barry S.
                                                                                                                                                                     TYPE: PRT
ORGANISM: Mycoplasma gallisepticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6123
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56.2%;
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Best Local Similarity 47.4%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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US-09-902-540-14436
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                                                                                                                                                                                                                                                                      APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
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Patent No. 6936707
GENERAL INFORMATION:
APPLICANT: Nippon Zeon Co., Ltd.,
TITLE OF INVENTION: Modified DNA molecules, Recombinants and uses thereof
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                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Maltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature;
CCATION: (B) LOCATION 1...525;
SEQUENCE DESCRIPTION: SEQ ID NO: 5095:
US-09-107-532A-5095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMUNICATION INFORMATION:
TELEPHONE: (781)893-8277
INFORMATION FOR SEQ ID NO: 5095:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                          Sequence 5095, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 525 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LSSATTLSAVKADDFDAQI 19
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                              1 LSSATTLSAVKADDFDA 17
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Sequence 29343, Application US/09252991A

Sequence 29343, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS.
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT PILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PELICATION NUMBER: US 60/094,190

PRIOR PELICATION NUMBER: US 60/094,190

PRIOR PILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.5%; Score 40; DB 2; Length 238; 55.6%; Pred. No. 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
PRIOR APPLICATION NUMBER: DE 19940831.9
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
PRIOR PLING DATE: 1999-08-27
PRIOR PLING DATE: 1999-08-31
PRIOR PRICATION NUMBER: DE 19941378.9
PRIOR PLING DATE: 1999-08-31
PRIOR PRILING DATE: 1999-08-31
PRIOR PLING DATE: 1999-08-31
PRIOR PLING DATE: 1999-08-31
PRIOR PLING DATE: 1999-09-03
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US-09-248-796A-19179
; Sequence 19179, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa
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77 AAQTLSAETADDPDTVLA 94
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147 LASVRLDDLDLQVA 160
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Best Local Similarity 55.6
Matches 10; Conservative
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US-09-252-991A-29343
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US-09-252-991A-29343
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      Indels
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     Mismatches
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APPLICATION NUMBER: DE 19940830.0
FILING DATE: 1999-08-27
                                                                                                                                                Sequence 92, Application US/09602787A Patent No. 6696561 GENERAL INFORMATION:
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668 LNGATTLTAEKPDSID 683
                                     1 LSSATTLSAVKADDFD
     Conservative
     6
     Matches
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GENERAL INFORMATION:
APPLICANT: Johnston, Robert E.
APPLICANT: Davis, Nancy L.
APPLICANT: Davis, Nancy L.
APPLICANT: Simpson, Dennis A.
TITLE OP INVENTION: System for the In Vivo Delivery and
TITLE OP INVENTION: Expression of Heterologous Genes in the Bone Marrow
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell Seltzer Park & Gibson, P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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43.5%; Score 40; DB 1; Length 2500;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 10; Conservative 3; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.5%; Score 40; DB 2; Length 249
50.0%; Pred. No. 1.2e+03;
Mismatches 7; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,263A
FILING DATE: 19-FEB-1997
CLASSIFICATION: S14
ATTORNEY/AGENT INFORMATION:
NAME: S1bley, Kenneth D.
REGISTRATION NUMBER: 31,665
REGISTRATION NUMBER: 5470-147
TELECCOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
PRIOR APPLICATION NUMBER: 09/902,537
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 2492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1211 East Morehead Street CITY: Charlotte STATE: No. 5811407th Carolina COUNTRY: USA
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2500 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 50.0<sup>1</sup>
Matches 10; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNES: 107196-132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR PILING DATE: 1999-02-13
PRIOR PILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
ROWHER OF SEQ ID NOS: 28208
SEQ ID NO 19179
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APPLICANT: Maughan, Maureen
APPLICANT: Johnston, Robert
APPLICANT: Johnston, Robert
APPLICANT: Johnston, Robert
APPLICANT: Swanstrom, Ronald
TITLE OF INVENTION: VACCINES
TITLE OF INVENTION: VACCINES
TITLE OF INVENTION: VACCINES
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TITLE OF INVENTION: V
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APPLICANT: Nagata, Lealie P.
APPLICANT: Wagata, Jonathan P.
TITLE OF INVENTION: A STRAIN OF THE WESTERN EQUINE ENCEPHALITIS VIRUS (AS AMENDED)
FILE REPERENCE: NEL-001
CURRENT APPLICATION NUMBER: US/10/023,649A
CURRENT FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 49
SPRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 614
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Pred. No. 2e+02;
4; Mismatches 3; Trair
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43.5%; Score 40; DB 2; Length 614;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches 10; Conservative 3; Mismatches 7; Indels
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Patent No. 6783939
GENERAL INFORMATION:
APPLICANT: Olmsted, Robert
APPLICANT: Ceith, Paula
APPLICANT: Caley, Ian
APPLICANT: Maughan, Maureen
APPLICANT: Johnston, Robert
APPLICANT: Sanstrom, Robert
APPLICANT: Swanstrom, Robert
APPLICANT: Swanstrom, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/10023649A Patent No. 6800289
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Best Local Similarity 50.0%;
Matches 7; Conservative
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104 LEMIQAPDFDSQLA 117
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US-09-991-258-3
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SEQUENCE CHARACTERISTICS:
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US-08-801-263A-9
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Sequence 2, Application US/09102248

Sequence 2, Application US/09102248

Fatent No. 6008035

GENERAL INFORMATION:

APPLICANT: Davis, Nancy L.

APPLICANT: Davis, Nancy L.

TITLE OF INVENTION: Expression of Heterologous Genes in the Bone Marrow NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Bell Seltzer Park & Gibson, P.A.

STREET: 1211 East Morehead Street

CITY: Charlotte

COUNTRY: USA
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APPLICANT: Johnston, Robert E.
APPLICANT: Simpson, Dennis A.
APPLICANT: Simpson, Dennis A.
TITLE OF INVENTION: System for the In Vivo Delivery and
TITLE OF INVENTION: Expression of Heterologous Genes in the Bone Marrow
WINGHER OF SKQUENCES: 12
CORRESPONDENCE: Bell Seltzer Park & Gibson, P.A.
STREFT: 1211 East Morehead Street
CITY: Charlotte
STRET: No. 6583121th Carolina
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43.5%; Score 40; DB 2; Length 2500;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 10; Conservative 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                     ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/102,248
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION BATA:
APPLICATION NUMBER:
IS 19-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-147
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEPHONE: 919-420-2200
TELEPHONE: 919-881-3175
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Patent No. 6583121
GENERAL INFORMATION:
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MEDICATION:
PRIOR APPLICATION
FILEMENT NEORANTING:
NAME: Sibley Kameth D.
FILIAGO DATE: JP-88-1937
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Matches 20; Conservative
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41619, A
51310, A
3145, Ap
37656, A
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score greater than or equal to the score of the result being printed
and is derived by analysis of the total score distribution.
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(cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

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cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                         GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd
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US-10-424-599-252326
US-10-437-963-158213
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                                                                                                                                                                                                                                                                                                                                                                                             1867569 seqs, 417829326 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                         OM protein - protein search, using sw model
                                                                                                                                                  January 25, 2006, 19:13:51
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Maximum DB seq length: 200000000
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28 42 45.7 227 4 US-10-425-115-250586 Sequence 250586, 29 42 45.7 427 4 US-10-369-493-769 Sequence 769, App 31 41 44.6 127 6 US-11-097-143-9270 Sequence 9170, Ap 32 41 44.6 310 6 US-11-097-143-9270 Sequence 9270, Ap 32 41 44.6 310 6 US-11-097-143-9270 Sequence 194501, 34 41 44.6 705 4 US-10-424-599-194501 Sequence 194501, 35 41 44.6 943 4 US-10-424-599-194501 Sequence 194501, 36 40 43.5 127 4 US-10-282-1264591 Sequence 164591, 37 40 43.5 127 4 US-10-282-1264591 Sequence 266224, 37 40 43.5 127 4 US-10-26-212644 Sequence 21797, Ap 40 43.5 186 4 US-10-369-493-21797 Sequence 21797, Ap 40 43.5 190 4 US-10-186-2603-334 Sequence 21797, Ap 40 43.5 223 3 US-10-369-493-21797 Sequence 3234, Ap 41 40 43.5 223 3 US-10-369-493-1233 Sequence 22, Appl 42 40 43.5 224 4 US-10-66-1860 Sequence 12323, Ap 44 40 43.5 224 4 US-10-369-493-1233 Sequence 12323, Ap 44 40 43.5 271 4 US-10-186-761-8135 Sequence 1332, Ap 45 40 43.5 271 4 US-10-186-761-8135 Sequence 39937, Ap 45 40 43.5 323 4 US-10-167-701-39937
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ALIGNMENTS

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RESULT 2
US-10-797-821-5
US-10-797-821-5
Sequence 5, Application US/10797821
Sequence 5, Application US/10797821
Sequence 5, Application Wo. US20050031633A1
GENERAL INFORMATION:
APPLICANT: Smith, Daniel J.
TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens
FILE REPERENCE: 2566-9-020
CURRENT FILING DATE: 2004-03-09
FRIOR PLILING DATE: 2001-03-07
PRIOR PAPLICATION NUMBER: 00/363,209
FRIOR PLILING DATE: 2002-03-07
PRIOR PLILING DATE: 2002-08-08
PRIOR PLILING DATE: 2002-08-08
PRIOR PLILING DATE: 2002-08-08
PRIOR PLILING DATE: 2002-08-08
PRIOR PLILING DATE: 2002-08-08

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RESULT 6
US-10-797-821-29
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US-10-383-930-33
  SEQ ID NO 30
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; Publication No. US20040127400A1
; Fublication No. US20040127400A1
; GENERAL INFORMATION:
   APPLICANT: Smitch, Daniel J
   APPLICANT: Taubman, Martin A
; TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
   FILE REFERENCE: 25669-018
; CURRENT APPLICATION NUMBER: US/10/383,930
; CURRENT FILING DATE: 2003-03-07
; PRIOR PILICATION NUMBER: 60/402,483
; PRIOR PLICATION NUMBER: 60/402,483
; PRIOR PLICATION NUMBER: 60/363,209
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH 431
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Publication No. US20040127400A1

GENERAL INFORMATION:

APPLICANT: Smith, Daniel J

APPLICANT: Taubman, Martin A

TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein

FILE REFERENCE: 25669-018

CURRENT APPLICATION NUMBER: US/10/383,930

CURRENT APPLICATION NUMBER: 60/3-07

PRIOR FILING DATE: 2002-08-08

NUMBER: OF SEQ ID NOS: 41
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100.0%; Score 92; DB 4; L
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 20; Conservative 0; Mismatches 0;
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100.0%; Score 92; DB 5; I
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 20; Conservative 0; Mismatches 0;
PRIOR FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: 60/081,550
PRIOR PILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.2
IENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LSSATTLSAVKADDFDAQIA 20
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                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial
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| Sequence 29, Application US/10797821
| Sequence 29, Application US/10797821
| Publication No. US20000031633A1
| GENERAL INFORMATION:
| APPLICANT: Smith, Daniel J.
| APPLICANT: Taubman, Martin A.
| TITLE OF INVENTION: Glucan Binding Frotein and Glycosyltransferase Immunogens
| FILER REFERENCE: 25669-020
| CURRENT FILING DATE: 2004-03-09
| PRIOR PAPLICATION NUMBER: 10/383,930
| PRIOR PAPLICATION NUMBER: 10/383,930
| PRIOR PAPLICATION NUMBER: 60/363,209
| PRIOR PAPLICATION NUMBER: 60/402,483
| PRIOR PAPLICATION NUMBER: 60/402,483
| PRIOR PAPLICATION NUMBER: 60/402,483
| PRIOR PAPLICATION NUMBER: 60/402,483
| PRIOR PAPLICATION NUMBER: 60/115,142
| PRIOR PAPLICATION NUMBER: 60/115,142
| PRIOR PLLING DATE: 1999-04-13
| PRIOR PLLING DATE: 1999-01-08
| PRIOR PLLING DATE: 1999-01-08
| PRIOR PLLING DATE: 1999-01-08
| PRIOR PLLING DATE: 1999-01-08
| PRIOR PLLING DATE: 1999-01-08
| PRIOR PLLING DATE: PALENTING NUMBER: 60/115,142
| PRIOR PLLING DATE: PALENTING NUMBER: 60/115,142
| PRIOR PLLING DATE: PALENTING NUMBER: 60/105,142
| SEQ ID NO 29
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APPLICANT: Smith, Daniel J
APPLICANT: Taubman, Martin A
FITTLE OF INVENTION: Immunogenicity of Glucan Binding Protein
FITER ERFERENCE: 25669-018
CURRENT APPLICATION NUMBER: US/10/383,930
CURRENT FILING DATE: 2003-03-07
FRIOR APPLICATION NUMBER: 60/402,483
FRIOR APPLICATION NUMBER: 60/363,209
FRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.2
SEQ ID NO 33
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                                                                                                                                                     Score 92; DB 4; 1 Pred. No. 1.4e-06;
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100.0%; Score 92; DB
Best Local Similarity 100.0%; Pred. No. 1.4
Matches 20; Conservative 0; Mismatches
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; ORGANISM: Streptococcus mutans
US-10-383-930-33
LENGTH: 431
TYPE: PRT
ORGANISM: Streptococcus mutans
US-10-383-930-30
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PRIOR APPLICATION NUMBER: 60/081,550
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR PLING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.2
SEQ ID NO 33
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Sequence 30, Application US/10797821

Publication No. USC3050031633A1

GENERAL INFORMATION:
APPLICANT: Smith, Daniel J.
APPLICANT: Smith, Daniel J.
APPLICANT: Taubman, Martin A.
TITLE OF INVENTION: GUOGA-03-09
CURRENT APPLICATION NUMBER: US/10/797,821

CURRENT APPLICATION NUMBER: US/383,930

PRIOR PILING DATE: 2003-09-09
PRIOR PLING DATE: 2003-09-09

PRIOR PLING DATE: 2002-03-07

PRIOR PLING DATE: 2002-09-06

PRIOR PLING DATE: 2002-09-06

PRIOR PLING DATE: 1999-04-12

PRIOR PLING DATE: 1999-04-12

PRIOR PLING DATE: 1999-04-13

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Sequence 33, Application US/1079821

Publication No. US20050031633A1

GENERAL INFORMATION:

APPLICANT: Smith, Daniel J.

APPLICANT: Taubman, Martin A.

TITLE OF INVENTION Glucan Binding Protein and Glycosyltransferase Immunogens
FILE REFERENCE: 256.9-0.0

CURRENT APPLICATION NUMBER: US/10/797,821

CURRENT FILING DATE: 2004-03-09

PRIOR APPLICATION NUMBER: 60/363,209

PRIOR FILING DATE: 2002-03-07

PRIOR FILING DATE: 2002-03-07

PRIOR FILING DATE: 2002-08-08

PRIOR PILING DATE: 2002-08-08

PRIOR PILING DATE: 2002-08-08

PRIOR FILING DATE: 1999-04-12
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100.0%; Score 92; DB 5; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 20; Conservative 0; Mismatches 0; Indels
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                            ; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-10-797-821-29
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US-10-797-821-30
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   LENGTH: 431
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US-10-797-821-32

Sequence 32, Application US/10797821

Sequence 32, Application US/10797821

Sequence 32, Application US/0050031633A1

SEQUENCE 32, Application No. USCO05003163A1

GENERAL INFORMATION:

APPLICANT: Smith, Daniel J.

TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens

FILE REFERENCE: 25669-020

CURRENT FILING DATE: 2004-03-09

PRIOR FILING DATE: 2003-03-07

PRIOR PLICATION NUMBER: 10/383,930

PRIOR PLILOR DATE: 2002-03-07

PRIOR PLILOR DATE: 1999-04-12

PRIOR PLILOR DATE: 1999-04-12
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US-10-383-930-32
Sequence 32, Application US/10383930
Sequence 32, Application US/10383930
Sequence 32, Application US/10383930
SHUDICATION OF US20040127400A1
GENERAL INFORMATION:
APPLICANT: Smith, Daniel J
APPLICANT: Taubman, Martin A
TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
FILE REFERENCE: 25669-018
CURRENT FILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: 60/402,483
PRIOR APPLICATION NUMBER: 60/363,209
PRIOR APPLICATION NUMBER: 60/363,209
PRIOR PILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn version 3.2
SEQ ID NO 32
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100.0%; Score 92; DB 5; Length 431; 100.0%; Pred. No. 1.4e-06; ive 0; Mismatches 0; Indels
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                                                                                                                       1 LSSATTLSAVKADDFDAQIA 20
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APPLICANT: et al.

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

FILE REFERENCE: CLOO0728

CURRENT APPLICATION NUMBER: US/11/097,143

CURRENT PLING DATE: 2005-04-04

PRIOR APPLICATION NUMBER: 60/157,832

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-19

PRIOR PRILING DATE: 1999-10-19

PRIOR PRILING DATE: 1999-10-19

PRIOR APPLICATION NUMBER: 60/16/,769

PRIOR PILING DATE: 1999-11-12

PRIOR FILING DATE: 1999-11-12

PRIOR FILING DATE: 1999-11-12

PRIOR FILING DATE: 1999-11-12

PRIOR FILING DATE: 1999-12-28

PRIOR FILING DATE: 2000-02-24

PRIOR FILING DATE: 2000-02-24

PRIOR FILING DATE: 2000-02-24

PRIOR FILING DATE: 2000-03-33

NUMBER OF SEQ ID NOS: 43008

SOUTHWARE: PRESEED FOR WINDOWN VERSION 4.0
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Pred. No. 1e+02;
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; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Verter, J. Craig
; APPLICANT: Verter, T. Craig
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                           98.9%; Score 91; DB 5; 1
95.0%; Pred. No. 2.1e-06;
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PRIOR APPLICATION NUMBER: 60/115,142
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.2
SEQ ID NO 31
LENGTH: 432
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US-10-797-821-31
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Best Local Similarity 64.3.
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Best Local Similarity 95.0*
....hes 19; Conservative
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US-11-097-143-41619
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US-11-097-143-38595
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Sequence 31, Application US/10383930

Publication No. US20040127400A1

Sequence 31, Application US/10383930

Publication No. US20040127400A1

APPLICANT: Smith, Daniel J

APPLICANT: Smith, Daniel J

TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein

FILE REFERENCE: 25669-018

CURRENT PAPLICATION NUMBER: US/10/383,930

CURRENT FILING DATE: 2003-03-07

PRIOR APPLICATION NUMBER: 60/402,483

PRIOR APPLICATION NUMBER: 60/363,209

PRIOR APPLICATION NUMBER: 60/363,209

PRIOR APPLICATION NUMBER: 60/363,209

NUMBER OF SEQ ID NOS: 41

SEQ ID NO 31

LENGTH: 432
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100.0%; Score 92; DB 5; Length 432;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 20; Conservative 0; Mismatches 0; Indels
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Pred. No. 2.1e-06;
1; Mismatches 0; Indels
         PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION WUMBER: 60/115,142
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.2
SEQ ID NO 32
LENGTH: 432
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                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Streptococcus mutans
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Best Local Similarity 95.0%;
Matches 19; Conservative
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ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE DROSOPHILA GENES.
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Pred. No. 1e+03;
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/20,335
PRIOR PILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/230,337
PRIOR PILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/245,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-10-23
PRIOR PELING DATE: 2000-10-23
               FILE OF INVENTION: DROSOPHILA GENES.

FILE REFERENCE: CLOOD728

CURRENT APPLICATION NUMBER: US/11/097,143

CURRENT FILING DATE: 2005-04-04

PRIOR APPLICATION NUMBER: 60/157,832

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-19

PRIOR FILING DATE: 1999-10-19

PRIOR FILING DATE: 1999-10-18

PRIOR FILING DATE: 1999-10-28

PRIOR FILING DATE: 1999-10-28

PRIOR FILING DATE: 1999-10-28

PRIOR FILING DATE: 1999-11-12

PRIOR FILING DATE: 1999-11-2

PRIOR FILING DATE: 1999-12-28

PRIOR FILING DATE: 1999-12-28

PRIOR FILING DATE: 2000-01-12

PRIOR FILING DATE: 2000-01-12

PRIOR FILING DATE: 2000-01-12

PRIOR FILING DATE: 2000-03-23

NUMBER OF SEQ ID NOS: 43008

SOFTWARE: PESESEQ FOR WINDOWS VEFSION 4.0

SEQ ID NO 41619
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Carr, Grant
APPLICANT: Famamoto, Robert
APPLICANT: Forsyth, R.
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61.1%;
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Best Local Similarity 61.1
Matches 11; Conservative
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US-10-282-122A-51310
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APPLICANT:
APPLICANT:
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Sequence 6432, Application US/10467657

Publication No. US20050260581A1

GENERAL INFORMATION:

APPLICANT: CHIRON SpA

APPLICANT: FONTANA Maria Rita

APPLICANT: PUZZA Mariagrazia

APPLICANT: MASIGNANI Vega

APPLICANT: MONACI Elisabetta

TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

FILE REFERENCE:

CURRENT FILING DATE: 2003-08-11

PRIOR PILING DATE: 2001-02-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 20; Conserv
US-11-052-554A-210
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US-10-467-657-6432
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TYPE: PRT
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Sequence 1846, Ap
Sequence 8, Appli
Sequence 120, App
Sequence 120, App
Sequence 15, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 182, Appli
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218, App
118, App
15, App
1467, Ap
2720, Ap
4976, Ap
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145, App
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                                                                                                     January 25, 2006, 19:15:26; Search time 5.5 Seconds (without alignments) 39.378 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd
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US-10-457-6432

US-10-454-437-8

US-11-055-822-608

US-11-055-822-608

US-11-059-120

US-10-981-873-15

US-10-981-873-15

US-10-981-873-15

US-11-169-630-4

US-11-169-630-4

US-11-169-630-6

US-11-169-630-6

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US-11-169-630-6

US-11-182-188

US-11-073-62-118

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Match Length DB
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92
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Sequence 210, Application US/11052554A

Sequence 210, Application US/11052554A

Publication No. US2005028866A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
CURRENT APPLICATION NUMBER: US 60/589,227

PRIOR FILING DATE: 2004-07-20

PRIOR FILING DATE: 2004-07-20

PRIOR FILING DATE: 2004-02-06

NUMBER OF SEQ ID NOS: 763

SOFTWARE: Patentin version 3.3

SEQ ID NO 2.00
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                                                         1074, Ap
1076, Ap
1068, Ap
1070, Ap
1066, Ap
27, Appl
54, Appl
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14, Appl
58, Appl
54, Appl
56, Appl
40, Appl
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US-11-186-284-141

US-11-145-554A-149

US-11-052-554A-149

US-11-052-554A-169

US-10-453-372-1074

US-10-453-372-1076

US-10-453-372-1066

US-10-453-372-1066

US-11-186-284-49

US-11-186-284-49

US-11-186-284-49

US-10-453-372-1082

US-10-453-372-1082

US-10-453-372-1082

US-10-453-372-1082

US-10-453-372-1082

US-10-453-372-1082

US-10-453-372-1082

US-10-356-263A-58

US-10-336-263A-56

US-10-336-263A-56
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PRIOR APPLICATION NUMBER: DE 19932127.2
PRIOR APPLICATION NUMBER: DE 19932128.0
PRIOR PILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-19
PRIOR PELIOR SPELICATION NUMBER: DE 19932129.9
PRIOR APPLICATION NUMBER: DE 19932226.0
PRIOR PILING DATE: 1999-07-09
PRIOR PILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19932920.6
PRIOR APPLICATION NUMBER: DE 19932922.2
PRIOR APPLICATION NUMBER: DE 19932922.2
PRIOR PILING DATE: 1999-07-14
PRIOR PRIOR PRIOR DATE: 1998-07-14
PRIOR PRIOR PRIOR DATE: 1998-07-14
PRIOR PRIOR PRIOR DATE: 1998-07-14
PRIOR PORTION NUMBER: DE 19932922.2
PRIOR PRIOR PRIOR DATE: 1998-07-14
PRIOR PORTION NUMBER: DE 19932922.2
PRIOR PORTION NUMBER: DE 19932922.2
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NUMBER OF SEQ ID NOS: 1158
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APPLICANT: POMPEJUN:

APPLICANT: Rroger, Burkhard

APPLICANT: Schroder, Hartwig

APPLICANT: Schroder, Hartwig

APPLICANT: Schroder, Hartwig

APPLICANT: Schroder, Gregor

TITLE OF INVENTION: CORTNEBACTERIUM GLUTAMICUM GENES ENCODING

TITLE OF INVENTION: CORTNEBACTERIUM GLUTAMICUM GENES

FILE REFERENCE: BGI-121CPCN

CURRENT FILING DATE: 1090-06-23

PRIOR FILING DATE: 1999-06-25

PRIOR FILING DATE: 1999-06-25

PRIOR APPLICATION NUMBER: 60/142,101

PRIOR PILING DATE: 1999-07-01

PRIOR PILING DATE: 1999-07-01

PRIOR FILING DATE: 1999-07-01

PRIOR PILING DATE: 1999-07-01

PRIOR FILING DATE: 1999-07-01

PRIOR APPLICATION NUMBER: DE 19931418.7

PRIOR FILING DATE: 1999-07-08

PRIOR APPLICATION NUMBER: DE 19931418.7

PRIOR FILING DATE: 1999-07-08

PRIOR FILING DATE: 1999-07-08

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Pred. No. 15;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-454-437-8
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ORGANISM: Corynebacterium glutamicum
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Best Local Similarity 58.3%;
Matches 7; Conservative 4
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86 AIQADEDDAQVA 97
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LENGTH: 277
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Sequence 8, Application US/10454437

Publication No. US20050277115A1

Sequence 8, Application No. US20050277115A1

APPLICANT: Pompejus, Markus

APPLICANT: Rroger, Burkhard

APPLICANT: Schoder, Hartwig

APPLICANT: Schoder, Hartwig

APPLICANT: Calder, Oskar

TITLE OF INVENTION: CORVEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS

TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION

FILE REFERENCE: BGI-128CPCN

CURRENT PILING DATE: 2003-06-13

PRIOR PLICATION NUMBER: US 60/141031

PRIOR PPLICATION NUMBER: DE 19931636.8

PRIOR APPLICATION NUMBER: DE 19931636.8

PRIOR PPLING DATE: 1999-07-08

PRIOR PLING DATE: 1999-07-09

PRIOR PLING DATE: 1999-07-09
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APPLICANT: CHIRON SPA
APPLICANT: PONTANA Maria Rita
APPLICANT: PONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REPERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
FRIOR APPLICATION NUMBER: GB-0103424.8
FRIOR FILING DATE: 2001-02-12
NUMBER: OF SEQ ID NOS: 9218
SOFTWARE: SeQMin99, version 1.04
SEQ ID NO 1846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 42.4%; Score 39; DB 6; Length 255; Best Local Similarity 52.9%; Pred. No. 13; Matches 9; Conservative 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                 DB 6; Length 122,
                                                                                                                                                                                                                                                                                                                                                       3; Indels
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Pred. No. 5.6;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1846, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
                                                                                                                                               ; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1846
          NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 6432
LENGTH: 122
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Best Local Similarity 58.3%;
Matches 7; Conservative
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54 SVKTDDFDKAVA 65
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; Sequence 4, Application US/10981873
; Publication No. US20050250680A1
; GENERAL INFORMATION:
; APPLICANT: Walensky, Loren D.
; APPLICANT: Wordine, Gregory
; TITLE OF INVENTION: STABLIZED ALPHA HELICAL PEPTIDES AND
; TITLE OF INVENTION: USES THEREOF
; TITLE OF INVENTION: USES THEREOF
; CURRENT APPLICATION NUMBER: US 60/517,848
; PRIOR FLING DATE: 2004-11-05
; PRIOR FLING DATE: 2004-11-05
; PRIOR FLING DATE: 2004-07-27
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO 4;
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Pred. No. 43;
1; Mismatches
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Pred. No. 1.5;
1; Mismatches
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ORGANISM: Corynebacterium glutamicum ATCC31388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Naturally occurring peptide
US-10-981-873-4
   Pred. No. 1.3;
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TITLE OF INVENTION: Novel Transaldolase
FILE REPERENCE: 00005.001198
CURRENT PELINGE: 00005.001198
CURRENT FILING DATE: 2005-06-30
PRIOR APPLICATION NUMBER: US/10/088,594
PRIOR FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: US/10/088,594
PRIOR FILING DATE: 1999-09-21
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/11169630 Publication No. US20050266517A1 GENERAL INFORMATION:
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ilarity 63.6%;
Conservative
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Best Local Similarity 70.0%;
Matches 7; Conservative
   63.68;
   Best Local Similarity 63.0
Matches 7; Conservative
                                                     9 AVKADDFDAQI 19
                                                                                    7 AAMCDDFDAGM 17
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Beet Local Similarity
7; Conserve
                                                                                                                                      RESULT 8
US-10-981-873-4
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GENERAL INFORMATION:
APPLICANT: Walensky, Loren D.
APPLICANT: Walensky, Loren D.
APPLICANT: Wordine, Gregory
TITLE OF INVENTION: STABILIZED ALPHA HELICAL PEPTIDES AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 06530-124001
CURRENT APPLICATION NUMBER: US/10/981,873
CURRENT APPLICATION NUMBER: US 60/517,848
PRIOR APPLICATION NUMBER: US 60/517,848
PRIOR APPLICATION NUMBER: US 60/591,548
PRIOR APPLICATION NUMBER: US 60/591,548
PRIOR PILING DATE: 2004-07-27
NUMBER OF SEQ ID NOS: 117
SOFTWARE: FRSESEE for Windows Version 4.0
SEQ ID NO 15
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38; DB 7; Length 1060;
Pred. No. 1e+02;
4; Mismatches 3; Indels
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                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Naturally occurring peptide US-10-981-873-15
   Pred. No. 15;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40.2%; Score 37;
Best Local Similarity 58.3%; Pred. No. Matches 7; Conservative 4; Mismat
                                                                                                                             RESULT 6
US-11-090-739-120
Sequence 120, Application US/11090739
Publication No. US20050260539A1
GENERAL INFORMATION:
APPLICANT: NAKANURA, Yuguke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-981-873-15
; Sequence 15, Application US/10981873
; Publication No. US20050250680A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41.3%;
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735 TVSQVAAEDFDSGV 748
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Best Local Similarity 50.0
Matches 7; Conservative
                                                   9 AVKADDFDAQIA 20
                                                                      |::||: |||:|
86 AIQADEDDAQVA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-090-739-120
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Sequence 218, Application US/11074176
PUBLICATION No. US20050250135A1
GENERAL INFORMATION:
APPLICANT: Rusenhammer, Todd R.
APPLICANT: Rusell, William M.
APPLICANT: McAuliffe, Olivia
APPLICANT: Perill, Andrea Azcarate
APPLICANT: Perill, Andrea Azcarate
TITLE OF INVENTION: Usucleic Acid Sequences Encoding
TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1808, Application US/10467657
; Publication No. US20050260581A1
; Fublication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PASIGNANI Vega
; APPLICANT: MASIGNANI Vega
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT FILING DATE: 2003-08-11
; PRIOR PILING DATE: 2001-02-12
; NUMBER: OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1808
; LENGTH: 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37; DB 6; Length 1107;
Pred. No. 1.6e+02;
3; Mismatches 6; Indels
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              APPLICANT: Foster, Simon APPLICANT: Mond, James TITLE OF INVENTION: Antigenic Polypeptides FILE REFERENCE: P100629W0 CURRENT FILING DATE: 2004-02-02 PRIOR APPLICATION NUMBER: GB 0118825.9 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-09 PRIOR PILING DATE: 2002-01-09 PRIOR SEQ ID NOS: 424 SOFTWARE: Patentin version 3.1
Biosynexus Incorporated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LSSATTLSAVKADDFDAQIA 20
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; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1808
                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-485-517-145
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.0%;
Matches 9; Conservative
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US-11-074-176-218
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LENGTH: 1107
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Pred. No. 53;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 37; DB 7; Length 360;
Pred. No. 43;
1; Mismatches 2; Indels
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; ORGANISM: Corynebacterium glutamicum ATCC31388

US-11-169-630-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 182, Application US/10485517
; Publication No. US20050256299A1
; GRNERAL INFORMATION:
GRNERAL INFORMATION:
GRNERAL INFORMATION:
APPLICANT: University of Sheffield
APPLICANT: Biosynexus Incorporated
APPLICANT: Foster, Simon
APPLICANT: Mond, James
ITLE OF INVENTION: Antigenic Polypeptides
FILE REFERENCE: P100629W0
CURRENT PAPLICATION NUMBER: US/10/485,517
CURRENT FILING DATE: 2004-02-02
PRIOR APPLICATION NUMBER: GB 0118825.9
PRIOR APPLICATION NUMBER: GB 0200349.9
PRIOR FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIN version 3.1
                                                                                    Sequence 6, Application US/11169630

Publication No. US20050266517A1

GENERAL INFORMATION:

APPLICANT: KVOWA HAKKO KOGYO CO., LTD

TITLE OF INVENTION: Novel Transaldolase

FILE REFERENCE: 00005.001198

CURRENT APPLICATION NUMBER: US/11/169,630

CURRENT FILING DATE: 2005-06-30

PRIOR APPLICATION NUMBER: US/10/088,594

PRIOR PILING DATE: 1999-09-21

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 6

LENGTH: 360
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GRNERAL INFORMATION: APPLICANT: University of Sheffield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          i ORGANISM: Staphylococcus aureus
US-10-485-517-182
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 40.2
Best Local Similarity 70.0
Matches 7; Conservative
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240 ADEFDVQIA 248
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54 KGDSYDAQIA 63
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US-11-169-630-6
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Publication No. US20050255478A1
GENERAL INFORMATION: US20050255478A1
GENERAL INFORMATION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT PILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 118
LENGTH: 571
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                                                                                                                                                                                                                                                                                                           Query Match 39.1%; Score 36; DB 7; Length 182; Best Local Similarity 50.0%; Pred. No. 29; Matches 7; Conservative 3; Mismatches 4; Indels
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FILE REFERENCE: 5051-694
CURRENT APPLICATION NUMBER: US/11/074,176
CURRENT FILING DATE: 2005-03-07
FRIOR APPLICATION NUMBER: 60/551,161
PRIOR FILING DATE: 2004-03-08
NUMBER OF SEQ ID NOS: 381
SOFTWARE: FESTSEQ for Windows Version 4.0
SEQ ID NO 218
LENGTH: 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: January 25, 2006, 20:11:08 Job time : 6.5 secs
                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
US-11-074-176-218
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Best Local Similarity 66.7
Matches 6; Conservative
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US-10-793-626-118
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January 25, 2006, 18:48:24; Search time 68.2 Seconds (without alignments) 128.850 Million cell updates/sec
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Copyright (c) 1993 - 2006 Compugen Ltd.
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Maximum Match 100%
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                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES Description	AD034626 Streeton	0300000	Adx37249	ADD93649 ADD93649 Streptoco	ADD93650 Streptoco	ADD93653 Streptoco	ADX37272 Streptoco	ADX37273 Streptoco	ADX37276 Adx37276 Streptoco	AEB91500 Aicrobial	ADD93651 Streptoco	ADD93652 Streptoco	ADX37274 Streptoco	ADX37275 Streptoco	ADD93627 ALTEDTOCO	ADX37250 . Adx37250 Streptoco	AAY22579 Bacterial	ABU02747 S. pheumo	ADK47859 Atreptoco	ADTS0227 S pneumon	ADT50226 Spneumon	ADT50165 S pneumon	ADR94595 Adr94595 Novel S.	AEA58465 Streptoco	
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* Query Match	100.0		100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	81.9	81.9	78.7	78.7	78.7	78.7	78.7	78.7	78.7	78.7	
Score	94	: :	94	94	94	94	94	94	94	94	94	94	94	94	77	77	74	74	74	74	74	74	74	74	
Result No.	1	۱ ،	7	e	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	

Adr83884 S. pyogen Abp91542 Microbial Abp29684 Streptoco Adv68322 Streptoco Adv88392 Streptoco Adv8889 Streptoco Adv8889 Streptoco Adv9888 Streptoco Adv9888 Streptoco Adv97888 Micheni Abr75182 Micheni Abr75182 Micheni Abr76182 Micheni Abr677 Pruit fly Adv86412 Drosophil Adv66779 Fruit fly Adv66779 Fruit fly Adv66779 Fruit fly Adv870956 Plant ful Ady70856 Plant ful Ady70826 Pseudomon Abo66368 Klebsiell Abu29734 Protein e	ptide; 20 AA. intry) glucan binding protein-B peptide fragment. n-B; GbpB; vaccine; anticaries; epitope; immunogen. 13632099.	Smith DJ, Taubman MA; WPI; 2003-845091/78. Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein. Claim 11; Page 10; 49pp; English. The present sequence is that of a peptide comprising amino acid residues 33-52 of the glucan binding protein-B (GbpB) of Streptococcus mutans strain SM23 ADD9349; The peptide binds to a major histocompatibility complex (MHC) class II protein. It was identified as a potential B cell epitope using a matrix-based algorithm for epitope prediction, which was complex (MHC) class II protein. It was identified as a potential B cell epitope using a matrix-based algorithm for epitope prediction, which was used to search the primary amino acid sequence of GbpB for known MHC class II binding motifs. The peptide can be used in immunogenic compositions and subunit vaccines for dental caries. These comprise MHC class II protein-binding GbpB peptides covalently linked with peptide class II protein-binding GbpB peptides covalently linked with peptide subunits (preferably from the catalytic domain) of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Diepitopic or multiepitopic polypeptides can be
ADR83884 ARP21542 ABP21542 ABP29684 ADR09524 ADV08332 ADV08332 ADV081808 ADV79643 ABB57775 ABB77775 ABB677175 ADR066779 ADV066779 ADV16553 ADM16553 ADM16553 ADM16553 ADM16553 ADM270956 AAX70956 AAX709782 ABB66194 ABB66194 ABB66194 ABB66194 ABB66194 ABB66194 ABB66194 ABB66194 ABB66194 ABC66368 ABU29734	i; 20 AA. In binding prote GbpB; vaccine; 62.	vaccines for dental caries cin-B binding to a major hist p; English. E that of a peptide comprisinding protein-B (GbpB) of Streen. The peptide binds to a major protein. It was identified rabased algorithm for epitope mary amino acid sequence of S. The peptide can be used if twacines for dental carient vaccines for dental carient two the catalytic domain) of used in a claimed method of election.
® Q N B B B B D 4 A B D D D D A B A A W D A	(1) (2) (3) (3) (3) (3) (3) (3) (3) (3) (3) (3	ein-B bin pp; Engli pp; Engli is that o inding pr The pept The pept imary ami fis. The pi all. Diepi
3 3 9 9 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	(first entry) mutans glucan g protein-B; Gb; mutans. A2. 2003WO-US006962 2002US-0363209P TH INST.	, Taubman MA; 3-845091/78. ion useful as vacc binding protein-B protein. ; Page 10; 49pp; E; the glucan bindin the glucan bindin the glucan bindin the glucan bindin the glucan bindin the brimary binding motifs. Ty brotein-binding G (preferably from ostitions are used ody in a mammal. D
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	6 standard; p 6; 2004 (first coccus mutans binding prote coccus mutans 75845-A2. 2003; 2003WO- 2002; 2002US- 2002; 2002US- FORSYTH INST	7. Taubman 3-845091/71 ion useful binding pi protein. 7. Page 10; ent sequen the glucan
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	362 3362 7AN- 7AN- 3an 9030 9030 1AR- 1AR- 1AR-	WPI; 2003-845091/78. Composition useful a a glucan binding proclass II protein. Claim 11; Page 10; 4; The present sequence 33-52 of the glucan strain SK32 ADD93649 compositions and subtrained to search the prolass II protein-bin subunits (preferably The compositions and subunits (preferably The compositions as an amam amam amam a mam a subunits (preferably The compositions are an amam amam an an amam a subunits (preferably The compositions are an amam amam an amam a subunits (preferably The compositions are an amam amam amam an amam an amam a subunits (preferably The compositions are amam amam an amam amam an amam amam an amam amam amam a subunits (preferably amam amam amam amam amam amam amam am
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Matches

88888

RESULT 2

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Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
                                                                                                                              Streptococcus mutans glucan binding protein-B.
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/note= "HLA-binding peptide"
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/note= "HLA-binding peptide"
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te= "HLA-binding peptide"
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re= "HLA-binding peptide"
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:e= "HLA-binding peptide"
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189. .308
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                                                  ADD93649 standard; protein; 431 AA.
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08-AUG-2002; 2002US-0402483P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a composition comprising a fragment of a glucan binding protein-B (GbpB) and a biocompatible microparticle, where the fragment binds to a major histocompatibility complex (MRIC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds to a Streptococcus mutans GbpB-derived peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gabs
                                                                                                        Gaps
prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in passive immunisation.
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                                                                                                                                                                                                                                                                                                                             immunogenicity; immune stimulation; glucan binding protein-B;
microparticle; major histocompatibility complex; tooth disease.
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Pred. No. 2.9e-08;
                                                                           100.0%; Score 94; DB 7; Length 20; 100.0%; Pred. No. 2.9e-08; ive 0; Mismatches 0; Indels
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                                                                                                                                  1 QIASQDSKINNLTAQQQAAQ 20
                                                                                                                                                 Query Match 100.0%; Sc
Best Local Similarity 100.0%; Pr
Matches 20; Conservative 0;
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08-JAN-1999; 99US-0115142P.
12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-03632209P.
08-AUG-2003; 2003US-0402483P.
07-MAR-2003; 2003US-00383930.
                                                                                                                                                                                                                           ADX37249 standard; peptide; 20
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                                                                                                                                                                                                                                                                                                                                                                          Streptococcus mutans.
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TAUBMAN M A.
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                                                                                Query Match
Best Local Similarity
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The compositions comprise major histocompatibility

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Gaps

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0; Indels

Mismatches

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100.0%;

22

OLASODSKINNLTAGOGAAQ

33

QIASQDSKINNLTAQQQAAQ 20

Score 94; DB 7; Length 431; Pred. No. 1e-06;

us-10-797-821-6.rag

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class II protein binding GDDB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Dispitopic or multi-epitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GDpB can be used in
                                                                                                                                                                                                                                                                                                                                                                                                      Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
                                                                                                                                                                                                                                                                                                                                                                             Streptococcus mutans glucan binding protein-B.
                                                                                                                                                                                                                                                                                               ADD93653 standard; protein; 431 AA
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                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith DJ, Taubman MA;
                                                                                          passive immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus mutans.
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                                                                                                                     Sequence 431 AA;
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                                                                                                                             protein B (GppB) of Streptococcus mutans strain SK32. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions comprise major human vaccines for dental caries. The compositions comprise major human specially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Diepitopic or multiepitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in
                                     Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                  The present sequence is the protein sequence of the glucan binding
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                                                                                                                                                                                                                                                                                                                       100.0%; Score 94; DB 7; Length 431; 100.0%; Pred. No. 1e-06; ive 0; Mismatches 0; Indels
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                                                                                          Claim 6; Page 7; 49pp; English.
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nes 20; Conservative
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2003-845091/78
            GENBANK; AY046410
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Matches
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protein-B (GbpB) of Streptococcus mutans strain SSM3. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions comprise major histocompatiblity complex (MHC) class II protein-binding GbpB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Diepitopic or multiepitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in
                                                                                                                Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
                                                                                                                                                                                                                                                                                                                                                                            The present sequence is the protein sequence of the glucan binding
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Pred. No. 1e-06;
                                                                                                                                                                                                                                                                                          Claim 5; Page 8-9; 49pp; English.
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2003-845091/78.
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                                       GENBANK; AY046414.
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The present sequence is the protein sequence of the glucan binding protein-B (GappB) of Streptococcus mutans strain 3VF4. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental

Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.

07-MAR-2003; 2003WO-US006962 07-MAR-2002; 2002US-0363209P.

18-SEP-2003.

Taubman MA;

Smith DJ,

WPI; 2003-845091/78.

GENBANK; AY046411.

(FORS-) FORSYTH INST.

Claim 5; Page 8; 49pp; English.

Matches

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ADX37272

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The invention relates to a composition comprising a fragment of a glucan binding protein-B (GbpB) and a biocompatible microparticle, where the fragment binds to a major histocompatibility complex (MRIC) class II protein. The composition is useful for producing an antibody for immunizing mammala against dental caries. This sequence corresponds to a Streptococcus mutans GbpB protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
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microparticle; major histocompatibility complex; tooth disease
                                                                immunogenicity; immune stimulation; glucan binding protein-B; microparticle; major histocompatibility complex; tooth disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 94; DB 9; Length 431; 100.0%; Pred. No. 1e-06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus mutant glucan binding protein B variant #5.
                               Streptococcus mutant glucan binding protein B variant #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; SEQ ID NO 30; 73pp; English.
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08-JAN-1999; 99US-0115142P.
12-APR-1999; 99US-00120049.
07-MAR-2002; 2002US-0363209P.
08-AUG-2002; 2002US-0402483P.
07-MAR-2003; 2003US-00383930.
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21-APR-2005 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Taubman MA;
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                                                                                                                        Streptococcus mutans
                                                                                                                                                                                                                                                                                                                                                                                       (SMIT/) SMITH D J.
(TAUB/) TAUBMAN M A.
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microparticle; major histocompatibility complex; tooth disease.
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Pred. No. 1e-06;
                                                                                                                                                                                                                                                                    Streptococcus mutant glucan binding protein B variant #1.
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100.0%; Pred. No. 100.0%; Mismatches
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08-JAN-1999; 99US-0115142P.
12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-0363209P.
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Best Local Similarity 100.
Matches 20; Conservative
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Taubman MA;
                                                                                                                                                                                                                                                                                                                                                            Streptococcus mutans.
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RESULT 7 ADX37273

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The present invention relates to a computational method (M1) for identifying adhesin and adhesin-like proteins, by computing the sequence-based attributes of protein sequences using five attribute modules of a neural network software, training an artificial neural network (ANN) for each of the computed five attributes, and identifying the adhesin and adhesin having probability of being an adhesin (Pad) as equal or greater than 0.51. Also claimed is a set of 274 annotated genes encoding adhesin and adhesin-like proteins, having 274 fully defined 162-ccc lists base pair (SEQ ID NO: 385-658) sequences; a set of 105 hypothetical genes encoding adhesin and adhesin-like proteins, having 105 fully defined 306-18876 base pairs (SEQ ID NO: 629-763); a set of 105 hypothetical adhesin-like proteins, having 105 fully defined 53-3716 base pair (SEQ ID NO: 1-279); a set of 105 hypothetical adhesin and adhesin-like proteins, having 105 fully defined 106-5291 base pair (SEQ ID NO: 1-279); a set of 105 hypothetical adhesin and adhesin-like proteins, having 105 fully defined 106-5291 base pair (SEQ ID NO: 280-384) sequences; and a fully connected multilayer feed forward ANN (I) based pair (SEQ ID NO: 1-279); a set of 105 hypothetical adhesin and adhesin-like proteins, of therapeutic potential. And identifying and short-listing proteins for further testing in development of new vaccine formulations consecuted adhesins and adhesins from discovery and preventing therapeutics for whooping cough, pneumonia, cuseful for identifying putative adhesins at hat are important in drug distantly related organisms, and from bacteria belonging to a wide consecution of the proteins. (M1) is capable of predicting adhesive nature of phylogenetic spectrum. (M1) is capable of predicting adhesive nature of cultique proteins. The present sequence is a microbial pathogen adhesin
 Computational method for identifying adhesin and adhesin like molecules, comprises computing sequence-based attributes of protein sequences using neural network software and training an artificial neural network.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 94; DB 9; Length 431;
Pred. No. 1e-06;
Mismatches 0; Indels
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                                                                     Claim 16; SEQ ID NO 210; 402pp; English
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  algorithm; adhesin; pharmaceutical; vaccine; drug screening; bordecella pertuesis infection; antibacterial; preumonia; antiinflammatory; respiratory-gen.; gastric ulcer; antiulcer; gastrointestinal-gen.; urinary tract infection; antimicrobial; uropathic.
                                                                                                                                                                                                                                                                           New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing
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                                                                                                                                                                                                                                                                                                                                                                   Claim 3; SEQ ID NO 33; 73pp; English.
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99US-0115142P.
99US-00290049.
2002US-0363209P.
2002US-0402483P.
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09-MAR-2004; 2004US-00797821
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2004US-0589227P
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                                                                                                                                                       (SMIT/) SMITH D J.
(TAUB/) TAUBMAN M A.
                                                                                                                                                                                                                                          WPI; 2005-151644/16.
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Matches 20; Conserv
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07-MAR-2002;
08-AUG-2002;
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20-JUL-2004;
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The present sequence is the protein sequence of the glucan binding protein-B (GbpB) of Streptococcus mutans strain 15JP2. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions comprise major histocompatiblity complex (MHC) class II protein-binding GbpB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Dispitopic or multispitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in
       Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex
                                                                                                                                                                                                                                                                                                                                 1 QIASQDSKINNLTAQQQAAQ 20
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                                     class II protein.
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                                                                                                                                                                                                                                                        Sequence 432 AA;
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100.0%; Score 94; DB 7; Length 432; 100.0%; Pred. No. 1e-06; red. No. 1e-06; Mismatches 0; Indels

100.0%;

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The present sequence is the protein sequence of the glucan binding protein-B (GbpB) of Streptococcus mutans strain 3SN1. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions comprise major histocompatibility complex (MHC) class II protein-binding GbpB peptides, especially HLA-binding peptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
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ADD93652 standard; protein; 432 AA
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08-AUG-2002; 2002US-0402483P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing
covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Dispitopic or multipeptopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in
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Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                              100.0%; Score 94; DB 7; Length 432; 100.0%; Pred. No. 1e-06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus mutant glucan binding protein B variant #3.
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07-MAR-2002; 2002US-0363209P.
08-AUG-2002; 2002US-0402483P.
07-MAR-2003; 2003US-00383930.
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                                                                                                                                                                  Best Local Similarity 100.
Matches 20; Conservative
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(TAUB/) TAUBMAN M A.
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                                                                                      passive immunisation
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The present sequence is that of a peptide comprising amino acid residues 37-56 of the glucan binding protein-B (GbpB) of Straptococcus mutans stray AbD93649. The peptide binds to a major histocompatibility complex (WHC) class II protein. It was identified as a potential B cell epitope using a matrix-based algorithm for epitope prediction, which was used to search the primary amino acid sequence of GapB for known MHC class II binding motifs. The peptide can be used in immunogenic compositions and subunit vaccines for dental caries. These comprise MHC class II protein-binding GbpB peptides covalently linked with peptide cubunits (preferably from the catalytic domain) of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Diepitopic or multiepitopic polypeptides can be related against MHC class II binding fragments of GbpB can be used in caised against MHC class II binding fragments of GbpB can be used in
                                                                                                                                                                                                                                                                                                                                                                                                                           Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
                                          Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
  Streptococcus mutans glucan binding protein-B peptide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunogenicity; immune stimulation; glucan binding protein-B;
microparticle; major histocompatibility complex; tooth disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus mutant glucan binding protein B peptide #7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 77; DB 7; L
Pred. No. 1.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADX37250 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 10; 49pp; English
                                                                                                                                                                                                     07-MAR-2003; 2003WO-US006962.
                                                                                                                                                                                                                                           07-MAR-2002; 2002US-0363209P.
08-AUG-2002; 2002US-0402483P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 ODSKINNLTAQQQAAQ 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QDSKINNLTAQQQAAQ 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                Taubman MA;
                                                                                    Streptococcus mutans
                                                                                                                                                                                                                                                                                                        (FORS-) FORSYTH INST.
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                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-845091/78.
                                                                                                                       WO2003075845-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2005031633-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-APR-2005
                                                                                                                                                               18-SEP-2003
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                                                                                                                                                                                                                                                                                                                                              Smith DJ,
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ADX37250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New composition comprising a fragment of a glucan binding protein-B (GDBB) that binds to MRC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a composition comprising a fragment of a glucan binding protein-B (GbpB) and a biocompatible microparticle, where the fragment binds to a major histocompatibility complex (MHC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds to a Streptococcus mutans GbpB protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                      immunogenicity; immune stimulation; glucan binding protein-B;
microparticle; major histocompatibility complex; tooth disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 94; DB 9; Length 432; 100.0%; Pred. No. 1e-06;
                                                                                                                                                                                                                                                                Streptococcus mutant glucan binding protein B variant #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; SEQ ID NO 32; 73pp; English.
                                                                                                                                      ADX37275 standard; protein; 432 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADD93627 standard; peptide; 20 AA.
                  QIASQDSKINNLTAQQQAAQ 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QIASQDSKINNLTAQQQAAQ 20
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OIASODSKINNLTAQQQAAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-APR-1998; 98US-0081550P.
08-JAN-1999; 99US-0115142P.
12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-0362209P.
08-AUG-2002; 2002US-0402483P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-MAR-2004; 2004US-00797821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-MAR-2003; 2003US-00383930
                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Taubman MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SMIT/) SMITH D J.
(TAUB/) TAUBMAN M A.
                                                                                                                                                                                                                                                                                                                                                                 Streptococcus mutans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2005-151644/16.
                                                                                                                                                                                                                                                                                                                                                                                                        US2005031633-A1.
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                                                                                                                                                                                                                      21-APR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                10-FEB-2005
                                     33
                                                                                                                                                                              ADX37275;
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ADD93627 RESULT

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The invention relates to a composition comprising a fragment of a glucan binding protein-B (GbpB) and a biocompatible microparticle, where the fragment binds to a major histocompatibility complex (MHC) class II protein. The composition is useful for producing an antibody for immunizing mammala against dental caries. This sequence corresponds to a Streptococcus mutans GbpB-derived peptide of the invention.
                                                                                                                                                                                                                                                                                         New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

81.9%; Score 77; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; SEQ ID NO 7; 73pp; English.
                                  13-APR-1998; 98US-0081550P.
08-JAN-1999; 99US-0115142P.
12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-036209P.
08-AUG-2002; 2002US-0402483P.
07-MAR-2003; 2003US-00383930.
09-MAR-2004; 2004US-00797821.
                                                                                                                                                                                                                        Taubman MA;
                                                                                                                                                                (SMIT/) SMITH D J.
(TAUB/) TAUBMAN M A.
                                                                                                                                                                                                                                                       WPI; 2005-151644/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 AA;
                                                                                                                                                                                                                        Smith DJ,
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Search completed: January 25, 2006, 19:01:43 Job time : 68.2 secs

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Gapa ;

GenCore version 5.1.6 Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

2006, 18:48:55; Search time 9.1 Seconds (without alignments) 211.465 Million cell updates/sec January 25,

US-10-797-821-6 94 Perfect score:

1 QIASQDSKINNLTAQQQAAQ 20 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ok			COLUMNIES	٠
Result		Query				
No.	Score	Match	Match Length	DB	qi	Description
г	74	78.7	392	0	G95258	secreted 45 kd pro
7	74	78.7	392	~	B98124	Btres
m	47	50.0	507	~	805542	tical pr
4	46	48.9	238	~	D75477	hypothetical prote
S	46	48.9	503	7	AB2734	NADH dehydrogenase
9	46	48.9	503	~	D97515	NADH dehydrogenase
7	45	47.9	526	~	E88940	protein C05E4,9 [i
80	44	46.8	308	~	AF1990	hypothetical prote
6	44	46.8	505	~	\$15194	sucrose porin'scrY
10	44	46.8	947	~	T23107	hypothetical prote
11	43	45.7	397	N	G83699	malate oxidoreduct
12	43	45.7	427	~	A43453	A-kinase anchor pr
13	43	45.7	461	~	G59093	hypothetical prote
14	43	45.7	542	~	S20466	
15	43	45.7	1302	Н	JC6009	surface-located me
16	42.5	45.2	2692	N	T23768	hypothetical prote
17	42	44.7	197	~	D91063	heat shock protein
18	42	44.7	197	~	H85907	heat shock protein
19	42	44.7	213	N	H75482	hypothetical prote
20	42	44.7	235	~	A56757	14-3-3 regulatory
21	42	44.7	347	7	T35518	probable secreted
22	42	44.7	353	~	G81120	I protein, probabl
23	42	44.7	420	~	D82709	colicin V secretio
24	42	44.7	649	~	T22254	hypothetical prote
25	42	44.7	722	~	Н97217	uncharacterized co
56	42	44.7	769	~	T22256	hypothetical prote
27	42	44.7	1189	~	AH2154	WD-repeat protein
28	42	44.7	1668	~	A60272	E E
29	41	43.6	110	7	B40785	ORF2 protein - ric

hypothetical prote heat shock protein	hypothetical prote uroporphyrin-III C	uroporphyrinogen I uroporphyrinogen I	hypothetical prote gene CARSR12 prote	cytoskeleton assem diaphanous-related	<pre>multimerin, endoth hypothetical prote</pre>	hypothetical prote	probable membrane hypothetical prote
S16667 S01240	T26828 S02185	E91220 G86066	T50010 S16595	T18255 T17454	A57384 T44045	T44231 A11987	H81850 F81090
0 0	01 01	01 01	0 0	0 0	0 0	0 0	00
110	245 393	6 6 6 6 7 7	414	1063	1228	1520	184
44	ဖွဲ့ဖ	ဖွဲ့ဖ	ب ب	ب ب	ب ب	6 6	9.9
43.43	43	43	43	43	£ 4 £ 8	43	42.6
41 41	41	4 4	4 4	4 4	44	41	44
30	33 33	34 35	36 37	38 30 80	41	4 4 2 6	4 4 4 C

ALIGNMENTS

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secreted 45 kd protein [imported] - Streptococcus pneumoniae (strain TIGR4)

G;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Datesion: 035288
B;Tettelin, H.; Nelson, K.B.; Paulsen, I.T.; Bisen, J.A.; Read, T.D.; Peterson, S.; Heir on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, B.K.; Holt, I.B.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A;Accession: 039258
A;Accession: 039258
A;Accession: 039258
A;Acteus: preliminary
A;Accession: DNA
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A;Residues: 1-392 <KUR>
A;Cross-references: UNIPROT:Q9DMY4; UNIPARC:UPI000051B81; GB:AE005672;
A;Cross-references: UNIPROT:Q9TMS5; UNIPROT:Q8DMY4; UNIPARC:UPI000051B81; GB:AE005672;
C;Genetics:
A;Gene: SP2216

Gaps ö Length 392; 1; Indels Query Match 78.7%; Score 74; DB 2; I Best Local Similarity 75.0%; Pred. No. 0.00026; Matches 15; Conservative 4; Mismatches 1;

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1 QIASODSKINNLTAQQQAAQ 20

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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-392 <KUR>
A;Cross-references: UNIPROT:Q97N55; UNIPROT:Q8DMY4; UNIPARC:UPI0000051B81; GB:AE007317;
C;Genetics:

A;Gene: gsp-781

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A;Cross-references: UNIPROT:QBUFW5; UNIPARC:UPI0000D1AD8; GB:AE008688; PIDN:AAL42288.1; A;Experimental source: strain C58 (Dupont)
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WADH dehydrogenase I chain m (NADH-ubiquinone oxidoreductase chain m) AGR_C_2362 [import C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: D97515
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: UNIPROT: QSUFWS; UNIPARC: UPI0000D1AD8; GB: AE007869; PIDN: AAK87077.1;
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A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elc A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: E88940
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A,Molecule type: DNA
A,Residues: 1-526 <STO>
A,Cross-references: UNIPROT:Q10663; UNIPARC:UPI0000176000; GB:chr_V; PIDN:AAB71278.1; PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
        ; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                      ster, E.W.
A;Itle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
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C.Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C.Accession: E88940
F.anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
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Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 503;
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                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: circular chromosome
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: AGR C 2362
A;Map position: circular chromosome
C;Superfamily: NADH dehydrogenase (ubiquinone) chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein C05E4.9 [imported] - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
48.9%; Score 46; DB
Best Local Similarity 61.1%; Pred. No. 13;
Matches 11; Conservative 1; Mismatches
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1 Similarity 61.1%;
11; Conservative 1
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-503 <KUR>
                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-503 <KUR>
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                                                                                                                                                                                  A; Accession: AB2734
                                                                                                                                                                                                                                                                                                                                                                                   A:Gene: nuoM
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A,Reference number: A75250, MUID:20036896, PMID:10567266
A,Accession: D75477
A,Accession: D75477
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-238 cWH1.
A,Cross-references: UNIPROT:09RW98, UNIPARC:UPI00000C1802; GB:AE001932; GB:AE000513; NIC
A,Experimental source: strain R1
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ద
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as Lys
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NADH dehydrogenase I chain M nuoM [imported] - Agrobacterium tumefaciens (strain C58,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: D75477
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, B.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
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                                                                                                                                                                                                                                                                                          Aypothetical protein, 54K - Enterococcus faecium
C;Species: Enterococcus faecium
C;Species: Enterococcus faecium
C;Species: Enterococcus faecium
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: 805542
R;Fuerst, P.; Moesch, H.U.; Solloz, M.
Nucleic Acids Res. 17, 6724, 1989
Nucleic Acids Res. 17, 6724, 1989
A;Title: A protein of unusual composition from Enterococcus faecium.
A;Reference number: 805542; MUID:89385998; PMID:2780297
A;Accession: 805542
A;Molecule type: DNA
A;Residues: 1-507 <FUE>
A;Residues: 1-507 <FUE>
A;Residues: 1-507 <FUE>
A;Rossereferences: UNIRROT:P13692; UNIPARC:UPI000016F6FC; GB:X16421; EMBL:1
A;Note: the authors translated the codon CGT for residues 221 and 223 as Lyi
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C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
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     Score 74; DB 2; Length 392;
Pred. No. 0.00026;
4; Mismatches 1; Indels
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                                                                                                                            1 QIASQDSKINNLTAQQQAAQ 20
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           78.7%;
75.0%;
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63 VAPQKSRFNDLTAQQ 77
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Best Local Similarity 60.0%
These 9; Conservative
Query Match
Best Local Similarity 75.0°
Matches 15; Conservative
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R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir Mucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUD:20512582; PMID:11058132
A;Accession: G83699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Molecule type: DNA
A;Residues: 1-397 <STO-3
A;Cross-references: UNIPROT:Q9KFS8; UNIPARC:UPI00000D73B6; GB:AP001508; GB:BA000004; NI
A;Experimental source: strain C-125
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C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A44453
R;Carr, D.W.; Stofko-Hahn, R.E.; Fraser, I.D.; Cone, R.D.; Scott, J.D.
J. Biol. Chem. 267, 16816-16823, 1992
A;Title: Localization of the cAMP-dependent protein kinase to the postsynaptic densitie
A;Reference number: A43453; MUID:92380978; PMID:1512224
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A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-427 <CAR>
A,CAR>
A,CCOSS-references: UNIPROT:P24588; UNIPARC:UPI0000125759; GB:M90359; NID:g178323; PID:A,Experimental source: thyroid
                                                                                                                                                                                                                                                                  A;Residues: 1-947 <WIL>
A;Cross-references: UNIPROT:Q9XXK5; UNIPARC:UPI000007E68B; EMBL:AL023493; PIDN:CAA18898
A;Experimental source: clone H20J18
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N;Alternate names: AKAP 79; cAMP-dependent protein kinase RII subunit-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 malate oxidoreductase (NAD) (malic enzyme) BH0399 [imported] - Bacillus halodurans C;Species: Bacillus halodurans C;Species: Bacillus halodurans C;Decies: Dec-2000 #sequence_revision 01-Dec-2000 #text_change 05-Oct-2004 C;Accession: G83699 R;Takami, H;; Nakasone, K;; Takaki, Y;; Maeno, G;; Sasaki, R.; Masui, N.; Fuji, F.;
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A;Map position: X
A;Introns: 20/3; 328/2; 587/1; 631/3; 676/3; 764/2; 794/3; 830/3; 886/1; 910/3
hypothetical protein H20J18.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23107
R;Steward, C.
submitted to the EMBL Data Library, May 1998
A;Reference number: Z19679
A;Accession: T21107
A;Accession: T21107
A;Status: preliminary; translated from GB/EMBL/DDBJ
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52;
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30;
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Pred. No.
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Pred. No.
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Best Local Similarity 55.6%;
Matches 10, Conservative
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49 QIAEQPDKVNSLTSR 63
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Best Local Similarity
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A,Gene: BH0399
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 21-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: S15194
S;Cshnid, K.; Ebner, R.; Jahrels, K.; Lengeler, J.W.; Titgemeyer, P.
Mol. Microbiol. S; 941-950, 1991
A;Title: A sugar specific porin, ScrY, is involved in sucrose uptake in enteric bacteria A;Reference number: S15193; MUD:91312133; PMID:1649946
A;Accession: S15194
A;Status: preliminary; translation not shown
A;Residues: 1-505 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-308 «KUR»
A;Cross-references: UNIPROT:08YWW9; UNIPARC:UPI0000CEODC; GB:BA000019; PIDN:BAB77841.1;
C;Genetics:
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C;Genetics:
A;Gene: scrY
                                                                                                                                                                                                                                                                                                                                                                                                        C.Species: Nostoc sp. PCC 7120
A,Note: Nostoc sp. PCC 7120
A,Note: Nostoc sp. etrain PCC 7120
C,Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
R,Kaneko, T.; Nakamura v ....
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C;Species: Klebsiella pneumoniae
C;Date: 21-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: S15194
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                                                                                                                                        DB 2; Length 526;
19;
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47.9%; Score 45;
Best Local Similarity 58.8%; Pred. No. 3
Matches 10; Conservative 3; Mismatcl
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435 VASQDERILSLTAQNVA 451
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     C,Genetics:
A,Gene: CO5E4.9
A,Map position: 5
C,Superfamily: isocitrate lyase
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Best Local Similarity
Matches 9; Conserv
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Length 1302;

Score 43; DB 1; Length 130 Pred. No. 1.1e+02; 4; Mismatches 7; Indels

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J. Bacteriol. 178, 2775-2784, 1996
A:Title: Analysis of 0.5-kilobase-pair repeats in the Mycoplasma hominis lmp gene system A;Title: Analysis of 0.5-kilobase-pair repeats in the Mycoplasma hominis lmp gene system A;Reference number: JC6009; MUID:96213016; PMID:8631664
A;Accession: JC6009
A;Molecule type: DNA
A;Residues: 1-1302 <LAD>
A;Residues: 1-1302 <LAD>
C;Gross-references: UNIPROT:Q49547; UNIPARC:UPI00000B0501; EMBL:X95601; NID:g1197335; PJI
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.Superfamily: surface-located membrane protein lmp3; tetratricopeptide repeat homology C.Superfamily: surface-located membrane protein (SIG)  
2.124/Domain: signal sequence #status predicted <SIG>  
7.124/Domain: signal sequence #status predicted <SIG>  
7.25-1302/Pomain: signal sequence #status predicted capacity  
7.25-1302/Domain: tetratricopeptide repeat homology <TT1>  
7.992/Domain: tetratricopeptide repeat homology <TT2>  
7.993-1026/Domain: tetratricopeptide repeat homology <TT3>  
7.1120/Domain: tetratricopeptide repeat homology <TT3>  
7.114-1190/Domain: tetratricopeptide repeat homology <TT3>  
7.114-1190/Domain: tetratricopeptide repeat homology <TT4>  
7.114-1190/Domain: tetratricopeptide repeat homology <TT4-  
7.114-1190/Domain: tetratrico
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Best Local Similarity 45.v.
Best Local 9; Conservative
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
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A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: UNIPROT:09X2Z4; UNIPARC:UPI00000B735E; GB:AF065404; NID:g4894216; PI
A;Experimental source: strain Sterne
A;Mote: similar to hypothetical gene (609 aa) Clostridium difficile (X98606), 249/390 pc
C;Genetics: pX01-23
A;Genome: plasmid
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R;Okinaka, R.T.; Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Koehler
J. Bacteriol. 181, 6509-6515, 1999
A;Title: Sequence and organization of pXO1, the large Bacillus anthracis plasmid harbori
A;Reference number: A59091; MUID:99445483; PMID:10515943
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C;Species: Mycoplasma hominis
C;Species: Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JC6009
R;Ladefoged, S.A.; Jensen, L.T.; Brock, B.; Birkelund, S.; Christiansen, G.
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C;Species: Fusarium oxysporum
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Bacillus anthracis
.Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004
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      A;Note: sequence extracted from NCBI backbone (NCBIN:111869, NCBIP:111870)
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                                                                                                                                 Query Match 45.7%; Score 43; DB 2; Length 427; Best Local Similarity 66.7%; Pred. No. 33; Matches 8; Conservative 3; Mismatches 1; Indels
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414 EMASDDNKINNL 425
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Sequence:

Scoring table:

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MEDLINE=21481971; PubMed=11598068;

MEDLINE=21481971; PubMed=11598068;

MINITED GGraner R.O., Jin S., King W.F., Chen T., Smith D.J.,

MATCHOS Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,

Duncan M.J.;

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Last sequence update)
Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Glucan-binding protein B.
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100.0%; Pred. No. 1.9e-06;
ive 0; Mismatches 0;
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051219 BRANE

061380 BIRA

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Glucan-binding protein B.
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Q4P5Q8 USTWA
Q6RKH4 G1BZE
Q9AZ34 BPHK6
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Maximum Match 100%
Listing first 45 summaries
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Q8P318
Q5M6K4
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Q55EG2
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Q810C2
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
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Chia J.-S., Chang L.-Y., Lee Y.-Y., Chen J.-Y.; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases
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DOI=10.1128/IAI.69.11.6931-6941.2001;
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PRINTS; PR01823; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
SEQUENCE 431 AA, 44592 MW;
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les 20; Conservative
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EMBL; AX046410; AAK94500.1; -; Genomic_DNA.

EMBL; AX046410; AAK94500.1; -; Genomic_DNA.

InterPro; IPR007921; CHAP.

InterPro; IPR009148; SibA.

Pfam; PP05257; CHAP; 1.
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DOI=10.1128/IAI.69.4.2493-2501.2001;
Chia J.S., Lee Y.Y., Huang P.T., Chen J.Y.;
Identification of stress-responsive genes in Streptococcus mutans by differential display revorse transcription-PCR.";
Infect. Immun. 69:2493-2501(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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MEDLINE=21481977; PubMed=11598074;

DOI=10.1128/IA1.69.11.6987-6998.2001;

Chia J.S., Chang L.Y., Shun C.T., Chang Y.Y., Chen J.Y.;

Chia J.S., Chang L.Y., Shun C.T., Chang Y.Y., Chen J.Y.;

"A 60-kilodalton immunodominant glycoprotein is essential for cell
wall integrity and the maintenance of cell shape in Streptococcus
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01-JUN-2001 (TrEMBLrel. 27, Last sequence update)
01-GLFEB-2005 (TrEMBLrel. 29, Last annotation update)
Immunodominant glycoprotein IDG-60 (Glucan-binding protein B)
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      Streptococcus mutans.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                   Jin S., Duncan M.J., Taubman M.A., Smith D.J.; "Cloning of the gbpB gene from Streptococcus mutans."; J. Dent. Res. 79:224-224 (2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21481971; PubMed=11598068;
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PROSITE; PS50911; CHAP; 1.
SEQUENCE 431 AA; 44620 MW;
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Best Local Similarity 100...
Best 20; Conservative
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NUCLEOTIDE SEQUENCE.
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                                                                                             NCBI_TaxID=1309;
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                                                                                                                                                                                                        STRAIN=SJ32;
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09AG98 STRMU
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Duncan M.J.;
"Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates.";
Infect. Immun. 69:6931-6941(2001).
EMBL; AR338445; AAK08104.1; -; Genomic_DNA.
EMBL; AX046411; AAK94501.1; -; Genomic_DNA.
InterPro; IPR007921; CHAB.
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MEDLINR=22295063; PubMed=12397186; DOI=10.1073/pnas.172501299;
Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Acarson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P.,
Qian Y., Li S., Zhu H., Najar F.Z., Lai H., White J., Roe B.A.,
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Putative secreted antigen GbpB/SagA, putative peptidoglycan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 94; DB 2; Length 431;
; Pred. No. 1.9e-06;
0; Mismatches 0; Indels
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
STRAIN=3VF4;
Jin S., Duncan M.J., Taubman M.A., Smith D.J.;
Jin S., Duncan M.J., Taubman M.A., Smith D.J.;
"Cloning of the ghpB gene from Streptococcus mutans.";
J. Dent. Res. 79:224-224 (2000).
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Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002).
EMBL, AE014855, AANST811.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR0079248; SibA.
Plam: PPG0557; CHAP; 1.
PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PSG0911; CHAP; 1.
Complete protecome.
SEQUENCE 431 AA; 44620 MM; 2DICA685248CCD3E CRC64.
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Pred. No. 1.9e-06;
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MEDLINE=21429245; PubMed=11544234;
DOI=10.1128/JB.183.19.5709-5717.2001;
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NUCLEOTIDE SEQUENCE.
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"Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates.";
        Gaps
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Pred. No. 1.9e-06;
Mismatches 0; Indels
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DOI=10.1128/IAI.69.11.6931-6941.2001;
Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
        Indels
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Bacteria, Pirmicutes, Lactobacillales; Streptococcaceae,
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Jin S., Duncan M.J., Taubman M.A., Smith D.J.;
"Cloning of the gbpB gene from Streptococcus mutans.";
J. Dent. Res. 79:224-224(2000).
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DR-2004 (TrEMBLrel. 26, Last annotation update)
Glucan-binding protein B.
Streptococcus mutans.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Glucan-binding protein B.
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EMBL; AX046413; AAK94503.1; -; Genomic_DNA.
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PROSITE; PS50911; CHAP; 1.
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Q938V1;
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MEDLINE=21461971; PubNed=11598068;

MEDLINE=21461971; PubNed=11598068;

DOI=10.1128/IAI.69.11.6931-6941.2001;

Mattoe-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,

Duncan M.J.;

Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in Cinical isolates.";

Infect. Immun. 69:6931-6941(2001).

EMBL; AY046412; AA894502.1; -; Genomic_DNA.

InterPro; IPR007921; CHAP.

InterPro; IPR007921; CHAP.
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                                                                                                                                                                                                                                                                                                                                                                                                        Score 94; DB 2; Length 432;
Pred. No. 1.9e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Peruzzi F., Piggot P.J., Daneo-Moore L.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U78607; AAD00288.1; -; Genomic_DNA.
NON_TER 211 211 211
                                                                                                                                                                                                                                                                                                                                                          432 AA; 44648 MW; E769B2504AEE50E9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-OCT-2002 (TrEMBLrel. 22, Last annotation update) Putative secreted protein (Fragment).
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1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
General stress protein GSP-781.
                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Scc...
100.0%; Pred. No....
0; Mismatches
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                                                                                                                                                                                                                                                                                Pfam, PF05257, CHAP, 1.
PRINTS, PR01852, SIBAPROTEIN.
PROSITE, PS50911, CHAP, 1.
SEQUENCE 432 AA, 44648 MW;
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Best Local Similarity 100.00.
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Best Local Similarity 100.0
watches 17; Conservative
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Q9ZAS7;
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QBDMY4;
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Query Match
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Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S., DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C., Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E., LeBlanc D.J., Lee L.N., Lekkowitz B.J., Lu J., Mateushima P., McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I., Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P., Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G., Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud P.L.,
                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                 Glass J.I.; "Genome of the bacterium Streptococcus pneumoniae strain R6.";
                                                                                                                                                                                                                                                                                                                  Query Match 78.7%; Score 74; DB 2; Length 392; Best Local Similarity 75.0%; Pred. No. 0.0028; Matches 15; Conservative 4; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  392 AA
                                                                                                                                           J. Bacteriol. 183:5709-5717(2001).

EMBL, AE008566; AAL00823.1; -; Genomic_DNA.

PIR; B98124; B98124.

PIR; G95258; G95258.

InterPro; IPR007921; CHAP.

InterPro; IPR009148; SibA.

Pfam; PP05257; CHAP; 1.
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EMBL; AE007509; AAK76264.1; -; Genomic_DNA.
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PROSITE; PS50911; CHAP; 1.
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InterPro, IPR007921; CHAP.
InterPro, IPR009148; SibA.
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Q97NSS;
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PIR; G95258; G95258.
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                                                                                                                                                                                                                                                                             Complete proteome. SEQUENCE 392 AA;
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Best Local Similarity
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MEDLINE-STRIP / ATCC 700294 / Serotype M1;
MEDLINE-STRIP SERVE G., McShan W.M., Ajdit D.U., Savic D.U., Savic G., Lyon K., Primeaux C., Scrate S., Strorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Noce B.A., McLaughlin R.E., "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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PROSITE; PS50911; CHAP; 1.
Complete protecome.
SEQUENCE 398 AA; 42028 MW; 5DCEDA78CB863B60 CRC64;
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09A128; Q7BH59;
01-UUN-2001 (TEMBLrel. 17, Created)
01-UTX-2001 (TEMBLrel. 17, Last sequence update)
10-MAY-2005 (TEMBLrel. 30, Last annotation update)
                                                                                                                                                                                                                                      25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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Pred. No. 0.24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M6 strain.";
J. Infect. Dis. 190:727-738(2004).

EMBL; CP0000003; AAT86152.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR001448; SibA.
Pfam; PF05257; CHAP; 1.
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4; Mismatches
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PubMed=15272401; DOI=10.1086/422697;
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                                            1 QIASQDSKINNLTAQQQAAQ 20
                                                                   33 KIAAQDNKISNLTAQQQEAQ 52
                                                                                                                                                                                                                                                                                                                             OrderedLocusNames=M6_Spy0017;
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                                                                                                                                                                                             QSXEL1 STRP6 PRELIMINARY;
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    15; Conservative
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                                                                                                                                                                                                                                                                                                           Secreted protein.
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13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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NUCLEOTIDE SEQUENCE
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Best Local Similarity
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Fagan P.K., Reinscheid D., Gottschalk B., Chhatwal G.S.; Indentification and characterization of a novel secreted protein from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smoot J.C., Barbian K.D., Van Gompel J.J., Smoof L.M., Chaussee M.S., Sylva G.L., Sturdevant D.E., Ricklefe S.M., Porcella S.F., Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q., Kapur V., Daly J.A., Veasy L.G., Musser J.M.; "Genome sequence and comparative microarray analysis of serotype MI$ group A Streptococcus strains associated with acute rheumatic fever outbreaks."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=MGAS8232 / Serotype M18;
MEDLINE=21927593; PubMed=11917108; DOI=10.1073/pnas.062526099
                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 62; DB 2; Length 398;
Pred. No. 0.24;
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Streptococcus pyogenes (Serotype M18).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                       group A streptococcus.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB006474; AAK33158.1; -; Genomic_DNA.
EMBLF, AR131999; AAL73135.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
                                                                                                                                                                                                                                                                                                                                                                                     398 AA; 41899 MW; 28A9B3F7195E969B CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                            66.0%; Score 62; DB 2 65.0%; Pred. No. 0.24;
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InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
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                                                                                                                                                                                                                                  Pfam, PF05257, CHAP, 1.
PRINTS, PRO1825, SIBARROTEIN.
PROSITE, PS50911, CHAP, 1.
Complete proteome; Signal.
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PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
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Q7CNQ7;
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Best Local Similarity
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Best Local Similarity
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Hayashi H., Hattori M., Hamada S., "Genome sequence of an M3 strain of Streptococcus pyogenes reveals a large-scale genomic rearrangement in invasive strains and new insights
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Bolotin A., Quinquis B., Renault P., Sorokin A., Ehrlich S.D.,
Kulakauskas S., Lapidus A., Goltsman E., Mazur M., Pusch G.D.,
Fonstein M., Overbeek R., Kyprides N., Purnelle B., Prozzi D.,
Ngui K., Masuy D., Hancy F., Burteau S., Boutry M., Delcour J.,
Goffeau A., Hols P.;
"Complete sequence and comparative genome analysis of the dairy
bacterium Streptococcus thermophilus.";
                                                                                                                                                                                                                                                                           STRAIN=SSI-1 / Serotype M3;
MEDLINE=22883270; PubMed=12799345; DOI=10.1101/gr.1096703;
Nakagawa I., Kurokawa K., Yamaabhita A., Nakata M., Tomiyasu Y.,
Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Pred. No. 0.24;
4; Mismatches 3; Indels
                                                                  Streptococcus pyogenes (serotype-M3).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae;
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EMBL; BA000034; BAC63110.1; -; Genomic_DNA.
EMBL; AR014136; AAM76821.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Glucan binding protein (PosB).
Name=pcsB; OrderedLocusNames=stu0022;
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Putative secreted protein.
OrderedLocusNames=SPs0015, SpyM3_0014;
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PROSITE; PS50911; CHAP; 1.
Complete proteome.
SEQUENCE 398 AA; 42028 MW;
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QSM6K4;
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                                                                                        Borges F., Layec S., Thibessard A., Fernandez A., Gintz B., Hols P., Decaris B., Leblond-Bourget N.;

"cse, a Chimeric and Variable Gene, Encodes an Extracellular Protein Involved in Cellular Segregation in Streptococcus thermophilus.";

J. Bacteriol. 187:2737-2746(2005).

EMBL; CP000023; AAV59752.1; -; Genomic_DNA.

EMBL; AY730643; AAM82375.1; -; Genomic_DNA.

InterPro; IPR009148; SibA.

PFEMP; PFEMPS; CHAPP.
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NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

NUMBRIGALISTAIRING DOI-10.1038/nbt1034;

A Bolotin A., Quinquis B., Renault F., Sorokin A., Ehrlich S.D.,

Nulakauskas S., Lapidus A., Goltsman E., Mazur M., Pusch G.D.,

Nulakauskas S., Lapidus A., Goltsman E., Mazur M., Pusch G.D.,

A Goffeau A., Hols P.,

"Complete sequence and comparative genome analysis of the dairy

bacterium Streptococcus thermophilus.";

"Complete sequence and comparative genome analysis of the dairy

bacterium Streptococcus thermophilus.";

NAL Blotechnol. 22:1554-1558 (2004).

REMBL; CP000024; AAV61641.1; -; Genomic_DNA.

RINCEPTO; IPR00148; SibA.

PROSITE; PRO1852; SIBARROTEIN.

R PROSITE; PS0911; CHAP; 1.

R Complete proteome.

SW Complete proteome.
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58.5%; Score 55; DB 2; Length 485;
Best Local Similarity 55.0%; Pred. No. 3.9;
Matches 11; Conservative 6; Mismatches 3; Indels
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
01-Can binding protein.
Name-pcsB; OrderedLocusNames=str0022;
Streptococcus thermophilus (strain CNRZ 1066).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  474 AA; 48142 MW; 1BAC6A9E0A0A200D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            485 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO1852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
COMPLE PrOLEOME.
SEQUENCE 474 AA; 48142 MW;
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OSM212 STRT1 PRELIMINARY;
AC 01-FEB-2005 (TrEMBLrel. 29,
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DT 01-FEB-20
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Ap

3, A

70, A

Appli

Appli
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                                                                                                                      ; Search time 16.6 Seconds (without alignments) 99.609 Million cell updates/sec
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Sequence 437,
Sequence 323
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/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
5.1.6
Compugen Ltd.
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US-09-270-767-31753

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US-09-134-000C-5990

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US-09-270-767-4780

US-09-270-767-4780

US-09-270-767-4780

US-09-270-767-4780

US-09-2480-039A-11667

US-09-107-532A-5095

US-09-107-532A-5095

US-09-107-532A-1067

US-09-134-0010-4733

US-09-134-0010-4733

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US-09-248-039A-11849

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US-09-248-039A-11849
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US-09-134-001C-4054
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US-09-949-016-10398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -08-696-944-20
                                                                                                                                                                                                                                                                                                                                                           572060 seqs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
GenCore version
Copyright (c) 1993 - 2006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                   OM protein - protein search, using sw model
                                                                                                                        January 25, 2006, 18:50:05
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94
1 QIASQDSKINNLTAQQQAAQ 20
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                            length: 0
length: 2000000000
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Match Length
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Maximum DB seq
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VS-001-583-110-4374

i Sequence 4374, Application US/09583110

i Partent No. 6699703

i Farent No. 6699703

i GRNERAL INFORMATION:

i TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

i TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

i TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

i TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

i TITLE OF INVENTION: NUMBER: US/09/583,110

cURRENT APPLICATION NUMBER: US 60/0107,433

PRIOR FILING DATE: 1998-06-30

i PRIOR FILING DATE: 1998-05-12

i RIOR FILING DATE: 1998-05-12

i RIOR FILING DATE: 1998-03-12

i RIOR FILING DATE: 1998-03-13

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                                                                Sequence 44851, A Sequence 9709, Ap Sequence 18849, A Sequence 10, Appli Sequence 17, Appli Sequence 75, Appl Sequence 73, Appl Sequence 73, Appl Sequence 23759, A Sequence 23759, A Sequence 23759, A Sequence 1736, Appl Sequence 1736, Appl Sequence 14607, Appl
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                          Sequence Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Youngan, Philip
APPLICANT: Fritz, Chrisian
APPLICANT: Fritz, Chrisian
APPLICANT: Murphy, Christopher
APPLICANT: Guzann, Luz-Maria
TITLE OF INVENTION: ESSENTIAL BACTERIAL GENES AND THEIR USE
FILE REFERENCE: 07334/060001
CURRENT APPLICATION NUMBER: US/09/222, 938A
CURRENT FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 74; DB 2; Length 210;
Pred. No. 0.00015;
4; Mismatches 1; Indels
US-09-902-540-12902
US-09-550-163-4
US-09-248-796A-18683
US-09-270-767-44851
US-09-949-016-9709
US-09-698-295-10
US-09-698-295-10
US-09-698-295-10
US-09-978-309A-75
US-09-540-236-3705
US-09-134-011C-2983
US-09-134-011C-2983
US-09-248-796A-2375
US-09-248-796A-2375
US-09-248-796A-14607
US-09-248-796A-14607
US-09-978-309A-77
US-09-248-796A-14607
US-09-978-309A-77
                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 67, Application US/09222938A Patent No. 6437108 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QIASQDSKINNLTAQQQAAQ 20
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33 KIAAQDNKISNLTAQQQEAQ 52
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    Query Match
Best Local Similarity
Matches 15; Conserv
    US-09-222-938A-67
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SEQ ID NO 67
LENGTH: 210
        TYPE: PRT
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                                                Sequence 31753, Application US/09270767

Patent No. 6703491
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HONDURGER et al.
TITLE OF INVENTION: Nucleic acide and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT PILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SEQ ID NO 31753
LENGTH: 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-09-270-767-46970
Sequence 46970, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFRENCE: File Reference: 7326-094
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SSEQ ID NO 46970
LENGTH: 168
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ilarity 62.5%; Pred. No. 2.3;
Conservative 2; Mismarchee
                                                                                                                                                                                                                                                                                                                                                                                                        Score 48; DB 2;
Pred. No. 2.3;
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Sequence 4, Application US/09972784

Sequence 4, Application US/09972784

Sequence 4, Application US/09972784

Patent No. 656608

SEQUENT: No. 656608

TILLE OF INVENTION: Proly1-4-Hydroxylases

FILE REFERENCE: UTSD0871

CURRENT APPLICATION NUMBER: US/09/972,784

CURRENT APPLICATION NUMBER: US/09/972,784

CURRENT FILING DATE: 2001-10-04

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patentin Ver: 2.1

SEQ ID NO 4

LENGTH: 325

TYPE: PRT

ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                          ORGANISM: Drosophila melanogaster US-09-270-767-31753
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US-09-270-767-46970
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Best Local Similarity
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US-09-107-433-3230
US-09-107-433-3230

; Sequence 3230, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; THERAPEUTICS

THERAPEUTICS
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                                                                               78.7%; Score 74; DB 2; Length 392; ilarity 75.0%; Pred. No. 0.00031; Conservative 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: CULKIDWIN-
OPERATING SYSTEM: «UNKIDWIN-
SOFTWARE: «UNKIDWIN-
SOFTWARE: «UNKIDWIN-
APPLICATION NUMBER: US/09/107,433
FILING DATA:
APPLICATION NUMBER: 60/085131
FILING DATA:
APPLICATION NUMBER: 60/051553
FILING DATE: May 12, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...399
SEQUENCE DESCRIPTION: SEQ ID NO: 3230:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 893-807
INFORMATION FOR SEQ ID NO: 3230:
SEQUENCE CHARACTERISTICS:
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4374
                                                                                                                                                                                            33 KIAAQDNKISNLTAQQQEAQ 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 399 amino acide TYPE: amino acid
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40 KIAAQDNKISNLTAQQQEAQ 59
                                                                                                                                                                        1 QIASQDSKINNLTAQQQAAQ 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                 Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-107-433-3230
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US-09-605-703B-894

i Sequence 894, Application US/09605703B

j Requence 894, Application US/09605703B

j Retent No. 69628-10.

j APPLICANT: Pompejus, Markus

j APPLICANT: Schooder, Hartwig

j APPLICANT: Achooder, Hartwig

j APPLICANT: Aberhauer, Greger, Brawig

j APPLICANT: Aberhauer, Greger, Trille OF INVENTION: CORYNBBATTERIUM GLUTAMICUM GENES ENCODING NOVEL,

j TITLE OF INVENTION: CORYNBBATTERIUM GLUTAMICUM GENES ENCODING NOVEL,

j TITLE OF INVENTION: CORYNBBATTERIUM GLUTAMICUM GENES ENCODING NOVEL,

j TITLE OF INVENTION: CORYNBBATTERIUM GLUTAMICUM GENES ENCODING NOVEL,

j TITLE OF INVENTION: CORYNBBATTERIUM GLUTAMICUM GENES ENCODING NOVEL,

j TITLE OF INVENTION: CORYNBBATTERIUM GLUTAMICUM GENES ENCODING NOVEL,

j FILE REFERENCE: BGI-129CP.

j CURRENT PLILING DATE: 1999-07-06

j RIOR APPLICATION NUMBER: 60/142,764

j PRIOR APPLICATION NUMBER: 60/142,764

j PRIOR PILLING DATE: 1999-07-09

j NUMBER OF SEQ. ID NOS: 2934

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APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
TAPLICANT: Aberhauer. Gregor
TITLE OF INVENTION: FROTBINS
TITLE OF INVENTION: PROTBINS
FILE REFERENCE: BGI-129CP
CURRENT APPLICATION NUMBER: US/09/605,703B
CURRENT PILING DATE: 1990-00-06-27
PRIOR FILING DATE: 1999-07-06
PRIOR FILING DATE: 1999-07-06
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 2934
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Length 497;
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red. No. 13;
Mismatches 3
50.0%; Score 47; DB 2;
50.0%; Pred. No. 12;
ive 3; Mismatches
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Pred. No.
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Patent No. 6862989
GENERAL INFORMATION:
APPLICANT: Pompejus, Markus
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                                                                                                                                                 1 QIASQDSKINNLTAQQQAAQ 20
                                                                                                                                                                                                          48 KIQQQDQKINALTSOMSDAE 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 AAKQARVDELVAQKQAAQ 250
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Query Match 50.0
Best Local Similarity 50.0
Matches 10; Conservative
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Best Local Similarity 44.4
Matches 8; Conservative
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Matches 8; Conservative
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US-09-605-703B-892
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ORGANISM:
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APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: DROSOPHILA HOMOLOGUES OF GENES AND PROTEINS IMPLICATED IN CANCE
TITLE OF INVENTION: DROSOPHILA HOMOLOGUES OF GENES AND PROTEINS IMPLICATED
TITLE OF INVENTION: DROSOPHILA HOMOLOGUES OF GENES AND PROTEINS IMPLICATED
TITLE OF INVENTION: DROSOPHILA HOMOLOGUES OF GENES AND PROTEINS IMPLICATION NUMBER: 60/170,832
PRIOR PAPLICATION NUMBER: 60/170,838
PRIOR PILING DATE: 1999-12-14
PRIOR PILING DATE: 2000-01-29
PRIOR PILING DATE: 2000-01-29
PRIOR PILING DATE: 2000-02-29
PRIOR PILING DATE: 2000-02-29
PRIOR PILING DATE: 2000-03-01
PRIOR PILING DATE: 2000-03-01
PRIOR PILING DATE: 2000-03-01
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Sequence 5990, Application US/09134000C

Sequence 5990, Application US/09134000C

GENERAL INFORMATION:

TITLE OF INFORMATION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: BYTERROCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT APPLICATION NUMBER: US 60/055,778

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: Patentin version 3.1

SEQ ID NO 5990
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                                  Score 48; DB 2; Length 325;
Pred. No. 4.9;
2; Mismatches 4; Indels
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/09738946
Patent No. 6579701
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                                                                                                                                                                                                                      115 ENSKTNNLAAQAQAQQ 430
                              Query Match
Best Local Similarity 62.5%;
Matches 10; Conservative
                                                                                                                                                                        5 QDSKINNLTAQQQAAQ 20
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Best Local Similarity 62.5%;
Matches 10; Conservative
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US-09-738-946-6
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Sequence 5095, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FARCIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 525;
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
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                                                                                                                                                                 DB 2;
39;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 MAY 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                   Score 44; DB 2
Pred. No. 39;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...525
SEQUENCE DESCRIPTION: SEQ ID NO: 5095:
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REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Enterococcus faecium
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MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QIASQDSKINNLTAQQQAAQ 20
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                                                                      ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12885
                                                                                                                                                                                                                                                                                                            73 ASAEQKVQQLTQQQQQTQ 90
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STATE: Massachusetts
COUNTRY: USA
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                                                                                                                                                                 Query Match
Best Local Similarity 50.0%;
Matches 9; Conservative
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12885
LENGTH: 523
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APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 32643
LENGTH: 328
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APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: 03/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 47860
LENGTH: 328
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Best Local Similarity 45.0%; Pred. No. 23;
Matches 9; Conservative 4; Mismatches 7; Indels
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                                                                                                                                                                 US-09-270-767-32643; Sequence 32643, Application US/09270767; Patent No. 6703491; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
US-09-270-767-47860
; Sequence 47860, Application US/09270767
; Patent No. 6703491
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US-09-270-767-47860
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Best Local Similarity 45.0%;
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RESULT 15
US-09-328-322-7956
IS-gquence 7956, Application US/09328352
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FATENCE OF THE NEWALTION:
TITLE OF INVENTION: BADMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-66-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7956
LENGTH: 243
FYPE: PRT
TYPE: PRT
TYPE: PRT
CORRANTSM: Acinetobacter baumannii
US-09-328-352-7956
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Matches 9; Conservative 4; Mismatches 6; Indels
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Sequence 6, Application US/10797821
; Publication No. US20050031633A1
; GENERAL INPORMATION:
; APPLICANT: Smith, Daniel J.
; APPLICANT: Taubman, Martin A.
; TITLE OF INVENTION Glucan Binding Protein and Glycosyltransferase Immunogens; FILER REFERENCE: 25669-020
; CURRENT APPLICATION NUMBER: US/10/797,821
; CURRENT PELICATION NUMBER: 10/383,930
; PRIOR APPLICATION NUMBER: 60/363,209
; PRIOR FILING DATE: 2002-03-07
; PRIOR FILING DATE: 2002-03-07
; PRIOR FILING DATE: 2002-03-07
; PRIOR FILING DATE: 2002-08-08
; PRIOR FILING DATE: 2002-08-08
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Sequence 33, Appl
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Sequence 1330, Ap
Sequence 600, App
Sequence 117, App
Sequence 23781, A
Sequence 288800,
Sequence 40322, A
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Sequence 57658, A
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Sequence 147607,
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GenCore version 5.1.6
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US-10-437-963-147607
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; Publication No. US20040127400A1
; Publication No. US20040127400A1
; GREEAL INFORMATION:
; APPLICANT: Smith, Daniel J
; APPLICANT: Taubman, Martin A
; TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
; FILE REFERENCE: 25669-018
; CURRENT PAPLICATION NUMBER: 60/402,483
; CURRENT FILING DATE: 2003-03-07
; PRIOR FILING DATE: 2002-08-08
; PRIOR PLILING DATE: 2002-03-07
; RRIOR APPLICATION NUMBER: 60/363,209
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 6
; LENGTH: 20
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100.0%; Score 94; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels
US-10-437-963-147640

US-10-767-701-5332

US-10-805-684-18

US-10-425-114-52777

US-10-425-114-52777

US-10-425-114-52777

US-10-479-925-6

US-10-479-925-6

US-10-479-925-14656

US-10-424-599-149551

US-10-424-599-249978

US-10-424-599-24978

US-10-437-963-186821

US-10-282-1224-51562

US-10-282-1224-5162

US-10-282-1224-5162

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US-10-282-1224-5162
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US-10-797-821-29
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    SEQ ID NO 30
LENGTH: 431
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; Beduence 29, Application US/10383930
; Publication No. US20040127400A1
; GENERAL INFORMATION:
; APPLICANT: Smitch, Daniel J
; APPLICANT: Taubman, Martin A
; TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
; FILE REFERENCE: 25669-018
; CURRENT APPLICATION NUMBER: US/10/383,930
; CURRENT FILING DATE: 2003-03-07
; PRIOR PLING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/402,483
; PRIOR APPLICATION NUMBER: 60/402,483
; PRIOR PRILING DATE: 2002-03-07
; WUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 29
; LINGTH: 431
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US-10-383-930-30

i Sequence 30, Application US/10383930

j Sequence 30, Application US/10383930

j Sequence 30, Application US/10383930

j Publication No. US20040127400A1

j GRYERAL INFORMATION:

j APPLICANT: Taubman, Martin A

j TILLE OF INVENTION: Immunogenicity of Glucan Binding Protein

j TILLE OF INVENTION: Immunogenicity of Glucan Binding Protein

j FILE REPERENCE: 25669-018

j CURRENT APPLICATION NUMBER: US/10/383,930

j PRIOR APPLICATION NUMBER: 60/402,483

j PRIOR APPLICATION NUMBER: 60/363,209

j PRIOR APPLICATION NUMBER: 60/363,209

j RROR FILING DATE: 2002-08-08

j RROR FILING DATE: 2002-03-07

j NUMBER OF SEQ ID NOS: 41

c ; SOPTWARE: PatentIn version 3.2
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PRIOR FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: 60/081,550
PRIOR PLING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.2
SEQ ID NO 6
LENGTH: 20
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Best Local Similarity 100.0%; P. Matches 20; Conservative 0;
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; ORGANISM: Streptococcus mutans
US-10-383-930-29
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Best Local Similarity 100.0
Matches 20; Conservative
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                                                                                                                                                                                                                   TYPE: PRI
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sequence 29, Application US/10797821
; Sequence 29, Application US/10797821
; Publication No. US20050031633A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Daniel J.
; APPLICANT: Smith, Daniel J.
; APPLICANT: Taubman, Martin A.
; TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens
; FILE REPRENCE: 25669-020
; CURRENT FILING DATE: 2004-03-09
; PRIOR PLILING DATE: 2003-03-07
; PRIOR PLILING DATE: 2002-03-07
; PRIOR PLILING DATE: 2002-03-07
; PRIOR PLILING DATE: 2002-08-08
; PRIOR PLILING DATE: 2002-08-08
; PRIOR PLILING DATE: 2002-08-08
; PRIOR PLILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/081,550
; PRIOR PLILING DATE: 1999-04-13
; PRIOR PLILING DATE: 1999-04-13
; PRIOR PLILING DATE: 1999-04-13
; PRIOR PLILING DATE: 1999-04-13
; PRIOR PLILING DATE: 1999-04-13
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; Sequence 33, Application US/10383930
; Publication No. US20040127400A1
; GENERAL INFORMATION:
    APPLICANT: Smith, Daniel J
    APPLICANT: Taubman, Martin A
    TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
    TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
    TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
    CURRENT APPLICATION NUMBER: US/10/383,930
    CURRENT FILING DATE: 2003-03-07
    PRIOR PELING DATE: 2002-08-08
    PRIOR PELING DATE: 2002-08-08
    PRIOR APPLICATION NUMBER: 60/363,209
    PRIOR APPLICATION NUMBER: 60/363,209
    NUMBER OF SEQ ID NOS: 41
    SOFTWARB: Patentin version 3.2
    SEQ ID NO 33
    IRPAGENTAL A.3.
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                                                                                                                            Length 431;
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                                                                                                                      Query Match 100.0%; Score 94; DB 4; 1
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 20; Conservative 0; Mismatches 0;
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; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-10-383-930-30
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SOFTWARE: Patentin version 3.2
SEQ ID NO 29
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Best Local Similarity 100.0
Matches 20; Conservative
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PRIOR APPLICATION NUMBER: 60/081,550
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR FILING DATE: 1999-01-08
NUMBER: OF SEQ ID NOS: 45
SOFTWARE: PATENTIN Version 3.2
SEQ ID NO 33
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; ORGANISM: Streptococcus mutans
US-10-383-930-31
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SOFTWARE: Patentin version 3.2
SEQ ID NO 32
LENCTH: 432
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LENGTH: 432
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US-10-797-821-30

Sequence 30, Application US/10797821

Publication Wo. US20050031633A1

Sequence 30, Application US/10797821

Publication Wo. US20050031633A1

APPLICANT: Smith, Daniel J.

TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens

FILE REFERENCE: 25669-020

CURRENT APPLICATION NUMBER: US/10/797,821

CURRENT FILING DATE: 2003-03-07

PRIOR PPLING DATE: 2002-03-07

PRIOR APPLICATION NUMBER: 60/402,483

PRIOR PLING DATE: 1998-04-12

PRIOR PPLING DATE: 1998-04-12

PRIOR PPLING DATE: 1998-04-13

PRIOR PPLING DATE: 1998-04-13

PRIOR PLING DATE: 1998-01-08

NUMBER OF SEQ ID NOS: 45

SOFTWARE: Patentin version 3.2

SEQ ID NO 30

LENGTH: 431
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| Publication No. US20050031633A1
| GENERAL INFORMATION |
| GENERAL INFORMATION |
| GENERAL INFORMATION |
| APPLICANT: Smitch, Daniel J. |
| TITLE OF INVENTION Clucan Binding Protein and Glycosyltransferase Immunogens |
| TITLE OF INVENTION NUMBER: US/10/797,821 |
| CURRENT PILING DATE: 25669-020 |
| CURRENT PILING DATE: 2004-03-09 |
| PRIOR PILING DATE: 2003-03-07 |
| PRIOR FILING DATE: 2003-03-07 |
| PRIOR PILING DATE: 2002-03-07 |
| PRIOR PILING DATE: 10999-04-12 |
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100.0%; Score 94; DB 5; Length 431;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 20; Conservative 0; Mismatches 0; Indels
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Pred. No. 2.1e-06;
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100.0%; Score 94; DE
Best Local Similarity 100.0%; Pred. No. 2.1
Matches 20; Conservative 0; Mismatches
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                                                 ; ORGANISM: Streptococcus mutans US-10-797-821-29
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US-10-797-821-33
  LENGTH: 431
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US-10-383-930-31
i Sequence 31, Application US/10383930
j Sequence 31, Application US/10383930
j Publication No. US20040127400A1
j GENERAL INPORMATION:
j APPLICANT: Smith, Daniel J
j TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
fILE REFERENCE: 25669-018
j TITLE OF INVENTION: UNBER: US/10/383,930
j CURRENT FILING DATE: 2003-03-07
j PRIOR APPLICATION NUMBER: 60/402,483
j PRIOR APPLICATION NUMBER: 60/402,483
j PRIOR APPLICATION NUMBER: 60/363,209
j PRIOR APPLICATION NUMBER: 60/363,209
j PRIOR SEQ ID NOS: 41
j SOFTWARE: PatentIn version 3.2
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| Sequence 32, Application US/10383930
| Sequence 32, Application US/10383930
| Publication No. US20040127400A1
| GENERAL INFORMATION:
| APPLICANT: Smith, Daniel J
| APPLICANT: Smith, Martin A
| TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
| FILE REFERENCE: 25669-018
| CURRENT FILING DATE: 2003-03-07
| PRIOR PILING DATE: 2003-03-07
| PRIOR PILING DATE: 2002-08-08
| PRIOR PILING DATE: 2002-08-08
| PRIOR PILING DATE: 2002-03-07
| PRIOR PILING DATE: 2002-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 94; DB 4; Length 432; Best Local Similarity 100.0%; Pred. No. 2.1e-06; Matches 20; Conservative 0; Mismatches 0; Indels
100.0%; Score 94; DB 5; Length 431; 100.0%; Pred. No. 2.1e-06; ive 0; Mismatches 0; Indels
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RESULT 14
US-10-797-821-7
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| Sequence 31, Application US/10797821
| Publication No. US20050031633A1
| GENERAL INFORMATION:
| APPLICANT: Smith, Daniel J. |
| APPLICANT: Taubman, Martin A. |
| TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens FILE REFERENCE: 25669-200 |
| CURRENT FILING DATE: 2004-03-09 |
| PRIOR APPLICATION NUMBER: US/10/797,821 |
| CURRENT FILING DATE: 2004-03-09 |
| PRIOR APPLICATION NUMBER: 60/402,483 |
| PRIOR FILING DATE: 2002-08-08 |
| PRIOR FILING DATE: 1999-04-12 |
| PRIOR FILING DATE: 1999-04-12 |
| PRIOR FILING DATE: 1999-04-12 |
| PRIOR FILING DATE: 1999-04-12 |
| PRIOR FILING DATE: 1999-04-13 |
| PRIOR FILING DATE: 1999-01-08 |
| NUMBER OF SEQ ID NOS: 45 |
| SEQ ID NO 31 |
| LENGTH: 432 |
| TYPE: PRI FILING CANTER FILING C
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| Sequence 32, Application No. US20050031633A1
| Publication No. US20050031633A1
| GENERAL INFORMATION:
| APPLICANT: Smith, Daniel J. |
| APPLICANT: Taubman, Martin A. |
| TITLE OF INVENTION:
| TITLE REFERENCE: 25669-020
| FILLE REFERENCE: 25669-020
| FILLE REFERENCE: 25669-020
| FILLE REFERENCE: 25669-030
| FRIOR APPLICATION NUMBER: US/10/797,821
| CURRENT FILLNG DATE: 2004-03-09
| PRIOR PILLNG DATE: 2003-03-07
| PRIOR FILLNG DATE: 2002-03-07
| PRIOR FILLNG DATE: 2002-03-07
| PRIOR PILLNG DATE: 2002-08-08
| PRIOR PILLNG DATE: 2002-08-08
| PRIOR PILLNG DATE: 1999-04-12
| PRIOR FILLNG DATE: 1998-04-13
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100.0%; Score 94; DB 4; L
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 20; Conservative 0; Mismatches 0;
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; ORGANISM: Streptococcus mutans
US-10-383-930-32
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APPLICANT: Smith, Daniel J.
APPLICANT: Smith, Daniel J.
APPLICANT: Smith, Daniel J.
TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens
FILE REFERENCE: 25669-020
CURRENT APPLICATION NUMBER: US/10/797,821
CURRENT FILING DATE: 2004-03-09
PRIOR PELICATION NUMBER: 60/403,930
PRIOR APPLICATION NUMBER: 60/403,209
PRIOR PILING DATE: 2002-03-07
PRIOR PLILNG DATE: 2002-03-07
PRIOR PLILNG DATE: 2002-04-12
PRIOR PLILNG DATE: 2002-04-12
PRIOR FILING DATE: 2002-04-12
PRIOR FILING DATE: 2004-04-12
PRIOR PLILNG DATE: 1999-04-12
PRIOR PLILNG DATE: 1998-04-13
PRIOR PLILNG DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/081,550
PRIOR APPLICATION NUMBER: 60/081,550
PRIOR APPLICATION NUMBER: 60/115,142
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Pred. No. 3.4e-05;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                               ; Score 94; DB 5; L; Pred. No. 2.1e-06; 0; Mismatches 0;
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.2
SRQ ID NO 32
LENGTH: 432
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Best Local Similarity 100.0%; P:
Matches 16; Conservative 0;
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                                                                                                                                                                                                   100.0%;
                                                                                                                          ; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-10-797-821-32
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SOFTWARE: Patentin version 3.2
SEQ ID NO 7
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Best Local Similarity 100.
Matches 20; Conservative
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; Sequence 67, Application US/10154251
; Publication No. US20030092024A1
; GENERAL INFORMATION:
    APPLICANT: Youngman, Philip
    APPLICANT: Winphy, Christian
    APPLICANT: Murphy, Christian
    APPLICANT: Murphy, Christian
    APPLICANT: Murphy, Christopher
    APPLICANT: Murphy, Christopher
    APPLICANT: Murphy, Christopher
    APPLICANT: GLAMMAN: LUZ-Maria
    TITLE OF INVENTION: ESSENTIAL BACTERIAL GENES AND THEIR USE
    FILE REFERENCE: 06286-060002
    CURRENT FILING DATE: 2002-09-16
    PRIOR FILING DATE: 2002-09-16
    PRIOR FILING DATE: 2002-05-22
    NUMBER OF SEQ ID NOS: 102
    SOFTWARE: PASELEDG for Windows Version 3.0
    SEQ ID NO 67
    LENGTH: 210
    TYPE: PRT
    ORGANISM: Streptococcus pneumoniae
    US-10-154-251-67
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PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.2
SEQ ID NO 7
LENGTH: 20
TYPE: PRT
PRE: PRT
PRE: PRT
PRE: PRT
PRE: PRT
CRGANISM: Artificial
FRATURE:
COTHER INFORMATION: GDDB peptide
US-10-797-821-7
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Search completed: January 25, 2006, 20:10:03
Job time : 60 secs

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Sequence 10, Appl
Sequence 1432, Ap
Sequence 1382, Ap
Sequence 59, Appl
Sequence 12, Appl
Sequence 174, Appl
Sequence 174, Appl
Sequence 16, Appl
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Sequence 169; App
Sequence 11, Appl
Sequence 8726, Ap
Sequence 10, Appl
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Sequence 212, App
Sequence 4, Appli
Sequence 48, Appli
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Sequence 252, App
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                                                                January 25, 2006, 19:15:26; Search time 5.5 Seconds (without alignments) 39.378 Million cell updates/sec
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Sequence 130
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1: /cgn2_6/ptodata/2/pubpaa/USO8 NEW FUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO6 NEW FUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO7 NEW FUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW FUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO7 NEW FUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO7 NEW FUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USIO_NEW FUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USIO_NEW FUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USIO_NEW FUB.pep:*
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Compugen Ltd.
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US-10-467-657-4336
US-10-678-556A-169
US-10-673-075-11
US-10-673-707-11
US-10-613-744-10
US-10-913-656-1432
US-11-019-711-59
US-11-019-711-59
US-11-019-711-59
US-11-019-711-59
US-11-019-711-6136
US-11-074-176-136
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GenCore version
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Listing first 45 summaries
                                            protein search, using sw model
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US-11-069-834-48

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Sequence 210, Application US/11052554A

Sequence 210, Application US/11052554A

Publication No. US20050288866A1

GENERAL INFORMATION:

TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE

TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL

TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL

FILE REFERENCE: 30653/40359A

CURRENT FILING DATE: 2004-07-20

PRIOR FILING DATE: 2004-07-20

PRIOR FILING DATE: 2004-07-20

PRIOR FILING DATE: 2004-02-06

NUMBER OF SEQ ID NOS: 763

SEQ ID NOS: 763

LENGTH: 431
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Publication No. US20050288866A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sachdeva.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-20
FRIOR APPLICATION NUMBER: IN 173/DEL/2004
NUMBER OF SEQ ID NOS: 763
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                                                                                                                          Sequence 1002, Ap Sequence 20, Appl Sequence 2, Appl Sequence 1114, Ap Sequence 1003, Ap Sequence 1001, Ap Sequence 998, App Sequence 998, App Sequence 997, App Sequence 18, App Sequence 18, App Sequence 18, App
                                         64, Appl
66, Appl
216, App
66, Appl
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US-11-069-834-50
US-110-734-55
US-110-734-64-82
US-110-508-263-66
US-11-052-554A-216
US-11-052-554A-216
US-11-052-554A-216
US-11-052-554A-216
US-11-097-657-3988
US-11-095-561-1002
US-11-097-49-2
US-110-995-561-1003
US-110-995-561-1004
US-10-995-561-1004
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Matches 20; Conservative
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US-11-052-554A-252
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APPLICANT: RESSELET, Maria
APPLICANT: Zelinski, Thomas
APPLICANT: Alinski, Thomas
APPLICANT: Hauer, Bernardian Serial
TITLE OF INVENTION: L-RHAMNOSE-INDUCIBLE EXPRESSION SYSTEMS
TITLE OF INVENTION: L-RHAMNOSE-INDUCIBLE EXPRESSION SYSTEMS
FILE REPERENCE: 12810-00091-US
CURRENT APPLICATION NUMBER: 2005-06-01
PRIOR APPLICATION NUMBER: PCT/EP2003/013367
PRIOR FILING DATE: 2005-06-01
PRIOR APPLICATION NUMBER: DE 102 56 381.0
PRIOR FILING DATE: 2002-11-27
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: FORTANA Maria Rita

APPLICANT: FORTANA Maria Rita

APPLICANT: FORTANA Maria Rita

APPLICANT: MASIGANAI Vega

APPLICANT: MASIGANAI Vega

TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

FILE REFERENCE:

CURRENT APPLICATION NUMBER: 08/10/467,657

CURRENT FILING DATE: 2003-08-11

PRIOR APPLICATION NUMBER: GB-0103424.8

NUMBER OF SEQ ID NOS: 9218

SOFTWARE: SEGWIN99, version 1.04

SEQ ID NO 9726

TUNDON 09726
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Pred. No. 48;
2; Mismatches 6; Indels
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Publication No. US20050260581A1
                                                                                                                                                                    US-10-537-075-11

; Sequence 11, Application US/10537075
; Publication No. US20060014291A1
; GENERAL INFORMATION:
                                                         510 OIGDEDOKIONLEALLOKSK 529
                        1 QIASQDSKINNLTAQQQAAQ 20
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US-10-467-657-8726
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100 VAYRDSRTNGLMAQAQ 115
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Best Local Similarity 50.0%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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42.6%; Score 40; DB 6; Length 1404;
Best Local Similarity 45.0%; Pred. No. 82;
Matches 9; Conservative 3; Mismatches 8; Indels
                                                                                                                                                                    Query Match 66.0%; Score 62; DB 7; Length 398; Best Local Similarity 65.0%; Pred. No. 0.0049; Matches 13; Conservative 4; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4336, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SpA
APPLICANT: FOXTANA Maria Rita
APPLICANT: PASSIGNANI Vega
APPLICANT: MASSIGNANI Vega
APPLICANT: MASSIGNANI Vega
APPLICANT: MASSIGNANI Vega
APPLICANT: MASSIGNANI Vega
APPLICANT: MONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
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APPLICANT: Hoffmann La-Roche Inc.; TITLE OF INVENTION: HCV regulated protein expression; TILLE REFERENCE: 21762
CURRENT APPLICATION NUMBER: US/10/878,556A; CURRENT FILING DATE: 2004-06-28
NUMBER OF SEQ ID NOS: 199; SOFTWARE: PatentIn version 3.1
SEQ ID NO 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: humangp/chr12-q14221
DATABASE ENTRY DATE: 2003-04-22
US-10-878-556A-169
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                                                                                              ; ORGANISM: Streptococcus pyogenes MGAS8232
US-11-052-554A-252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 4336
LENGTH: 205
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; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4336
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 252
LENGTH: 398
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Best Local Similarity
Matches 9; Conserv
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APPLICANT:
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APPLICANT:
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           Sequence 10, Application US/10613744

Publication No. US20050272093A1

GENERAL INFORMATION.

APPLICANT: MacKinnon, Rederick

APPLICANT: The Rockefeller University

TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation

TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation

TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation

TITLE OF INVENTION: Cation Channel Proteins, and Uses Thereof

FILE REFERENCE: 018512-002901US

CURRENT APPLICATION NUMBER: US/09/275,252

FRIOR APPLICATION NUMBER: US 09/045,529

FRIOR PILING DATE: 1998-03-24

FRIOR APPLICATION NUMBER: US 09/045,529

FRIOR APPLICATION NUMBER: WO PCT/US99/06307

FRIOR PILING DATE: 1999-03-22

FRIOR PILING DATE: 1999-03-22

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 10

LENGTH: 731
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Sequence 1432, Application US/10793626

Sequence 1432, Application US/10793626

Publication No. US20050255478A1

GENERAL INFORMATION:
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626

CURRENT PILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472

SOFTWARE: Patentin Ver. 2.1
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US-10-793-626-1432
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Pred. No. 82;
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; Publication No. US20050255114A1
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Best Local Similarity 57.1%;
Matches 8; Conservative
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ORGANISM: Artificial Sequence
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655 QIGSLESKLEHLTA 668
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ORGANISM: Homo sapiens
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US-10-821-234-1382
US-10-613-744-10
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LENGTH: 1145
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APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Susan
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR APPLICATION NUMBER: US 60/462,047
NUMBER OF SEQ ID NOS: 1704
SEQ ID NO 1382
LENGTH: 261
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APPLICANT: Anderson, David W
APPLICANT: Padigaru, Muralidhara
APPLICANT: Taupier Jr, Raymond J
APPLICANT: Tinpier Jr, Raymond J
APPLICANT: Eisen, Andrew J
APPLICANT: Eisen, Andrew J
APPLICANT: Eisen, Andrew J
APPLICANT: Rich Andrew J
APPLICANT: Rich Andrew J
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CURRENT FILING DATE: 2004-12-21
PRIOR APPLICATION NUMBER: US/10/037,417
PRIOR PILING DATE: 2002-09-20
PRIOR FILING DATE: 2001-01-05
PRIOR PILING DATE: 2001-01-05
PRIOR PILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 60/260,360
PRIOR PILING DATE: 2001-01-08
PRIOR PILING DATE: 2001-01-08
PRIOR PLING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/272,411
PRIOR PILING DATE: 2001-03-08
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Publication No. US20060009634A1
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
APPLICANT: Alsobrook II, John P
APPLICANT: Tchernev, Velizar T
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Burgess, Catherine E
Vernet, Corine A.M.
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Sciore, Paul
Bllerman, Karen
Malyankar, Uriel M
Rothenberg, Mark
Stone, David J
Boldog, Ferenc L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 İLSQDSFYRVLTSEQKA 74
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Spytek, Kimberly A
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Grosse, William M
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                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Friesen, Robert H. E.

APPLICANT: Friesen, Robert H. E.

APPLICANT: Hektor, Harm

APPLICANT: Van Esch, Johannes H.

APPLICANT: Van Esch, Johannes H.

APPLICANT: ABELICANT: OF INVENTION: DELIVERY OF A SUBSTANCE TO A PRE-DETERMINED SITE

FILE REPREBENCE: 2183-6668US

CURRENT PAPLICATION NUMBER: PCT/NL/00256

FRIOR APPLICATION NUMBER: PCT/NL/00256

NUMBER OF SEQ ID NOS: 309

SOFTWARE: PATEURIN Version 3.2
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                                                                                                                                                                      39.4%; Score 37; DB 6; Length 1050; 40.0%; Pred. No. 1.8e+02;
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Pred. No. 7.1;
4; Mismatches
                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                   481 QIASESQKIPGMTLSSSVCQ 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 38.3%;
Best Local Similarity 41.2%;
Matches 7; Conservative 4
                NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
SEQ ID NO 47
LENGTH: 1050
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                                                                                                                                                        Query Match
Best Local Similarity 40.v.
Best Local 8; Conservative
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                                                                                                               ORGANISM: Homo sapiens
US-10-770-726-47
CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                         US-10-957-887B-174
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                                                                                               TYPE: PRT
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Publication No. US200506409A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei Lown, Eugene
TITLE OF INVENTION: CANCERS

FILE REFERENCE: AM10.079 (031896-010000)

CURRENT APPLICATION NUMBER: US/10/770,726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-523-477-12

Sequence 12, Application US/10523477

Sequence 12, Application No. US20050266406A1

Sequence 12, Application No. US20050266406A1

GENERAL INFORMATION: MASS AS MODIFIERS OF THE AXIM PATHWAY AND METHODS OF USE

TILE OF INTENTION: MASS AS MODIFIERS OF THE AXIM PATHWAY AND METHODS OF USE

FILE REFRENCE: EX03-051C-US

CURRENT APPLICATION NUMBER: US/10/523,477

CURRENT APPLICATION NUMBER: US 60/401,534

PRIOR FILING DATE: 2002-08-07

PRIOR FILING DATE: 2002-09-16

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin version 3.2

LENGTH: 1050

TYPE: PRI
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US-11-019-711-59
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39.4%; Score 37; DB 6; Length 1050;
Best Local Similarity 40.0%; Pred. No. 1.8e+02;
Matches 8; Conservative 2; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB 7; Length 860;
Pred. No. 1.4e+02;
5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 39.4%; Score 37; DB Best Local Similarity 33.3%; Pred. No. 1.4¢ Matches 6; Conservative 5; Mismatches
                PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/303,231
PRIOR APPLICATION NUMBER: 60/305,231
PRIOR PILING DATE: 2001-07-05
PRIOR PILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 60/318,405
PRIOR APPLICATION NUMBER: 60/318,700
PRIOR APPLICATION NUMBER: 60/318,700
PRIOR PILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 227
SEQ ID NO 59
LENGTH: 860
    APPLICATION NUMBER: 60/291,186
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; ORGANISM: Homo sapiens
US-10-523-477-12
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US-11-074-176-136

Sequence 136, Application US/11074176

Publication No. US20060250135A1

GENERAL INFORMATION:
APPLICANT: Klasenlammer, Todd R.
APPLICANT: Russell, William M.
APPLICANT: Russell, William M.
APPLICANT: Altermann, Eric
APPLICANT: Peril, Adrea Azcarate
TITLE OF INVENTION: Nucleic Acid Sequences Encoding
TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
FILE REPERRORE: 5051-694
CURRENT PILING DATE: 2005-03-07

PRIOR APPLICATION NUMBER: US/11/074,176

CURRENT FILING DATE: 2004-03-08

NUMBER OF SEQ ID NOS: 381

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 136

LIVER CONTROLES 
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                                                                                                      Query Match 38.3%; Score 36; DB 7; Length 89; Best Local Similarity 43.8%; Pred. No. 16; Matches 7; Conservative 3; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                              4 SQDSKINNLTAQQQAA 19
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38 SEEKVRNEPTQQQRA 53
US-11-145-631-16
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Search completed: January 25, 2006, 20:11:08 Job time : 5.5 secs

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Result		Query				
No.	Score	Match	Length DB	8	ΩI	Description
7	96	100.0	20	7	ADD93627	Add93627 Streptoco
7	96	100.0	20	0	ADX37250	Adx37250 Streptoco
е	96	100.0	431	7	ADD93649	Add93649 Streptoco
4	96	100.0	431	7	ADD93650	Add93650 Streptoco
ហ	96	100.0	431	7	ADD93653	Add93653 Streptoco
9	96	100.0	431	σ	ADX37272	Adx37272 Streptoco
7	96	100.0	431	6	ADX37273	Adx37273 Streptoco
œ	96	100.0	431	6	ADX37276	Adx37276 Streptoco
σ	96	100.0	431	σ	AEB91500	Aeb91500 Microbial
10	96	100.0	432	7	ADD93651	Add93651 Streptoco
11	96	100.0	432	7	ADD93652	Add93652 Streptoco
12	96	100.0	432	0	ADX37274	Adx37274 Streptoco
13	96	100.0	432	σ	ADX37275	Adx37275 Streptoco
14	77	80.2	20	7	ADD93626	Add93626 Streptoco
15	77	80.2	20	σ	ADX37249	Adx37249 Streptoco
16	73	76.0	210	N	AAY22579	Aay22579 Bacterial
17	73	76.0	392	9	ABU02747	Abu02747 S. pheumo
18	73	76.0	392	æ	ADK47859	Adk47859 Streptoco
19	73	76.0	392	œ	ADT50227	Adt50227 S pneumon
20	73	76.0	392	œ	ADT50226	S
21	73	76.0	392	80	ADT50165	Adt50165 S pneumon
22	73	76.0	399	œ	ADR94595	Adr94595 Novel S.
23	73	76.0	399	σ	AEA58465	Aea58465 Streptoco
24	61	63.5	398	Ŋ	ABP25919	Abp25919 Streptoco

	_		Abr40385 Fruitfly	Ads96412 Drosophil	Adc06779 Fruit fly	Abp29684 Streptoco	Adu69524 S agalact	Adv88392 Streptoco	Adv81808 Streptoco	Adv79645 Streptoco	Adv16553 E. faecal	Adh88105 Enterococ	Abg75182 M licheni	Abu43868 Protein e	Aab29586 Rat potas	Aau00216 Rat potas	Abb65663 Drosophil	Abg99869 S. cinnam	Abu29734 Protein e	Adc95468 E. faeciu	
ADR83884	AEB91542	ABB57775	ABR40385	ADS96412	ADC06779	ABP29684	ADU69524	ADV88392	ADV81808	ADV79645	ADV16553	ADH88105	ABG75182	ABU43868	AAB29586	AAU00216	ABB65663	ABG99869	ABU29734	ADC95468	
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25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein. Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen. Streptococcus mutans glucan binding protein-B peptide fragment ADD93627 standard; peptide; 20 AA. 07-MAR-2002; 2002US-0363209P. 07-MAR-2003; 2003WO-US006962. (first entry) Taubman MA; Streptococcus mutans. (FORS-) FORSYTH INST. WPI; 2003-845091/78. WO2003075845-A2 18-SEP-2003. Smith DJ,

Claim 11; Page 10; 49pp; English.

The present sequence is that of a peptide comprising amino acid residues 37-56 of the glucan binding protein-B (GbpB) of Streptococcus mutans strain SK13 ADD9549. The peptide binds to a major histocompatibility complex (MHC) class II protein. It was identified as a potential B cell epitope using a matrix-based algorithm for epitope prediction, which was used to search the primary amino acid sequence of GbpB for known MHC class II binding motifs. The peptide can be used in immunogenic compositions and subunit vaccines for dental caries. These comprise MHC class II protein-binding GbpB peptides covalently linked with peptide subunits (preferably from the catalytic domain) of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Diepitopic or multiepitopic polypeptides can be

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Streptococcus mutans glucan binding protein-B.
                                                         ADD93649 standard; protein; 431 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MfC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in passive immunisation.
                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                  immunogenicity; immune stimulation; glucan binding protein-B;
microparticle; major histocompatibility complex; tooth disease.
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                                                                                 Query Match 100.0%; Score 96; DB 7; Length 20; Best Local Similarity 100.0%; Pred. No. 7.8e-08; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                        Streptococcus mutant glucan binding protein B peptide #7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; SEQ ID NO 7; 73pp; English.
                                                                                                                                                                                                                             ADX37250 standard; peptide; 20 AA
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08-JAN-1999; 99US-0115142P.
12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-0363209P.
08-AUG-2002; 2002US-0402483P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-MAR-2003; 2003US-00383930
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                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                           Streptococcus mutans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SMIT/) SMITH D J.
(TAUB/) TAUBMAN M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2005-151644/16.
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Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
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== "HLA-binding peptide"
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'note= "HLA-binding peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide"
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/note= "HLA-binding peptide"
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'note= "HLA-binding peptide"
                                                                                                                                                                             "HLA-binding peptide"
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                                                         Location/Qualifiers
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289. .308
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                                                                                          The present sequence is the protein sequence of the glucan binding protein—B (GDpB) of Streptococcus mutans strain SK32. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions comprise major histocompatibility complex (WHC) class II protein-binding Gbp speptides, especially HLA-binding peptides, cowpositions are used in a claimed method of eliciting production of an antibody in a mammal. Dispitopic or multipelicipic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in
                             Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Composition useful as vaccines for dental caries comprises a fragmeht of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is the protein sequence of the glucan binding protein-B (GDpB) of Streptococcus mutans strain 3VF4. The sequence includes a number of human leucocyte antigen (HIA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dentain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
                                                                                                                                                                                                                                                                                     Gaps
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2.4e-06;
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                                                                                                                                                                                                                                                              100.0%; Score 96; DE
100.0%; Pred. No. 2.4
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    ADD93650 standard; protein; 431 AA.
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                                                                                                                                                                                                                                                                                                                     Claim 5; Page 8; 49pp; English.
                                                                        Claim 6; Page 7; 49pp; English.
                                                                                                                                                                                                                                                                                                           1 ODSKINNLTAQOQAAQAQVN
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08-AUG-2002; 2002US-0402483P.
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Taubman MA;
                                                                                                                                                                                                                    passive immunisation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus mutans
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          GENBANK; AY046410
                                                                                                                                                                                                                                          Sequence 431 AA;
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caries. The compositions comprise major histocompatibility complex (MHC) class II protein-binding GBpB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Dispitopic or multipeptopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 96; DB 7; Length 431; 100.0%; Pred. No. 2.4e-06;
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Pred. No. 2.4e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADD93653 standard; protein; 431 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ODSKINNLTAQOQAAQAQVN 56
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                                                                                                                                                                                                                                                                                                                                                                                                                  20; Conservative
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                                                                                                                                                                                                                           passive immunisation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             passive immunisation.
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                                                                                                                                                                                                                                                                                          Sequence 431 AA;
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21-APR-2005

ADX37272;

10-FEB-2005

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The invention relates to a composition comprising a fragment of a glucan binding protein-B (GbpB) and a biocompatible microparticle, where the fragment binds to a major histocompatibility complex (MHC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds to a Streptococcus mutans GbpB protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible nicroparticle, useful for producing an antibody (claimed) for immunizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunogenicity; immune stimulation; glucan binding protein-B;
microparticle; major histocompatibility complex; tooth disease.
                                                              immunogenicity; immune stimulation; glucan binding protein-B; microparticle; major histocompatibility complex; tooth disease.
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                                Streptococcus mutant glucan binding protein B variant #2.
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100.0%; Pred. No. 2.4e-06;
ive 0; Mismatches 0;
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08-JAN-1999; 99US-011542P.
12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-0363209P.
08-MUG-2002; 2002US-0402483P.
07-MAR-2003; 2003US-00383930.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               microparticle, useful for prod
mammals against dental caries.
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21-APR-2005 (first entry)
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                                                                                                                          Streptococcus mutans
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TAUBMAN M A.
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Pred. No. 2.4e-06;
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 0; Mismatches
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                                   1 ODSKINNLTACOCAACACN 20
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08-JAN 1999; 99US-0115142P.
12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-03632209P.
08-AUG-2002; 2002US-0402483P.
07-MAR-2003; 2003US-00383930.
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Best Local Similarity 100.
Matches 20; Conservative
   Conservative
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                                                                                                                                                                                                                                                                                                                                                                    Streptococcus mutans.
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(TAUB/) TAUBMAN M A.
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Smith DJ,

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Gaps

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ADX37273

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RESULT 7 ADX37273

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The present invention relates to a computational method (M1) for identifying adhesin and adhesin-like proteins, by computing the sequence-based attributes of protein sequences using five attribute modules of a neural network software, training an artificial neural network (MNN) for each of the computed five attributes, and identifying the adhesin and adhesin-like proteins having probability of being an adhesin and adhesin-like proteins, having 274 annotated genes encoding adhesin and adhesin-like proteins, having 274 fully defined 162-1151 base pair (SEQ ID NO: 385-659) sequences; a set of 105 hypothetical adhesin and adhesin-like proteins, having 279 fully defined 162-1151 base pair (SEQ ID NO: 1279); a set of 105 hypothetical adhesin and adhesin-like proteins, having 279 fully defined 53-3716 base pair (SEQ ID NO: 1-279); a set of 105 hypothetical adhesin and adhesin-like proteins, having 279 fully defined 165-529 base pairs (SEQ ID NO: 12-39); a set of 105 hypothetical adhesin and adhesin-like proteins, having 105 fully defined 106-5291 base pair (SEQ ID NO: 280-384) sequences; and a fully connected multilayer feed forward ANN (I) based on (M1). (M1) is useful for identifying adhesin and adhesin-like proteins of therapeutic potential, and identifying and short-listing proteins for further testing in development of new vaccine formulations to eliminate diseases caused by various pathogenic organisms. (M1) is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful for identifying putative adhesins that are important in drug discovery and preventing therapeutics for whooping cough, pneumonia, gastric ulcer and urinary tract infections. (M1) identifies adhesins from distantly related organisms, and from bacteria belonging to a wide phylogenetic spectrum. (M1) is capable of predicting adhesive nature of unique proteins. The present sequence is a microbial pathogen adhesin
Computational method for identifying adhesin and adhesin like molecules, comprises computing sequence-based attributes of protein sequences using neural network software and training an artificial neural network.
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Pred. No. 2.4e-06;
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                                                                                           Claim 16; SEQ ID NO 210; 402pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADD93651 standard; protein; 432 AA
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100.0%;
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nes 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                        New composition comprising a fragment of a glucan binding protein-B (GpB) that binds to MfC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
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Pred. No. 2.4e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; SEQ ID NO 33; 73pp; English.
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                                         13-APR-1998; 98US-0081550P.
08-JAN-1999; 99US-0115142P.
12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-0363209P.
08-AUG-2002; 2002US-0402483P.
07-MAR-2003; 2003US-00383930.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 100.0%;
1 Similarity 100.0%;
20; Conservative 0;
  09-MAR-2004; 2004US-00797821
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                                                                                                                                                                                                                                                                            Smith DJ, Taubman MA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus mutans
                                                                                                                                                                                                                                 (TAUB/) TAUBMAN M A.
                                                                                                                                                                                                                                                                                                                            WPI; 2005-151644/16.
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Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                        SMITH D J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-AUG-2005
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Gaps

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The present sequence is the protein sequence of the glucan binding protein—B (GDpB) of Streptococcus mutans strain 15JP2. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental class II protein-binding GbpB peptides, especially HLA-binding peptides, cowplently linked with peptides supecially HLA-binding peptides, cowpositions are used in a claimed method of eliciting production of an antibody in a mammal. Dispitopic or multiepitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in
composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
                                                                                                                                                                                                                                              5; Page 8; 49pp; English
                                                                                                                                                                                                                                         Claim
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Score 96; DB 7; 1 Pred. No. 2.4e-06; Mismatches 1 ODSKINNLTAQQQAAQAQVN 20 ö 100.0%; 100.0%; Query Match 100. Best Local Similarity 100. Matches 20; Conservative Sequence 432 AA;

passive immunisation.

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Gaps

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Length 432; 0; Indels

> 37 ODSKINNLTAQOQAAQAQVN 56 ઠે g

ADD93652 standard; protein; 432 29-JAN-2004 ADD93652; RESULT 11

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Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen. Streptococcus mutans glucan binding protein-B. (first entry) Streptococcus mutans WO2003075845-A2.

07-MAR-2002; 2002US-0363209P. 08-AUG-2002; 2002US-0402483P

07-MAR-2003; 2003WO-US006962

18-SEP-2003

(FORS-) FORSYTH INST.

Smith DJ, Taubman MA; 2003-845091/78.

dental caries comprises a fragment of to a major histocompatibility complex Composition useful as vaccines for a glucan binding protein-B binding GENBANK; AY046413. class II protein

5; Page 8; 49pp; English. Claim

The present sequence is the protein sequence of the glucan binding protein-B (GbpB) of Streptococcus mutans strain 3SN1. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions comprise major histocompatibility complex (MHC) class II protein-binding GbpB peptides, especially HLA-binding peptides,

ö ö The invention relates to a composition comprising a fragment of a glucan binding protein-B (GbpB) and a biocompatible microparticle, where the fragment binds to a major histocompatibility complex (MHC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds to a Streptococcus mutans GbpB protein of the invention. composition comprising a fragment of a glucan binding protein-B pB) that binds to MHC class II protein, and a biocompatible reparticle, useful for producing an antibody (claimed) for immunizing covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of a antibbody in a mammal. Diepitopic or multiepitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in Gaps Gaps ö immunogenicity; immune stimulation; glucan binding protein-B; microparticle; major histocompatibility complex; tooth disease. ö Length 432; Length 432; Indels Indels Streptococcus mutant glucan binding protein B variant #3 Query Match 100.0%; Score 96; DB 9; L Best Local Similarity 100.0%; Pred. No. 2.4e-06; Matches 20; Conservative 0; Mismatches 0; 100.0%; Score 96; DB 7; I 100.0%; Pred. No. 2.4e-06; Mismatches Claim 3; SEQ ID NO 31; 73pp; English. ADX37274 standard; protein; 432 AA 1 QDSKINNLTAQQQAAQAQVN 20 56 ; 0 13-APR-1998; 98US-0081550P.
08-JAN-1999; 99US-0115142P.
12-ARR-1999; 99US-00290049.
07-MAR-2002; 2002US-0363209P.
08-AUG-2002; 2002US-0402463P.
07-MAR-2003; 2003US-00383939. mammals against dental caries. 37 ODSKINNLTAGOGAAGAGVN 09-MAR-2004; 2004US-00797821 (first entry) Conservative Smith DJ, Taubman MA; microparticle, useful Streptococcus mutans. passive immunisation (SMIT/) SMITH D J. (TAUB/) TAUBMAN M A. WPI; 2005-151644/16. Local Similarity les 20; Conserv Sequence 432 AA; US2005031633-A1. Sequence 432 AA; 21-APR-2005 10-FEB-2005. ADX37274; Query Match (GpbB) Best Loc Matches RESULT 12 ADX37274 ន្តដូន្តន្តន្តន្ត 8 셤

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The present sequence is that of a peptide comprising amino acid residues 33-52 of the glucan binding protein-B (GbpB) of Streptococcus mutans strain SK32 ADD93649. The peptide binds to a major histocompatibility complex (WHC) class II protein. It was identified as a potential B cell epitope using a matrix-based algorithm for epitope prediction, which was used to search the primary amino acid sequence of GapB for known MHC class II binding motifs. The peptide can be used in immunogenic compositions and subunit vaccines for dental caries. These comprise MHC class II protein-binding GapB peptides covalently linked with peptide subunits (preferably from the catalytic domain) of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Diepitopic or multiepitopic polypeptides can be raised against MHC class II binding fragments of GbpB can be used in raised against MHC class II binding fragments of GbpB can be used in
                                                                                                                                                                                                                                                                                                                                                                                                  Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
                                       Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
 Streptococcus mutans glucan binding protein-B peptide fragment
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microparticle; major histocompatibility complex; tooth disease.
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Pred. No. 6.9e-05;
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'... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 10; 49pp; English.
                                                                                                                                                                                         07-MAR-2003; 2003WO-US006962
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                                                                           Streptococcus mutans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New composition comprising a fragment of a glucan binding protein-B (dpB) that binds to MfC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                immunogenicity; immune stimulation; glucan binding protein-B;
microparticle; major histocompatibility complex; tooth disease.
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                                                                                                                                                                                                                                              Streptococcus mutant glucan binding protein B variant #4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; SEQ ID NO 32; 73pp; English.
                                                                                                                           ADX37275 standard; protein; 432 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADD93626 standard; peptide; 20 AA.
QDSKINNLTAQQQAAQAQVN 20
                                     26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QDSKINNLTAQQQAAQAVN 20
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                         37 QDSKINNLTAQQQAAQAQVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37 QDSKINNLTAQQQAAQAQVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-APR-1999; 98US-0081550P.
08-JAN-1999; 9US-0115142P.
12-APR-1999; 9US-0020049.
07-MAR-2002; 2002US-04052839P.
08-AUG-2002; 2002US-0405483P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-MAR-2004; 2004US-00797821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-MAR-2003; 2003US-00383930
                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Taubman MA;
                                                                                                                                                                                                                                                                                                                                            Streptococcus mutans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SMIT/) SMITH D J.
(TAUB/) TAUBMAN M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2005-151644/16.
                                                                                                                                                                                                                                                                                                                                                                              US2005031633-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JAN-2004
                                                                                                                                                                                                         21-APR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                     10-FEB-2005
 Н
                                                                                                                                                                   ADX37275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smith DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADD93626;
                                                                                           RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
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The invention relates to a composition comprising a fragment of a glucan binding protein-B (GbpB) and a biocompatible microparticle, where the fragment binds to a major histocompatibility complex (MHC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds to a Streptococcus mutans GbpB-derived peptide of the invention.
                                                                                                                                                                                                                                                                                               New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 80.2%; Score 77; DB 9; Length 20; Best Local Similarity 100.0%; Pred. No. 6.9e-05; Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; SEQ ID NO 6; 73pp; English.
                               13-APR-1998; 98US-0081550P.
08-JAN-1999; 99US-0115142P.
12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-0363209P.
08-AUG-2002; 2002US-0402483P.
07-MAR-2003; 2003US-00383930.
09-MAR-2004; 2004US-00797821.
                                                                                                                                                                                                                           Taubman MA;
                                                                                                                                                                     (SMIT/) SMITH D J.
(TAUB/) TAUBMAN M A.
                                                                                                                                                                                                                                                                WPI; 2005-151644/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20 AA;
                                                                                                                                                                                                                           Smith DJ,
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Gapa ..

Search completed: January 25, 2006, 19:01:44 Job time : 69.2 secs

1 ODSKINNLTAQQQAAQ 16

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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OM protein - protein search, using sw model

January 25, 2006, 18:48:55; Search time 9.1 Seconds (without alignments) 211.465 Million cell updates/sec Run on:

US-10-797-821-7 96 Title: Perfect score:

1 ODSKINNLTAQQQAAQAQVN 20 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printéd, and is derived by analysis of the total score distribution.

IIES	Description	Becreted 45 kd pro	8	tical br	succinate-CoA, liga	El protein - Muman	probable membane	hypothetical prote	hyaluronan recepto	competence ComEA p	probable membrane	light-induced.prot	hypothetical prote	hypothetical prote	probable lipoprote		probable RNA helic	probable helitase	pupal cuticule pro	exopolysaccharide	G protein-coupled	VPS27 protein - ye	protein V (fcrV)	RAE-28 - mouse	polyketide synthas	probable ppsB prot	polyketide synthas	ribosomal protein	ORF2 protein - ric	
SUMMARIES	13	G95258	B98124	S05542	C64189	836575	H81850	F81090	JC4298	D97056	AB0827	S16322	T50010	B86899	AD0976	JC1419	G91286	C86128	S41958	AB3616	S58868	845129	C64236	153172	873013	E70874	H87203	F69696	B40785	
	DB	10	N	~	~	N	~	N	N	7	N	N	N	~	~	N	~	~	~	N	~	N	N	N	~	~	~	N	~	
	Query Match Length	392	392	507	389	647	184	184	631	209	254	414	414	552	227	587	2113	2113	353	392	484	622	756	1012	1446	1538	1540	119	110	
de	Query Match	76.0	76.0	50.0	47.9	47.9	46.9	46.9	46.9	45.8	45.8	45.8	45.8	45.8	44.8	44.8	44.8	44.8	43.8	43.8	43.8	43.8	43.8	43.8	43.8	43.8	43.8	43.2	42.7	
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ACTA/ACTE family p	heat shock transcr	hypothetical prote	sucrose porin scrY	cloacin DF13 prote	WD-40 repeat regul	small GTP binding	conserved hypothet	multimerin, endoth	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	polyadenylate-bind	NADH dehydrogenase	NADH dehydrogenase	
E82436	S59539	T33065	S15194	CDECP3	JN0133	G01252	B83018	A57384	A11987	D75477	B85466	D86321	S41644	AB2734	D97515	
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334	370	495	505	561	713	810	1118	1228	67	238	404	404	465	503	503	
42.7	42.7	42.7	42.7	42.7	42.7	42.7	42.7	42.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7	
41	41	41	41	41	41	41	41	41	40	40	40	40	40	40	40	
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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Graces 45 kd protein [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Species: O3-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: G55258
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heiton, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: G95258
A;Accession: G95258
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-392 <KUR>
A;Coss-references: UNIPROT:Q97N55; UNIPROT:Q8DWY4; UNIPARC:UPI0000051B81; GB:AE005672;
A;Genetics:
A;Genetics:
A;Genetics:
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Gaps ö Length 392; 2; Indels Score 73; DB 2; Pred. No. 0.00058; 76.0%; Sco... 75.0%; Pred. No. v... Query Match
Best Local Similarity 75.0
Matches 15; Conservative

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A;Molecule type: DNA A;Residues: 1-392 <KUX> A;Cross-references: UNIPROT:Q97N55; UNIPROT:Q8DMY4; UNIPARC:UPI0000051B81; GB:AE007317; C;Genetics: A;Gene: gsp-781

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A;Cross-references: UNIPROT:P36730; UNIPARC:UPI0000138310; EMBL:X74481; NID:g397038; PII C;Superfamily: papillomavirus El protein
C;Keywords: early protein; nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable membrane lipoprotein NWA1581 [imported] - Neisseria meningitidis (strain 22491 C; Species: Neisseria meningitidis C; Species: Neisseria meningitidis C; Species: OS-May-2000 #text_change 09-Jul-2004 C; Accession: H81850 #squence_revision 05-May-2000 #text_change 09-Jul-2004 B; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel R; Parkhill, J.; Achtman, M.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000 A; May sequence of a serogroup A strain of Neisseria menigitidis Z2491. A; Reference number: A81775; MUID:20222556; PMID:10761919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q9UTY2; UNIPARC:UPI00000C4C19; GB:AL162756; GB:AL157959; NII A;Experimental source: serogroup A, strain Z2491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C,Accession: F81090
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.; R;Tettelin, H.; Saunders, N.J.; Heidelberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Oin, H.; Vanathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A;Reference number: A81000; MUID:20175755; PMID:10710307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-raferences: UNIPROT:Q9JYY6; UNIPARC:UPI00000C46C7; GB:AE002485; GB:AE002098; NII
A;Experimental source: serogroup B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein NMB1369 [imported] - Neisseria meningitidis (strain MC58 serogroup C;Species: Neisseria meningitidis C;Species: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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C;Superfamily: Neisseria meningitidis probable membrane lipoprotein NMA1581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: NMA1581
C;Superfamily: Neisseria meningitidis probable membrane lipoprotein NMA1581
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                                                                                                                                                                                                                                   Length 647
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                                                                                                                                                                                                                                                                                                6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.9%; Score 45; DB 2; 55.6%; Pred. No. 7.7;
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Pred. No. 7.7;
3; Mismatches
                                                                                                                                                                                                                                         5
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                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                      Score 46;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                          :| :||||||||
143 RDLNTRSLRAKQQAAQAQ 160
                                                                                                                                                                                                                                                                                                                                                         2 DSKINNLTAQQQAAQAQVN 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ODSKINNLTAQQQAAQAQ 18
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Best Local Similarity 55.6%;
Matches 10; Conservative
                                                                                                                                                                                                                                      47.9%;
52.6%;
                                                                                                                                                                                                                                                                 Best Local Similarity 52.6
Matches 10; Conservative
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      A; Reference number: S36469
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A Molecule type: DNA
A;Residues: 1-184 <TET>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-184 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 10: Conser
                                                         A; Molecule type: DNA
A; Residues: 1-647 <DEL>
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                                    A;Accession: S36575
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C; Species: Haemophilus influenzae
C; Species: Haemophilus influenzae
C; Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-Oct-2004
C; Accession: C44189
R; Pleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, R; Pleischmann, J.D.; Science 269, 496-512, 1995
A; Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A; Title: Whole-genome random sequencing and assembly of Amemophilus influenzae Rd.
A; Title: Mccession: C64189
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-389 < TICR>
A; Residues: 1-389 < TICR>
A; Residues: 1-389 < TICR>
A; Cross-references: UNIPROT: P45101; UNIPARC: UP1000013619E; GB:U32799; GB:L42023; NID:g15
                                                                                                                                                                                                                                                                                                                     hypothetical protein, 54K - Enterococcus faecium
C;Species: Enterococcus faecium
C;Species: Enterococcus faecium
C;Species: Enterococcus faecium
C;Species: Enterococcus faecium
C;Species: Enterococcus faecium
C;Species: S0542.
B;Puerst, P.; Moesch, H.U.; Solioz, M.
Nucleic Acids Res. 17, 6724, 1989
A;Fitle: A protein of unusual composition from Enterococcus faecium.
A;Reference number: S05542; MUID:89385998; PMID:2780297
A;Accession: S05542
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-507 <FUS-
A;Residues: 1-507 <FUS-
A;Accessives: Enterococcus faecium.
A;Residues: 1-507 <FUS-
A;Accessives: Enterococcus faecium.
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C;Superfamily: succinyl-CoA synthetase, beta subunit
C;Keywords: acid-thiol ligase; coenzyme A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ä
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El protein - human papillomavirus type 52
C;Species: human papillomavirus type 52
C;Species: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gарв
                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 50.0%; Score 48; DB 2; Length 507; Local Similarity 52.6%; Pred. No. 7.5; no 10; Conservative 4; Mismatches 5; Indels
   Length 392;
Score 73; DB 2; Length 392
Pred. No. 0.00058;
3; Mismatches 2; Indels
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3; Mismatches
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Pred. No.
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                                                                                                                                                 37 QDNKISNLTAQQQEAQKQVD 56
                                                                                                                      1 ODSKINNLTAQQQAAQAQVN 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 QDKKIADLQNQQASAQSQI 46
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      Query Match
Best Local Similarity 75.0%;
Matches 15; Conservative 3
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Best Local Similarity 57.1%;
Matches 12; Conservative
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Best Local S
Matches 10
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A;Molecule type: DNA
A;Residues: 1-209 <KUR>
A;Cross-references: UNIPROT:Q97JK6; UNIPARC:UPI00000CA14F; GB:AE001437; PIDN:AAK79239.1,
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC1268
                                                                                                                                                                                                                                                                                                                                                                            probable membrane protein STY2810 [imported] - Salmonella enterica subsp. enterica sero' C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AB0<u>0</u>27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R.Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K., A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero A;Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: UNIPARC: UP100000CDB90; GB: AL513382; PIDN: CAD02766.1; PID: 916503776;
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R; Weisshaar, B.; Armstrong, G.A.; Block, A.; da Costa e Silva, O.; Hahlbrock, K. EMBO J. 10, 1777-1786, 1991

A; Title: Light-inducible and constitutively expressed DNA-binding proteins recognizing A; Reference number: S16320; MUID: 91266906; PMID: 2050115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: mRMP.
A;Molecule type: mRMP.
A;Residues: 1.444 < WEI>
A;Cross-references: UNIPROT:Q99089; UNIPARC:UPI00001794BE; EMBL:X58575
C;Superfamily: BZIP &-box-binding protein; fosfylun DNA-binding domain homology
C;Keywords: DNA binding; nucleus; transcription regulation
F;267-307/Domain: fosfylun DNA-binding domain homology <FUD>
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                                                                                                                                                          Length 209,
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Pred. No. 16;
5; Mismatches
                                                                                                                                                            DB 2;
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                                                                                                                                                                                                   5; Mismatches
                                                                                                                                                            Score 44;
Pred. No. 1
                                                                                                                                                                                                                                                                     121 KDSKVTNTSSSQENTQPQQN 140
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                                                                                                                                                          A 45.8%;
Similarity 40.0%;
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ilarity 47.4%;
Conservative
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Best Local Similarity
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Matches 9; Conserv
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Best Local Similarity
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A;Molecule type: DNA
A;Status: preliminary
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                                                                                                                                                                                    C;Keywords: glycoprotein; receptor
F;260-387/Region: 21 residue repeats
F;560-574/Region: hyaluronan binding #status predicted
F;575-625/Region: hyaluronan binding #status predicted
F;575-625/Region: hyaluronan binding #status predicted
F;116,283,304,325,346,367,398,438,619/Binding site: carbohydrate (Asn) (covalent) #statu
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R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibs.; Daly, M.J.; Bennett, G.N.; Koonin, B.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing E A; Reference number: A96900; MUID:21359325; PMID:21359325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Clostridium acetobutylicum
                                                                                                                                                          hyaluronan receptor - mouse
C;Species: Mus musculus (house mouse)
                                      392 EDLKLENLTLQEKVAMAE 409
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                 ODSKINNLTAQQQAAQAQ
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Matches 8; Conservative
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Length 227; Indels

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A,Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; MUID:21534947; PMID:11677608
A,Accession: AD0976
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-227 <PAR>
A,Residues: 1-227 <PAR>
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A,Residues: 1
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C;Species: Streptococcus sp.
C;Accession: Ucl419; S17354
R;Accession: Ucl419; S17354
R;Smirnov, O.Y.; Denesyuk, A.I.; Zakharov, M.V.; Abramov, V.M.; Zav'yalov, V.P.
Gene 120, 27-32, 1992
A;Title: Protein V, a novel type-II IgG receptor from Streptococccus sp.: Sequence, homol A;Reference number: Ucl419; MUID:93013016; PMID:1398120
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A;Residues: 1-587 <SMI>
A;Cross-references: UNIPROT:QS5312; UNIPARC:UPI0000BCFF7; EMBL:X62467; NID:g47562; PIDN
A;Experimental source: strain 22/58'Valente'
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C;Keywords: duplication; immunoglobulin receptor
E;1-41Domain: signal sequence #status predicted <SIG>
F;1-42NProduct: IgG receptor II #status predicted <MAT>
F;234-268/Region: 35-residue repeat A
F;269-303/Region: 35-residue repeat A
F;304-318/Region: 35-residue repeat A
F;374-408/Region: 35-residue repeat A
F;374-408/Region: 35-residue repeat B
F;416-450/Region: 35-residue repeat B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fc gamma (1gG) receptor II precursor - Streptococcus sp. N;Alternate names: fcrV protein
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                                                                                                                                                                                                                                                                                                                                                                                                                     44.8%;
ilarity 40.0%;
Conservative 6
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137 KVNELSAQNKALQAE 151
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Best Local Similarity
Matches 8; Conserva
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                                                                                                                                                                                                        hypothetical protein T31P16.50 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: D2-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: T50010
R;Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Kalicki, J.; Wohldmann, P.; Sr
submitted to the Protein Sequence Database, May 2000
A;Recession: T50010
A;Accession: T50010
A;Accession: T50010
A;Accession: T50010
A;Accession: T50010
A;Accession: T50010
A;Experimental surce: Cultivar Columbia; BAC clone T31P16
C;Genetics:
A;Gene: AFGP: T31P16.50
A;Map position: 5
A;Introns: 55/3; 107/3; 219/3
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CiAccession: B86899
RiBolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: B86899
A;Status: preliminary
A;Residues: 1-552 <STO>
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C.Speciese: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
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R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
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hypothetical protein dnaH [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
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C;Genetics:
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Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
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                     303 KVDSLTAENMALKAEIN 319
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"Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates.";

Infect. Immun. 69:6931-6941(2001).

EMBL; ANO46441; ARV94540-1; -; Genomic_DNA.

InterPro; IPR007921; CHAP.

InterPro; IPR009148; SibA.

PRINTS; PR01852; SIBAPROTEIN.

PROSITE; PS050911; CHAP; 1.

SEQUENCE 431 AA; 44650 MW; 05D38D8D8BC4609F CRC64;
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MEDLINE=21481971; PubMed=11598068;
DOI=10.1128/IAI.69.11.6931-6941.2001;
Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Glucan-binding protein B.
Streptococcus micans.
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08JZ41_POLCB
05JTE2_SALCH
08JZ41_POLCB
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08JJM5_VIBPA
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Q938V3;
Q1-DEC-2001 (TEMBLE1. 19, C
01-DEC-2001 (TEMBLE1. 19, L
01-MAR-2004 (TEMBLE1. 26, L
Glucan-binding protein B.
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Q938V0;
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NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE.
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Q871Q7_STRP3
Q5MG14_STRT2
Q5MZ12_STRT1
Q810C2_DROME
Q9VN98_DROME
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KCNE2_CAVPO
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Infect. Immun. 69:6931-6941(2001).

EMBL; AY046410; AA94500.1; -; Genomic_DNA.

InterPro; IPR007921; CHAP.

InterPro; IPR009148; SibA.
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DOI=10.1128/IAI.69.4.2493-2501.2001;
Chia J.S., Liee Y.Y., Huang P.T., Chen J.Y.;
Tidentification of stress-responsive genes in Streptococcus mutans differential display reverse transcription-PCR.";
Infect. Immun. 69:2493-2501(2001).
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Chia J.S., Chang L.Y., Shun C.T., Chang Y.Y., Chen J.Y.;
"A 60-kilodalton immunodominant glycoprotein is essential for cell
wall integrity and the maintenance of cell shape in Streptococcus
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01-JUN-2001 (TrEMBLrel. 29, Last sequence update)
01-REB-2005 (TrEMBLrel. 29, Last annotation update)
Immunodominant glycoprotein IDG-60 (Glucan-binding protein B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 431;
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Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
                     Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                        Jin S., Duncan M.J., Taubman M.A., Smith D.J.; "Cloning of the gbpB gene from Streptococcus mutans."; J. Dent. Res. 79:224-224 (2000).
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Pred. No. 2.6e-06;
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MEDLINE=21481977; PubMed=11598074;
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PRINTS: PR01852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
SEQUENCE 431 AA; 44620 MG.
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Q9AG98;
    Streptococcus mutans.
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NCBI_TaxID=1309;
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Duncan M.J.;

"Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates."

Infect. Immun. 69:6931-6941(2001).

EMBL; AR338445; AAK08104.1; -; Genomic_DNA.

EMBL; AR046411; AAK084501.1; -; Genomic_DNA.

InterPro; IPR007921; CHAP.
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MEDLINE=22295063; PubMed=12397186; DOI=10.1073/pnas.172501299;
Ajdic D.J., McShan W.M., McLaughlin R.B., Savic G., Chang J.,
Ajdic D.J., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P.,
Qian Y., Li S., Zhu H., Najar F.Z., Lai H., White J., Roe B.A.,
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last amotation update)
Putative secreted antigen GbpB/SagA; putative peptidoglycan
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Pred. No. 2.6e-06;
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Chia J.-S., Chang L.-Y., Lee Y.-Y., Chen J.-Y.; submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                    Jin S., Duncan M.J., Taubman M.A., Smith D.J.; "Cloning of the gbpB gene from Streptococcus mutans."; J. Dent. Res. 79:224-224(2000).
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Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
Exacl. AE014855; AANS7811.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
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Pred. No. 2.6e-06;
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                                                                                                                                                                                                                                                                              STRAIN=3VF4;
MEDLINE=21481971; PubMed=11598068;
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PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
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PRINTS; PR01862; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
SEQUENCE 431 AA; 44592 MW;
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NCBI_TaxID=1309;
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Mattos-Grant R.O., Jin S., King W.F., Chen T., Smith D.J.,
Duncan M.J.;
Cloning of the Streptococcus mutans gene encoding glucan binding
protein B and analysis of genetic diversity and protein production in
clinical isolates.";
Infect. Immun. 69:6931-6941(2001).
EMBL; AXV046412; AAX94502.1; -; Genomic_DNA.
InterPro; IRR007921; GRAP.
InterPro; IRR007921; GRAP.
Fram; PRO5257; GRAP.
PRINTS; PRO1852; SIBAPROTEIN.
PROSITE; PSS0911; CHAP; 1.
SEQUENCE 432 AA; 44648 MW; E769B2504AEB50B9 CRC64;
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DOI=10.1128/JB.183.19.5709-5717.2001;
Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S., Hoskins J., Alborn W.E. Jr., Arnold J., Blassczak L.C., Burgett S., Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E., LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P., McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I., Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P., Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G., Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud P.L.,
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J. Bacteriol. 183:5709-5717(2001).
EMBL: AE008566; AAL00823.1; -; Genomic_DNA.
PIR; B98124; B98124.
PIR; G95258; G95286.
InterPro; IPR007921; CHAP.
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75.0%; Pred. No. 0.0085; 2; Indels
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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1-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
General stress protein GSP-781.
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                                                                  DOI=10.1128/IAI.69.11.6931-6941.2001;
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                                 MEDLINE=21481971; PubMed=11598068;
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PRINTS; PRO1852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
COMDLECE Proteome.
SEQUENCE 392 AA; 41697 MW;
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QBDMY4;
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Matches 20; Conservative
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NUCLEOTIDE SEQUENCE
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Best Local Similarity
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"Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates.";
      Gaps
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Pred. No. 2.6e-06;
; Mismatches 0; Indels
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Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
      Indels
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Jin S., Duncan M.J., Taubman M.A., Smith D.J.;
"Cloning of the gbpB gene from Streptococcus mutans.";
J. Dent. Res. 79:224-224(2000).
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                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Glucan-binding protein B.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DRC-2004 (TrEMBLrel. 26, Last annotation update)
Glucan-binding protein B.
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EMBL; AX046413; AAK94503.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
PF05257; CHAP; 1.
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100.0%; Score 96; DB
Best Local Similarity 100.0%; Pred. No. 2.6
Matches 20; Conservative 0; Mismatches
0; Mismatches
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                                                         1 ODSKINNLTAQOQAAQAQVN 20
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Q938V1;
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Q938V2;
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20; Conservative
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NCBI_TaxID=1309;
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MEDLINE-21357209; PubMed=11463916; DOI=10.1126/science.1061217;
MEDLINE-21357209; PubMed=11463916; DOI=10.1126/science.1061217;
Peterlin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
Peterson S.N., Heidelberg J.F., DeBoy R.T., Haft D.H., Dodson R.J.,
Durkin A.S., Gwinn M.L., Kolonay J.F., Nelson W.C., Peterson J.D.,
Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
Holtzapple B.K., Khouri H.M., Wolf A.M., Utterback T.R., Hansen C.L.,
McDonald L.A., Feldblyum T.V., Angiuoli S.V., Dickinson T.,
Hickey B.K., Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
"Complete genome sequence of a virulent isolate of Streptococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 76.0%; Score 73; DB 2; Length 392; 1 Similarity 75.0%; Pred. No. 0.0085; 15; Conservative 3; Mismatches 2: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus mutans.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Peruzzi F., Piggot P.J., Daneo-Moore L.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U78607; AAD00288.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                         Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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Last annotation update)
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Last annotation update)
                                                                    392 AA
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PIR; B98124; B98124.
PIR; G95258; G95258.
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01-MAY-1999 (TrEMBLrel. 10, Last seq
01-OCT-2002 (TrEMBLrel. 22, Last ann
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InterPro; IPR00148; Siba.
Pfam; PF02257; CHAP; 1.
PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
                                                                                                                   (TrEMBLrel. 18, (TrEMBLrel. 18, (TrEMBLrel. 26,
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Q9ZAS7 STRMU PRELIMINARY;
Q9ZAS7;
                                                                  Q97N55 STRPN PRELIMINARY;
Q97N55;
                                                                                                                                                                                     Secreted 45 kd protein.
OrderedLocusNames=SP2216;
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                                                                                                                                                                                                                                        Streptococcus pneumoniae
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Best Local Similarity
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Best Local Similarity
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MEDLINE=21192684; PubMed=11296296; DOI=10.1073/pnas.071559398;
MEDLINE=21192684; PubMed=11296296; DOI=10.1073/pnas.071559398;
MEDLINE=21192684; PubMed=11296296; DOI=10.1073/pnas.071559398;
Princeaux C., Seate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Noce B.A., McLaughlin R.E.;
"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=15272401; DOI=10.1086/422697;
Banks D.J., Porcella S.F., Barbian K.D., Beres S.B., Philips L.E.,
Voyich J.M., DeLeo F.K., Martin J.M., Somerville G.A., Musser J.M.;
"Progress toward characterization of the group A Streptococcus
metagenome: complete genome sequence of a macrolide-resistant serotype
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 398;
                                                                                                                                                                                                                                                                                                                                                         Streptococcus pyogenes (serotype M6).
Bacteria, Firmicutes, Lactobacillales; Streptococcaceae;
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                                                                                                                                                                                              25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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65.0%; Pred. No. 0.62;
iive 4; Mismatches
                                                                                                                                                                                                       398 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M6 strain.",
J. Infect. Dis. 190:727-738 (2004).
EMBL; CP000003; AAT86152.1; -; Genomic_DNA.
InterPro; IPR001921; CHAP.
InterPro; IPR009148; SibA.
1; Mismatches
                                            1 QDSKINNLTAQQQ-----AAQAQVN 20
                                                                                 ODSKINNLTAGOGOHKHKLITIQGOVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PERMIT PF05257; CHAP; 1.
PRINTS; PR01822; SIBAPROTEIN.
PR051TE; PS050911; CHAP; 1.
CCMD1ete proteome.
SEQUENCE 398 AA; 42028 MW;
                                                                                                                                                                                                                                                                                                                 Secreted protein.
OrderedLocusNames=M6_Spy0017;
                                                                                                                                                                                                       STRP6 PRELIMINARY;
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les 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=MGAS10394;
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13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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SEQUENCE 398 AA:
                                                                                                                                                                   Streptococcus.
NCBI_TaxID=301448;
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Fagan P.K., Reinscheid D., Gottschalk B., Chhatwal G.S., "Identification and characterization of a novel secreted protein from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S., Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F., Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q., Kapur V., Daly J.A., Veasy L.G., Musser J.M.; "Genome sequence and comparative microarray analysis of serotype M18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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STRAIN=MGAS8232 / Serotype M18;
MEDLINE=21927593; PubMed=11917108; DOI=10.1073/pnas.062526099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            group A Streptococcus strains associated with acute rheumatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.5%; Score 61; DB 2; Length 398; 65.0%; Pred. No. 0.62; 3; Indels ive 4; Mismatches 3; Indels
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                                                             group A streptococcus.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AE006474; AAK33158.1; -; Genomic_DNA.
EMBL; AF319999; AAK73135.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                           28A9B3F7195E969B CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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EMBL; AE009955; AAL96649.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
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Streptococcus pyogenes (Serotype M18).
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34 QDSIISNLTTEQKAAQNQVS 53
                                                                                                                                                                                                                                                                                                                                                                                                       398 AA; 41899 MW;
                                                                                                                                                                                                                                                Pfam; PF05257; CHAP; 1.
PRINTS; PRO1852; SIBABROTEIN.
PROSITE; PS50011; CHAP; 1.
Complete proteome; Signal.
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PROSITE; PS50911; CHAP; 1.
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Q7CNQ7;
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Matches 13; Conservative
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SEQUENCE 398 AA
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Q8P318 STR
ID Q8P31
AC Q8P31
DT 01-OC
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Hayashi H., Hattori M., Hamada S., "Genome sequence of an M3 strain of Streptococcus pyogenes reveals a large-scale genomic rearrangement in invasive strains and new insights
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MEDLINE=22133808; PubMed=12122206; DOI=10.1073/pnas.152298499;
MEDLINE=2213808; PubMed=12122206; DOI=10.1073/pnas.152298499;
MERCE S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S., Parkins L.D.,
Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlievert P.M., Musser J.M.;
Genome sequence of a serotype M3 strain of group A Streptococcus:
phage-encoded toxins, the high-virulence phenotype, and clone
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MEDLINE=22683278; PubMed=12799345; DOI=10.1101/gr.1096703;
Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
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Bolotin A., Quinquis B., Renault P., Sorokin A., Ehrlich S.D.,
Kulakauskas S., Lapidus A., Goltsman E., Mazur M., Pusch G.D.,
Fonstein M., Overbeek R., Kyprides N., Purnelle B., Prozzi D.,
Ngui K., Masuy D., Hancy F., Burteau S., Boutry M., Delcour J.,
Goffeau A., Hols P.;
"Complete sequence and comparative genome analysis of the dairy
bacterium Streptococcus thermophilus.";
Nat. Biotechnol. 22:1554-1558(2004).
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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Pred. No. 0.62;
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Putative secreted protein.
OrderedLocusNames=SP80015. SpyM3_0014;
Streptococcus pyogenes (serotype M3).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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EMBL; BA000034; BAC63110.1; -; Genomic_DNA.
EMBL; Ac014136; AAM76221.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
61ucan binding protein (PosB).
Name=posB; OrderedLocusNames=stu0022;
Streptococcus thermophilus (strain ATCC BAA-250 / L.
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PROSITE; PS50911; CHAP; 1.
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Best Local Similarity 65.09
Matches 13; Conservative
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                                                                                                                                    Decaris B., Leblond-Bourget N.;
"cse, a Chimeric and Variable Gene, Encodes an Extracellular Protein Involved in Cellular Segregation in Streptococcus thermophilus.";
J. Bacteriol. 187:2737-2746 (2005).
EMBL; CP000023; AAV59752.1; -; Genomic_DNA.
EMBL; AY730643; AAW82375.1; -; Genomic_DNA.
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NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

PubMed=15543133; DOI=10.1038/nbt1034;

Bolotin A., Quinquis B., Renault P., Sorokin A., Ehrlich S.D.,

Kulakauskas S., Lapidus A., Kgoltsamn E., Mazur M., Pusch G.D.,

Ronstein M., Overbeek R., Kypridas N., Purnelle B., Prozzi D.,

Ngui K., Masuy D., Hancy F., Burteau S., Boutry M., Delcour J.,

Goffeau A., Hols P.;

"Complete sequence and comparative genome analysis of the dairy

bacterium Streptococcus thermophilus.";

Nat. Biotechnol. 22:1554-1558 (2004).

EMBL; CRO00024; AAV61641.1; -; Genomic_DNA.

RINTERPO; IPR007921; CHAP.
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57.3%; Score 55; DB 2; Length 474;
Best Local Similarity 61.1%; Pred. No. 6.2;
Matches 11; Conservative 5; Mismatches 2; Indels
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
03. Created protein.
Name-pcsB; OrderedLocusNames=str0022;
Streptococcus thermophilus (strain CNRZ 1066).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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InterPro; IPR009148; SibA.
Pfam; PF05257; CHAP; 1.
PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
Complete proteome.
SEQUENCE 474 AA; 48142 MW;
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PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
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Best Local Similarity 61.1:
Matches 11; Conservative
[2]
NUCLEOTIDE SEQUENCE.
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January 25, 2006, 18:50:05 ; Search time 16.6 Seconds (without alignments) 99.609 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 67, Appl Sequence 3134, Ap Sequence 31781, Ap Sequence 46970, A Sequence 46970, A Sequence 6, Appli Sequence 5990, Ap Sequence 5990, Ap Sequence 5095, Appli Sequence 5095, Appli Sequence 5095, Appli Sequence 3, Appli Sequence 3513, Ap Sequence 2, Appli Sequence 11, Appl Appl Appli Appli Description Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence US-09-583-110-4374
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US-09-134-000C-5990
US-09-134-000C-5990
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Sequence

US-09-733-524A-20 US-10-189-977A-20

Sequence 894, App Sequence 892, App Sequence 1660, Ap Sequence 592, Ap Sequence 6592, Ap Sequence 6793, Ap Sequence 6029, Ap Sequence 6029, Ap Sequence 689, App Sequence 689, App Sequence 88, App Sequence 88, App Sequence 88, App Sequence 884, App Sequence 886, App	Sequence 12885, A
US-09-605-703B-894 US-09-605-703B-892 US-09-105-1660 US-09-134-001C-4820 US-09-949-016-6592 US-09-949-016-6592 US-09-949-016-11054 US-09-134-001C-4733 US-09-134-001C-4733 US-09-138-012-688 US-09-138-012-688 US-09-65-703B-884 US-09-605-703B-884 US-09-605-703B-886 US-09-6540-12972 US-09-617-811C-40	US-09-489-039A-12885
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## ALIGNMENTS

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VS-09-583-110-4374

i Sequence 4374, Application US/09583110

i Sequence 4374, Application US/09583110

i Sequence 4374, Application US/09583110

i Patent No. 6699703

i GRNERAL INFORMATION:

i APPLICANT: Lynn Doucette-Stamm et al.

i TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

i TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

i TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

i TITLE OF INVENTION: DATE: US 09/107,433

i FRIOR APPLICATION NUMBER: US 60/085,131

i PRIOR FILING DATE: 1998-06-30

i PRIOR FILING DATE: 1998-06-12

i PRIOR PRILING DATE: 1998-05-12

i PRIOR PILING DATE: 1998-05-12

i RIOR FILING DATE: 1998-05-13

i RIOR FILING DATE: 1998-05-12

i RIOR FILING DATE: 1998-05-13

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                                                                                                                         GENERAL INCOGNATION:
APPLICANT: Youngman, Philip
APPLICANT: Printsian
APPLICANT: Murphy, Christopher
APPLICANT: Guzman, Luz-Maria
TITLE OF INVENTION: ESSENTIAL BACTERIAL GENES AND THE
FILE REFERENCE: 07334,00001
CURRENT APPLICATION NUMBER: US/09/222,938A
CURRENT FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 102
SOFTWARE: FREEERO FOR UNIONE 102
SOFTWARE: PREFERO FOR UNIONE 102
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SOFTWARE: PREFERO FOR WINGONE 102
                               Sequence 67, Application US/09222938A Patent No. 6437108
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Best Local Similarity
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APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: TOWNER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 46970
LENGTH: 168
                                    %30-070-767-31753

Sequence 31753, Application US/09270767

Patent No. 6703491

SEQUENCE STATE OF INVENTION:

APPLICANT: Homburger et al.

TILE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster.

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0
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Sequence 4, Application US/09972784

Sequence 4, Application US/09972784

GENERAL INFORMATION:
APPLICANT: BATCHART:
TITLE OF INVENTION: Proly1-4-Hydroxylases
FILE REFERENCE: UTSD0871

CURRENT APPLICATION NUMBER: US/09/972,784

CURRENT FILING DATE: 2001-10-04

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patentin Ver: 2.1

SEQ ID NO 4

ILENGTH: 325
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                                                                                                                                                                                                                                                                                                                                                        , ORGANISM: Drosophila melanogaster US-09-270-767-31753
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Best Local Similarity
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US-09-270-767-46970
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LENGTH: 168
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                                                                                                                                                                                                                                                                                                                               Sequence 3230, Application US/09107433
Patent No. 6800744
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
                                                                                                                                  Gaps
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                                                                                    Query Match 76.0%; Score 73; DB 2; Length 392; Best Local Similarity 75.0%; Pred. No. 0.00077; Matches 15; Conservative 3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: GENOME THERAPEUTICS CORPORATION STREET: 100 Beaver Street CITY: Waltham STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: cUnknown CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...399
SEQUENCE DESCRIPTION: SEQ ID NO: 3230:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: GTC-011 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: «Unknown»
OPERATING SYSTEM: «Unknown»
  ; TYPE: PKT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4374
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37 QDNKISNLTAQQQEAQKQVD 56
                                                                                                                                                                         1 ODSKINNLTAQOQAAQAQVN 20
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INFORMATION FOR SEQ ID NO: 3230:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 02354
                                                                                                                                                                                                                                                                                     RESULT 3
US-09-107-433-3230
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TYPE: PRT
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Sequence 5095, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL LYUN A DOUCETTE STARM and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Seeti, Federico
APPLICANT: Seeti, Federico
APPLICANT: Splawski, Igor
APPLICANT: Splawski, Igor
APPLICANT: Splawski, Igor
APPLICANT: Goldstein, Steve A.N.
APPLICANT: University of Utah Research Foundation
APPLICANT: Vale University
TITLE OF INVENTION: MinK-Related Genes, Formation of Potassium Channels and
TITLE OF INVENTION: MinK-Related Genes, Formation of Potassium Channels and
TITLE OF INVENTION: WINGRES to al. US/09/550,163
CURRENT APPLICATION NUMBER: US/09/550,163
PRIOR APPLICATION NUMBER: US 60/129,404
PRIOR FILING DATE: 1999-04-15
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                                                            Gaps
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Length 497;
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                                                            Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
Score 52; DB 2;
Pred. No. 2.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/09/107,532A
FRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
Query Match
Best Local Similarity 57.9%; Pred. No. 2.4;
Matches 11; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
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Pred. No.
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COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09550163
Patent No. 6864364
                                                                                                                                                    52 QDQKINALTSQMSDAEAKV 70
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 50.0%;
Best Local Similarity 57.9%;
Matches 11; Conservative
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Sesti, Federico
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ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn Ve
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US-09-107-532A-5095
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LENGTH: 123
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APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: DROSOPHILA HOMOLOGUES OF GENES AND PROTEINS IMPLICATED IN CANCE
TITLE OF INVENTION: DROSOPHILA HOMOLOGUES OF GENES AND PROTEINS IMPLICATED IN CANCE
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: EXOO-043C
CURRENT APPLICATION NUMBER: US/09/738,946
CURRENT PILING DATE: 2000-12-14
PRIOR FILING DATE: 1999-12-14
PRIOR FILING DATE: 1999-12-14
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-02-29
PRIOR FILING DATE: 2000-02-29
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-15
NUMBER OF SEQ ID NOS: 14
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Sequence 5990, Application US/09134000C

Sequence 5990, Application US/09134000C

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: ENTERCOCCUS PAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR FILING DATE: 1997-08-15
                                                                                       Gaps
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                           DB 2; Length 325;
                                                                                    4; Indels
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                                                                                    3; Mismatches
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                        Query Match 56.2%; Score 54; Best Local Similarity 61.1%; Pred. No. Matches 11; Conservative 3; Mismatc
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Pred. No.
                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/09738946
Patent No. 6579701
                                                                                                                                                                            ::|| ||| || || || ||:
262 ENSKTNNLAAQAQAQAE 279
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ORGANISM: Drosophila melanogaster
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415 ENSKTNNLAAQAQAQAE 432
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SOFTWARE: Patentin version 3.1
SEQ ID NO 5990
LENGTH: 497
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Local Similarity 61.1%;
es 11; Conservative
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                                                                                                                                                                                                                                                                                      RESULT 7
US-09-738-946-6
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5; Mismatches
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                                                                                                                                                                                                            1 QDSKINNLTAQQQAAQAQ 18
                                                                                                                                                                                                                                                     2 EDLKLENLTLQEKVAMAE 19
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                                                                                                                                           Conservative
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                                                                    Query Match
Best Local Similarity
Matches 8; Conserv
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US-09-978-309A-75
             US-08-477-831C-41
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1. Similarity 50.0%; Pred. No. 23; Length 525;
10; Conservative 4; Mismatches 6; Indels
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APPLICANT: TURLEY, EVA A.
APPLICANT: BINDEN, ZHANG
APPLICANT: ENTWISTLE, JOYCELYN
TITLE OF INVENTION: HYALURONAN RECEPTOR PROTEIN
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 AVENUE OF THE AMERICAS
CITY: NEW YORK
COUNTRY: U.S.A.
ZIPE: 10020-1104
COMPUTER: IBM PC COMPALIAN
MEDIUM TYPE: Floppy disk
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC COMPALIAN
COMPUTER: PROPEN: NEW YORK
COMPUTER: OF THE AMERICAS
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ATTORNEY/AGENT INFORMATION:
NAME: ATTAIGHLO, Pamela Deneke
REGISTRATION NUMBER: 40,489
REGISTRATION NUMBER: 40,489
REFRENCE/DOCKET NUMBER: GTC-012
TELEPHONE: (781)893-8077
INFORMATION FOR SEQ ID NO: 5095:
SEQUENCE CHARACTERESTICS:
IENGTH: 525 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...525
; SEQUENCE DESCRIPTION: SEQ ID NO: 5095:
US-09-107-532A-5095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-08-477-831C-41
; Sequence 41, Application US/08477831C
; Patent No. 6429291
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 10; Conserva
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Sequence 73, Application US/09978309A

Sequence 73, Application US/09978309A

Sequence 73, Application US/09978309A

Sequence 73, Application US/09978309A

Sequence 73, Application US/09978309A

Sequence 73, Application

APPLICANT: Cruz, Tony

APPLICANT: Cruz, Tony

TITLE OF INVENTION: Injury and Other Proliferating Cell Disorders Regulated by

TITLE OF INVENTION: Hyaladherin and Hyaluronans

TITLE OF INVENTION: Hyaladherin and Hyaluronans

FILE REFERENCE: 033352-010

FILE REFERENCE: 033352-010

PRIOR PILING DATE: 2000-10-05

PRIOR PILING DATE: 2000-10-05

PRIOR PILING DATE: 2000-10-05

PRIOR PILING DATE: 1099-04-01

PRIOR PILING DATE: 1099-04-01

NUMBER OF SEQ ID NOS: 84

NUMBER OF SEQ ID NOS: 84
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                                  Gaps
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46.9%; Score 45; DB 2; Length 183; 44.4%; Pred. No. 10;
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US-09-978-309A-80

Sequence 80, Application US/09978309A

Patent No. 6911429

GENERAL INFORMATION:

APPLICANT: CTLX, TONI

TITLE OF INVENTION:

TITLE OF INVENTION: Hyaladherin and Hyaluronans

TITLE OF INVENTION: Hyaladherin and Hyaluronans

TITLE OF INVENTION: Hyaladherin and Hyaluronans

TITLE OF INVENTION Hyaladherin and Hyaluronans

TITLE OF INVENTION: WHOMER: US/09/978,309A

TITLE OF INVENTION WHOMER: US/09/978,309A

CURRENT FILING DATE: 2000-10-05

PRIOR FILING DATE: 2000-04-04

PRIOR PILING DATE: 2000-04-03

PRIOR APPLICATION NUMBER: US 09/541,522

PRIOR APPLICATION NUMBER: US 09/541,522

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PRIOR PRIOR APPLICATION NUMBER: US 09/541,522

PRIOR PRIOR APPLICATION NUMBER: US 00/127,457

PRIOR PRIOR APPLICATION NUMBER: US 00/127,457

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Sequence 77, Application US/09978309A

Patent No. 691429

GENERAL INPORMATION:

APPLICANT: Cruz, Tony

APPLICANT: Cruz, Tony

APPLICANT: Pastrak, Aleksandra

APPLICANT: Partley, Eva A.

ITILE OF INVENTION: Compositions and Methods for Treating Cellular Response to

ITILE OF INVENTION: Hyaladherin and Hyaluronans

TITLE OF INVENTION: Hyaladherin and Hyaluronans

TITLE OF INVENTION: Hyaladherin and Hyaluronans

TITLE OF INVENTION: Hyaladherin and Hyaluronans

CURRENT APPLICATION NUMBER: US/09/978,309A

CURRENT APPLICATION NUMBER: US 09/641,522

PRIOR FILING DATE: 2000-04-03

PRIOR FILING DATE: 2000-04-03

PRIOR FILING DATE: 1999-04-01

NUMBER OF SEQ ID NOS: 84

SOFTWARE: PastSEQ for Windows Version 4.0

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Best Local Similarity 44.4%; Pred. No. 20;
Matches 8; Conservative 5; Mismatches 5; Indels
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Best Local Similarity 44.4%; Pred. No. 27;
Matches 8; Conservative 5; Mismatches 5; Indels
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd
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No.
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28 46 47.9 524 4 US-10-282-122A-57658 Sequence 57658, A 30 45 46.9 190 4 US-10-767-701-32717 Sequence 32717, A 4 6.9 221 3 US-09-978-303A-75 Sequence 75, Appl 32 45 46.9 221 5 US-10-892-813-75 Sequence 75, Appl 33 45 46.9 221 5 US-10-994-157-3 Sequence 75, Appl 34 45 46.9 221 5 US-10-994-157-3 Sequence 18, Appl 35 46.9 313 3 US-09-978-303A-73 Sequence 2659, Appl 36 45 46.9 313 5 US-10-108-260A-2659 Sequence 2659, Appl 37 45 46.9 313 5 US-10-994-157-1 Sequence 17, Appl 39 45 46.9 415 5 US-10-994-157-1 Sequence 17, Appl 40 45 46.9 415 5 US-10-994-157-1 Sequence 10, Appl 41 45 46.9 476 3 US-09-978-303A-79 Sequence 10, Appl 42 46.9 476 3 US-09-978-303A-79 Sequence 10, Appl 42 46.9 476 5 US-10-994-157-1 Sequence 77, Appl 44 45 46.9 476 5 US-10-892-811-79 Sequence 77, Appl 44 45 46.9 476 5 US-10-994-157-7 Sequence 77, Appl 44 45 46.9 477 5 US-10-994-157-7 Sequence 77, Appl 45 46.9 477 5 US-10-994-157-7 Sequence 77, Appl 44 45 46.9 477 5 US-10-994-157-7 Sequence 77, Appl 44 45 46.9 477 5 US-10-994-157-7
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## ALIGNMENTS

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US-10-383-930-7

i Sequence 7, Application US/10383930

j Sequence 7, Application US/10383930

j Publication No. US20040127400A1

j GENERAL INFORMATION:
    APPLICANT: Smith, Daniel J

APPLICANT: Taubman, Martin A

j TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein

j TITLE OF INVENTION: 15669-018

CURRENT APPLICATION NUMBER: 60/402,483

FRIOR APPLICATION NUMBER: 60/402,483

FRIOR APPLICATION NUMBER: 60/363,209

FRIOR APPLICATION NUMBER: 60/363,209

FRIOR PILING DATE: 2002-03-07

FRIOR PILING DATE: 2002-03-07

SOFTWARE: PatentIn version 3.2

SEQ ID NO 7

LENGTH: 20

TYPE: PRT

OMETY MATCh

OMETY MATCh

OMETY MATCh

OMETY MATCh

Best Local Similarity 100.0%; Pred. No. 3.7e-08;

Matches 20; Conservative 0; Mismatches 0; Indels

QY

1 QDSKINNLTAQQQAAQAVN 20

OMETY MATCH

DD

1 QDSKINNLTAQQAAQAVN 20
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RESULT 2
US-10-797-821-7
Sequence 7, Application US/10797821
Sequence 7, Application US/10797821
Sequence 7, Application US/10797821
Sequence 7, Application No. US2005003163341
SEMERAL INFORMATION:
APPLICANT: Smith, Daniel J.
FILE REPERENCE: 25669-020
CURRENT APPLICATION NUMBER: US/10/797,821
CURRENT APPLICATION NUMBER: US/10/797,821
FRIOR APPLICATION NUMBER: US/383,930
PRIOR FILING DATE: 2004-03-07
PRIOR FILING DATE: 2003-03-07
PRIOR FILING DATE: 2002-03-07
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US-10-383-930-33
     SEQ ID NO 30
LENGTH: 431
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## Sequence 30, Application US/10383930

## Sequence 30, Application US/2040127400A1

## Sequence 30, Application US/2040127400A1

## SPELICANT: Smith, Daniel J

## APPLICANT: Taubman, Martin A

## TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein

## FILE REPERBNCE: 25669-018

## CURRENT APPLICATION NUMBER: US/10/383,930

## CURRENT PILING DATE: 2002-03-07

## PRIOR APPLICATION NUMBER: 60/42,483

## RIOR APPLICATION NUMBER: 60/363,209

## RIOR APPLICATION NUMBER: 60/363,209

## RIOR APPLICATION NUMBER: 60/363,209

## RIOR APPLICATION NUMBER: 5002-03-07

## NUMBER OF SEQ DI NOS: 41

** SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | CENERAL INFORMATION: |
| GENERAL INFORMATION: |
| APPLICANT: Taubman, Martin A |
| APPLICANT: Taubman, Martin A |
| APPLICANT: Taubman, Martin A |
| TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein |
| TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein |
| FILE REFERENCE: 25669-018 |
| CURRENT APPLICATION NUMBER: US/10/383,930 |
| CURRENT PILING DATE: 2003-03-07 |
| PRIOR APPLICATION NUMBER: 60/462,483 |
| PRIOR APPLICATION NUMBER: 60/363,209 |
| PRIOR FILING DATE: 2002-03-07 |
| NUMBER OF SEQ ID NOS: 41 |
| SOFTWARE: Patentin Version 3.2 |
| LENGTH: 431
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100.0%; Score 96, DB 4, I
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 20; Conservative 0; Mismatches 0;
PRIOR FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: 60/081,550
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOPTWARE: Patentin version 3.2
SEQ ID NO 7
LENGTH: 20
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                                                                                                                                                                                                                                                                                          ; FEATURE:
; OTHER INFORMATION: GbpB peptide
US-10-797-821-7
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; ORGANISM: Streptococcus mutans
US-10-383-930-29
                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Artificial
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Sequence 29, Application US/10797821

| Sequence 29, Application US/10797821
| Publication No. US20050031633A1
| Publication No. US20050031633A1
| GENERAL INFORMATION:
| APPLICANT: Smith, Daniel J. APPLICANT: Taubman, Martin A. ITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens FILE REFERENCE: 25669-020
| CURRENT FILING DATE: 2004-03-09
| PRIOR PLING DATE: 2003-03-07
| PRIOR APPLICATION NUMBER: 60/402,483
| PRIOR PLING DATE: 2002-03-07
| PRIOR PLING DATE: 2002-03-07
| PRIOR PLING DATE: 2002-03-07
| PRIOR PLING DATE: 1999-04-12
| PRIOR PLING DATE: 1999-04-13
| PRIOR PLING DATE: 1999-04-13
| PRIOR FILING DATE: 1999-04-13
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APPLICANT: Taubman, Martin A
ITILE OF INVENTION: Immunogenicity of Glucan Binding Protein
ITILE OP INVENTION: Immunogenicity of Glucan Binding Protein
FILE REFERENCE: 25669-018
CURRENT APPLICATION NUMBER: US/10/383,930
CURRENT PILING DATE: 2003-03-03-03
FRIOR FILING DATE: 2002-08-08
FRIOR FILING DATE: 2002-08-08
FRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.2
SEQ ID NO 33
LENGTH: 431
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Pred. No. 1.1e-06;
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Pred. No. 1.1e-06;
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100.0%; Pred. No....
0; Mismatches
                                                                                                                     Query Match
100.0%; Score 96; DB
Best Local Similarity 100.0%; Pred. No. 1.1
Matches 20; Conservative 0; Mismatches
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; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-10-383-930-30
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Best Local Similarity 100.0
Matches 20; Conservative
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US-10-383-930-31
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LENGTH: 432
TYPE: PRT
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Fublication No. US20050031633A1

GENERAL INFORMATION:

APPLICANT: Smith, Daniel J.

APPLICANT: Taubman, Martin A.

TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens

FILE REFERENCE: 25669-020

CURRENT FILING DATE: 2004-03-09

PRIOR APPLICATION NUMBER: US/10/797,821

CURRENT PILING DATE: 2003-03-07

PRIOR APPLICATION NUMBER: 60/363,209

PRIOR PRIOR PILING DATE: 2002-08-08

PRIOR FILING DATE: 2002-08-08

PRIOR PILING DATE: 1999-04-12

PRIOR PILING DATE: 1999-04-12

PRIOR PILING DATE: 1999-04-13

PRIOR FILING DATE: 1999-04-13

PRIOR FILING DATE: 1998-04-13

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PRIOR PILING DATE: 1998-04-13
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; Publication No. US20050031633A1
; GENERAL INFORMATION;
; APPLICANT: Smith, Daniel J.
; APPLICANT: Taubman, Martin A.
; TITLE OF INVENTION; Glucan Binding Protein and Glycosyltransferase Immunogens
; TITLE OF INVENTION NUMBER: US/10/797,821
; CURRENT APPLICATION NUMBER: US/10/797,821
; CURRENT PILING DATE: 2004-03-09
; PRIOR FILING DATE: 2003-03-07
; PRIOR PILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 60/402,483
; PRIOR PLILING DATE: 2002-03-07
; PRIOR PLILING DATE: 2002-03-07
; PRIOR PLILING DATE: 2002-03-07
; PRIOR FILING DATE: 2002-03-07
; PRIOR FILING DATE: 2002-03-07
; PRIOR FILING DATE: 1999-04-12
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Pred. No. 1.1e-06;
                                                                                                                                                    Length 431;
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100.0%; Score 96; DB
Best Local Similarity 100.0%; Pred. No. 1.1
Matches 20; Conservative 0; Mismatches
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                                                                                                                                                 100.0%;
                      ; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-10-797-821-29
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                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 20; Conservative
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US-10-797-821-33
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LENGTH: 431
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US-10-383-30-31

Sequence 31, Application US/10383930

Publication No. US20040127400A1

GENERAL INFORMATION:

APPLICANT: Smith, Daniel J

APPLICANT: Taubman, Martin A

TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein

FILE REPERENCE: 2569-018

CURRENT FILING DATE: 2003-03-07

FRIOR PAPLICATION NUMBER: 60/402,483

PRIOR PAPLICATION NUMBER: 60/363,209

PRIOR FILING DATE: 2002-08-08

PRIOR FILING DATE: 2002-08-08

PRIOR FILING DATE: 2002-08-08

PRIOR FILING DATE: 2002-08-08

NUMBER OF SEQ ID NOS: 41

SOPTWARE: Patentin version 3.2

SEQ ID NOS: 41
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### Sequence 32, Application US/10383930

### Sequence 32, Application US/10383930

### Sequence 32, Application US/20040127400A1

### Sequence 32, Application No. 10220040127400A1

### APPLICANT: Taubman, Martin A

### TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein

### PILE REFERENCE: 25669-018

### CURRENT APPLICATION NUMBER: US/10/383,930

### CURRENT PILING DATE: 2003-03-07

### PRIOR PILING DATE: 2002-08-08

### PRIOR PILING DATE: 2002-03-07

### NUMBER OF SEQ ID NOS: 41

### SOFTWARE: PatentIn version 3.2
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                                                                                                                                                                                                                                                                                                                                                   Length 431;
                                                                                                                                                                                                                                                                                                                                             100.0%; Score 96; DB 5; 1
nilarity 100.0%; Pred. No. 1.1e-06;
Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: 60/081,550
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PACENTIN VERBION 3.2
SEQ ID NO 33
LENGTH: 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ODSKINNLTAQQQAAQAQVN 20
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                                                                                                                                                                                                                                                         ; ORGANISM: Streptococcus mutans
US-10-797-821-33
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Matches 20; Conserv
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US-10-797-821-6
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j Sequence 31, Application US/2005031633A1

j Publication No. US20050031633A1

GENERAL INFORMATION:

APPLICANT: Smith, Daniel J.

APPLICANT: Taubman, Martin A.

TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens

FILE REFERENCE: 2569-02

CURRENT APPLICATION NUMBER: US/10/797,821

CURRENT FILING DATE: 2004-03-09

PRIOR PILING DATE: 2002-03-07

PRIOR PLING DATE: 2002-03-07

PRIOR PLING DATE: 2002-08-08

PRIOR PLING DATE: 1909-04-13

PRIOR APPLICATION NUMBER: 60/402,483

PRIOR PLING DATE: 1999-04-13

PRIOR PELING DATE: 1999-04-13

PRIOR PELING DATE: 1999-01-08

NUMBER: 60/115,142

PRIOR FILING DATE: 1999-01-08

NUMBER: PALCATION NUMBER: 60/115,142

PRIOR PLING DATE: 1999-01-08

NUMBER OF SEQ ID NOS: 45

SOFTWARE: PALCATION NUMBER: 60/115,142

PRIOR PLING DATE: 1999-01-08

NUMBER OF SEQ ID NOS: 45

SOFTWARE: PALCATION NUMBER: 60/115,142

PRIOR PLING DATE: 1999-01-08

NUMBER OF SEQ ID NOS: 45

SEQ ID NO 31

LEMCTH: 432

THE PARCENTE: 432
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Fublication No. US20050031633A1

GENERAL INFORMATION:

APPLICANT: Smith, Daniel J.

APPLICANT: Taubman, Martin A.

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/10/797,821

CURRENT APPLICATION NUMBER: 10/383,930

FRIOR APPLICATION NUMBER: 60/363,209

PRIOR FILING DATE: 2002-08-08

PRIOR FILING DATE: 2002-08-08

PRIOR FILING DATE: 2002-08-08

PRIOR FILING DATE: 2002-08-08

PRIOR FILING DATE: 2002-04-12

PRIOR PILING DATE: 1998-04-13

PRIOR FILING DATE: 1998-04-13
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; Pred. No. 1.1e-06;
                                                                            Query Match
100.0%; Score 96; DB 4; L
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 20; Conservative 0; Mismatches 0;
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; ORGANISM: Streptococcus mutans US-10-383-930-32
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Squence 6, Application US/10797821

Squence 6, Application US/10797821

Squence 6, Application No. US20050031633A1

GENERAL INFORMATION:

APPLICANT: Smith, Daniel J.

APPLICANT: Taubman, Martin A.

TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens

TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens

CURRENT APPLICATION NUMBER: US/10/79,821

CURRENT FILING DATE: 2069-03-09

PRIOR APPLICATION NUMBER: 00/363,209

PRIOR APPLICATION NUMBER: 60/402,483

PRIOR PLING DATE: 2002-03-07

PRIOR PLING DATE: 2002-09-04-12

PRIOR PLING DATE: 1999-04-12

PRIOR APPLICATION NUMBER: 09/290,049

PRIOR APPLICATION NUMBER: 60/081,550

PRIOR APPLICATION NUMBER: 60/081,550

PRIOR APPLICATION NUMBER: 60/081,550

PRIOR APPLICATION NUMBER: 60/115,142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 20;
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                                                                                                                                                                                               Score 96; DB 5; 1
Pred. No. 1.1e-06;
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PRIOR APPLICATION NUMBER: 60/115,142
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.2
SEQ ID NO 32
LENGTH: 432
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                                                                                                                     ; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-10-797-821-32
                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%;
Matches 20; Conservative 0
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US-10-154-251-67
is Sequence 67, Application US/10154251
spublication No. US20030092024A1
igeneral INFORMATION:
is APPLICANT: Youngman, Philip
is APPLICANT: Pritz, Christian
is APPLICANT: Whirphy, Christian
is APPLICANT: Guzman, Luz-Maria
is APPLICANT: Guzman, Luz-Maria
is TITLE OF INVENTION: ESSENTIAL BACTERIAL GENES AND THEIR USE
is FILE REPERBACE: 05266-060002
is CURRENT APPLICATION NUMBER: US/10/154,251
is FILENG DATE: 2002-09-16
is PRIOR FILING DATE: 2002-09-16
is PRIOR FILING DATE: 2002-09-16
is RIOR FILING DATE: 2002-05-22
is NUMBER of SEQ ID NOS: 102
is SOFTWARE: FastSEQ for Windows Version 3.0
is SEQ ID NO 67
is LENGTH: 210
it TYPE: PRT
is ORGANISM: Streptococcus pneumoniae
US-10-154-251-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 76.0%; Score 73; DB 4; Length 210; Best Local Similarity 75.0%; Pred. No. 0.0021; Matches 15; Conservative 3; Mismatches 2; Indels
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37 QDNKISNLTAQQQEAQKQVD 56
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PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.2
SEQ ID NO 6
LENGTH: 20
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ORGANISM: Artificial
FEATURE:
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Search completed: January 25, 2006, 20:10:03 Job time : 60 secs

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8, App 1
166, Ap
20, Ap 2
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2556, Ap
2988, Ap
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3154, Ap
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5562, Ap
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                                                                                             January 25, 2006, 19:15:26; Search time 5.5 Seconds (without alignments) 39.378 Million cell updates/sec
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1: /cgn2 6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*
2: /cgn2 6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*
3: /cgn2 6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*
4: /cgn2 6/ptodata/2/pubpaa/PCT_NEW PUB.pep:*
5: /cgn2 6/ptodata/2/pubpaa/NSO8 NEW PUB.pep:*
6: /cgn2 6/ptodata/2/pubpaa/USIO NEW PUB.pep:*
7: /cgn2 6/ptodata/2/pubpaa/USIO NEW PUB.pep:*
8: /cgn2 6/ptodata/2/pubpaa/USIO NEW PUB.pep:*
            GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd.
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US-10-793-626-1660

US-11-194-890-20

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US-10-467-657-2850

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US-10-467-657-145

US-10-793-626-3188

US-11-069-834-48

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US-11-052-554A-216
US-10-467-657-5432
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Gapop 10.0 , Gapext 0.5
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Sequence 210, Application US/11052554A

Publication No. US2005028866A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVERTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVERTION: PROTEINS OF THERAPEUTIC POTENTIAL
FILE REFREENCE: 30853/40359

CURRENT APPLICATION NUMBER: US/11/052,554A

CURRENT PILING DATE: 2004-02-07

PRIOR FILING DATE: 2004-07-20

PRIOR FILING DATE: 2004-02-06

NUMBER OF SEQ ID NOS: 763

SOFTWARE: Patentin version 3.3

SEQ ID NO 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 252, Application US/11052554A
Publication No. US20050288866A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC FOTENTIAL
FILE REPERENCE: 30853/40358A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT APPLICATION NUMBER: US 60/589,227
FRIOR FILING DATE: 2004-07-20
FRIOR FILING DATE: 2004-07-20
FRIOR FILING DATE: 2004-07-20
FRIOR FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
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   2484, Ap
1002, Ap
20, App
108, App
1514, Ap
1000, Ap
1004, Ap
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1001, Ap
998, App
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52, Appl
53, Appl
54, Appl
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US-10-467-657-2484
US-10-995-561-1002
US-11-113-837-20
US-11-113-837-20
US-11-037-243-108
US-10-995-561-1004
US-10-995-561-1004
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US-11-115-639-53
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Best Local Similarity 81.8%;
Matches 9; Conservative
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US-10-467-657-3078
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Fublication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: FONTANA Maria Rita
APPLICANT: MASIGNAN Vega
APPLICANT: MASIGNAN Vega
APPLICANT: MASIGNAN Vega
APPLICANT: MONACI Elisabetta
IIIE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLBIC ACIDS
FILE REPERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
                                                                                                            Query Match 63.5%; Score 61; DB 7; Length 398; Best Local Similarity 65.0%; Pred. No. 0.0086; Matches 13; Conservative 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 45; DB 6; Length 205;
Pred. No. 1.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                , ORGANISM: Streptococcus pyogenes MGAS8232
US-11-052-554A-252
                                                                                                                                                                            1 QDSKINNLTAQQQAAQAVN 20
                                                                                                                                                                                              34 QDSIISNLTTEQKAAQNQVS 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 9218
SOFTWARES SEGWHI99, version 1.04
SEQ ID NO 4336
LENGTH: 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4336
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milarity 55.6%;
Conservative 3
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SOFTWARE: Patentin version 3.3
SEQ ID NO 8
LENGTH: 515
TYPE: PRT
 SOFTWARE: PatentIn version 3.3 SEQ ID NO 252 LENGTH: 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Cryptococcus sp. US-11-132-142-8
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Best Local Similarity
                                                                                                                                                                                                                                                                        US-10-467-657-4336
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DB 7; Length 515;

45.8%; Score 44;

Query Match

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Publication No. UG2005025478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PUJ480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT PILING DATE: 1090-03-04
PRIOR FILLING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1660
LENGTH: 885
                                       Gaps
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Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNAT Vega
APPLICANT: MASIGNAT Vega
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22;
Pred. No. 6.5;
1; Mismatches
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Best Local Similarity 40.9%; Pred. No. 15;
Matches 9; Conservative 6; Mismatches
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CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
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Pred. No.
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371 AKVFDETAQSQKAEAQRN 388
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SOFTWARE: SegWin99, version 1.04
SEQ ID NO 3078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Neisseria gonorrhoeae US-10-467-657-3078
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Best Local Similarity Su.v.
Best Access 9; Conservative
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134 AQEQAAQAQAN 144
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Query Match
Best Local Similarity
Matches 9; Conserv
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    APPLICANT:
APPLICANT:
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          Sequence 20, Application US/11194890

Publication No. US20050287579A1

GENERAL INPORMATION:

APPLICANT: Wolfner, Mariana

APPLICANT: Lung, Oliver

APPLICANT: Lung, Oliver

TITLE OF INVENTION: GENES POR MALE ACCESSORY GLAND PROTEINS IN DROSOPHILA

TITLE OF INVENTION: WELANOGASTER

FILE REFERENCE: 19603/1791

CURRENT APPLICATION NUMBER: US/11/194,890

CURRENT PILING DATE: 2005-08-01

PRIOR APPLICATION NUMBER: US/10/114,774

PRIOR APPLICATION NUMBER: US/219,983

PRIOR PILING DATE: 1998-12-23

NUMBER OF SEQ ID NOS: 35

SOFTWARE: Patentin Ver: 2.1

SEQ ID NO 20

LENGTH: 716
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Pred. No. 50;
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42;
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APPLICANT: Biosynexus Incorporated
APPLICANT: Goster, Simon
APPLICANT: Goster, Simon
APPLICANT: Mond, James
TITLE OF INVENTION: Antigenic Polypeptides
FILE REFERENCE: P100629W0
CURRENT FILING DATE: 2004-02-02
PRIOR APPLICATION NUMBER: GB 0118825.9
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-09-03
PRIOR FILING DATE: 2001-09-03
NUMBER OF SEQ ID NOS: 424
SOFTWARE: Patentin version 3.1
SENGTH: 706
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US-10-467-657-2850
S. Sequence 2850, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 146, Application US/10485517; Publication No. US20050256299A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ; ORGANISM: Drosophila melanogaster US-11-194-890-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   337 QESKSNSLSQSQSQSQEQL 355
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; ORGANISM: Staphylococcus aureus
US-10-485-517-146
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Best Local Similarity 42.1%;
Matches 8; Conservative
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Best Local Similarity 52.9°
Matches 9; Conservative
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US-11-194-890-20
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Sequence 6750, Application US/10467657

Publication No. US20050260581A1

GENERAL INFORMATION:

APPLICANT: CHIRON SpA

APPLICANT: POUTANM Maria Rita

APPLICANT: POUTANM Maria Rita

APPLICANT: MASIGNAN Wega

APPLICANT: MASIGNAN Vega

APPLICANT: MASIGNAN Vega

APPLICANT: MASIGNAN Vega

APPLICANT: MONACI Eliasbetta

TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

FILE REPERENCE:

CURRENT APPLICATION NUMBER: US/10/467,657

CURRENT FILING DATE: 2001-02-12

NUMBER OF SEQ ID NOS: 9218

SOFTWARE: SEGWIN99, version 1.04

SEQ ID NO 6750
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT PILING DATE: 2003-08-11
PRIOR PILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: Sequing9, version 1.04
SEQ ID NO 2850
LENGTH: 298
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Pred. No. 22;
1; Mismatches 3; Indels
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Sequence 3988, Application US/10467657

Publication No. US20050260581A1

GENERAL INFORMATION:

APPLICANT: CHIRON SpA

APPLICANT: PONTANA Maria Rita

APPLICANT: PLZA Mariagrazia

APPLICANT: PLZA Mariagrazia

APPLICANT: MASIGNANI Vega

APPLICANT: MONACI Elisabetta

TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                               ORGANISM: Neisseria gonorrhoeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRGANISM: Neisseria gonorrhoeae US-10-467-657-6750
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Best Local Similarity 69.2%;
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Gaps

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Length 1279;

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Sequence 3154, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: STAPHYLOCCCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILLE REPRENCE: PUJ480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT APPLICATION NUMBER: 60/164,258
PRIOR APPLICATION NUMBER: 60/164,258
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4272
SOFTWARE: PATENTING DATE: 1999-11-09
LENGTH: 1095
                                                                                                                                                                                                                                                                                                                RESULT 14

US-11-069-834-48

i Sequence 48, Application US/11069834

j Publication No. US20050276811A1

general information.

APPLICANT: CARROLL, MICHAEL C.

APPLICANT: MOONE JR., FRANCIS D.

TILLE OF INVENTION: NATURAL IGM ANTIBODIES AND INHIBITORS THEREOF

TILLE OF INVENTION: NATURAL IGM ANTIBODIES AND INHIBITORS THEREOF

TILLE OF INVENTION: NATURAL IGM ANTIBODIES AND INHIBITORS THEREOF

TILLE OF INVENTION: NATURAL IGM ANTIBODIES AND INHIBITORS THEREOF

TILLE OF INVENTION NUMBER: 60/588,648

PRIOR FILING DATE: 2004-03-01

PRIOR FILING DATE: 2004-07-16

PRIOR FILING DATE: 2004-07-16

PRIOR FILING DATE: 2004-03-01

NUMBER OF SEQ ID NOS: 65

SEQ ID NOS: 65

SEQ ID NO 48

FERMINE PATENTION NUMBER: PATENTING NUMBER: PATENTING DATE: 2004-03-01

NUMBER OF SEQ ID NOS: 65
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       ; OTHER INFORMATION: Description of Artificial Sequence: synthetic; CTHER INFORMATION: amino acid sequence US-10-793-626-3188
                                                                                                         Query Match
38.5%; Score 37; DB 6; Length 127
Best Local Similarity 43.8%; Pred. No. 2.5e+02;
Matches 7; Conservative 4; Mismatches 5; Indels
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Pred. No. 4.1e+02;
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Pred. No. 2.5e+02;
4; Mismatches 5;
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ORGANISM: Artificial Sequence
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Best Local Similarity 47.4%;
Matches 9, Conservative
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Matches 7; Conservative
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ORGANISM: Mus musculus
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US-10-793-626-3154
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Publication No. US20050255478A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SEQ ID NO 3188
LENGTH: 1279
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                                                                                                                                                                                                                                                                    DB 6; Length 612;
51;
                                                                                                                                                                                                                                                                                                                                             7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 145, Application US/10485517
Publication No. US200502562991
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: University of Sheffield
APPLICANT: Biosynexus Incorporated
APPLICANT: Foster, Simon
APPLICANT: Roster, Simon
APPLICANT: Poster, Simon
CURRENT PROSERVED: P100629WO
FILE REFERENCE: P100629WO
CURRENT FILING DATE: 2004-02-02
PRIOR APPLICATION NUMBER: GB 0118825.9
PRIOR APPLICATION NUMBER: GB 0200349.9
PRIOR PILING DATE: 20001-089
NUMBER OF SEQ ID NOS: 424
SEQTWARE: PatentIN version 3.1
SEQ ID NO 145.
                                                                                                                                                                                                                                                                                           Query Match

40.6%; Score 39; DB
Best Local Similarity 47.4%; Pred. No. 51;
Matches 9; Conservative 3; Mismatches
CURRENT APPLICATION NUMBER: US/10/467,657
                  CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR PILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 3988
LENGTH: 612
TYPE: PRT
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3988
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ORGANISM: Artificial Sequence
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Best Local Similarity
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US-10-793-626-3188
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5; Indels

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Search completed: January 25, 2006, 20:11:08 Job time : 5.5 secs

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RESULT 1
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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93
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geneseqp1980s:* geneseqp2000s:* geneseqp2001s:* geneseqp2001s:* geneseqp2003as:* geneseqp2003as:* geneseqp2004s:*

A_Geneseq_21:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Add93628 Streptoco Adx37251 Streptoco				Aeb91500 Microbial Add93651 Streptoco		Adx37274 Streptoco Adx37275 Streptoco			Adresser Streptoco Adresses S. pyogen	Aeb91542 Microbial	Aay22579 Bacterial	Abu02747 S. pneumo	Adk47859 Streptoco	Adt50227 S pneumon	Adt50226 S_pneumon	Adt50165 S_pneumon
SUMMARIES	ADD93628 ADX37251	ADD93650 ADD93653	ADX37272	ADX37276	AEB91500 ADD93651	ADD93652	ADX37274 ADX37275	ADD93629	ADX37252	ADR83884	AEB91542	AAY22579	ABU02747	ADK47859	ADT50227	ADT50226	ADT50165
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8 ADR94595 9 ARA58465	5 ABP29684	8 ADU69524	8 ADV81808	8 ADV79645	7 ADD93622	9 ADX37245	5 ABB04822	4 AAG71388	8 ADS44071	5 ABB04818	5 ABB04824	9 ADW11843	3 AAB41087	5 ABB81459	5 ADG90450	6 ABR47614	7 ADE58866	7 ADD45522
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61.3	59.1	59.1	59.1	59.1	54.8	54.8	53.8	51.6	51.6	51.6	51.6	51.6	51.6	51.6	51.6	51,6	51.6	51.6
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### ALIGNMENTS

Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen. Streptococcus mutans glucan binding protein-B peptide fragment. ADD93628 standard; peptide; 20 AA. 07-MAR-2003; 2003WO-US006962. 07-MAR-2002; 2002US-0363209P. (first entry) Taubman MA; Streptococcus mutans. (FORS-) FORSYTH INST. WPI; 2003-845091/78. WO2003075845-A2. 29-JAN-2004 18-SEP-2003. Smith DJ, ADD93628; ADD93628 ID ADD 

Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.

Claim 11; Page 10; 49pp; English.

The present sequence is that of a peptide comprising amino acid residues 48-67 of the glucan binding protein-B (GbpB) of Streptococcus mutans strain SX23 ADD93649. The peptide binds to a major histocompatibility complex (MHC) class II protein. It was identified as a potential B cell epitope using a matrix-based algorithm for epitope prediction, which was used to search the primary amino acid sequence of GbpB for known MHC class II binding motifs. The peptide can be used in immunogenic compositions and subunit vaccines for dental caries. These comprise MHC class II protein-binding GbpB peptides covalently linked with peptide subunits (preferably from the catalytic domain) of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Diepitopic or multiepitopic polypeptides can be

Best Loca Matches

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Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
                                                                                                                                       Streptococcus mutans glucan binding protein-B.
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:e= "HLA-binding peptide"
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189. .308
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/note= "HLA-binding peptide"
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'note= "HLA-binding peptide"
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e= "HLA-binding peptide"
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note= "HLA-binding peptide"
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/note= "HLA-binding peptide"

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    /note= "HLA-binding peptide"

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te= "HLA-binding peptide"
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'note= "HLA-binding peptide"
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                                                       ADD93649 standard; protein; 431
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/note= ""
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                              RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in passive immunisation.
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                                                                                                                                                                                                                                                                                                                                               immunogenicity; immune stimulation; glucan binding protein-B;
microparticle; major histocompatibility complex; tooth disease.
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100.0%; Score 93; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.4e-08;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                  Length 20;
                                                                                                                                                                                                                                                                                                                    Streptococcus mutant glucan binding protein B peptide #8.
                                                                                                           Indels
                                                                                 100.0%; Score 93; DB 7; L
100.0%; Pred. No. 5.4e-08;
ive 0; Mismatches 0;
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08-JAN-1999; 99US-0115142P.
12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-0353209P.
08-AUG-2003; 2002US-0402483P.
07-MAR-2003; 2003US-0403493P.
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                                                                                  Query Match
Best Local Similarity 100.
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus mutans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SMIT/) SMITH D J.
(TAUB/) TAUBMAN M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2005-151644/16.
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The present sequence is the protein sequence of the glucan binding protein—B (GbpB) of Streptococcus mutans strain SK32. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions comprise major histocompatibility complex (WHC) class II protein-binding GbpB peptides, especially HLA-binding peptides, cowpositions are used in a claimed method of eliciting production of an antibody in a mammal. Dispitopic or multiepitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in
                                                         Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
                                                                                                                                                        Claim 6; Page 7; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              passive immunisation
                     GENBANK; AY046410.
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Score 93; DB 7; 1 Pred. No. 1.7e-06; 0; Mismatches 1 QQAAQAQVNTIQGQVSALQT 20 Query Match 100.0%; Best Local Similarity 100.0%; Matches 20; Conservative 0 ð

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Gaps

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Length 431; Indels

> 48 QQAAQAQVNTIQGQVSALQT 67 셤

ADD93650; RESULT 4 ADD93650

Streptococcus mutans glucan binding protein-B. ADD93650 standard; protein; 431 AA. (first entry) 29-JAN-2004

07-MAR-2003; 2003WO-US006962 Streptococcus mutans WO2003075845-A2. 18-SEP-2003 

Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.

07-MAR-2002; 2002US-0363209P.

(FORS-) FORSYTH INST.

Taubman MA;

Smith DJ,

WPI; 2003-845091/78.

GENBANK; AY046411.

Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex The present sequence is the protein sequence of the glucan binding protein-B (GbpB) of Streptococcus mutans strain 3VF4. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. Invention provides immunogenic compositions and vaccines for dental Claim 5; Page 8; 49pp; English. a glucan binuiny class II protein.

caries. The compositions comprise major histocompatibility complex (MHC) class II protein-binding GDpB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Dieptopic or multiepticpic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GDpB can be used in passive immunisation.

Sequence 431 AA; 8888888888888

Gaps ö 100.0%; Score 93; DB 7; Length 431; 100.0%; Pred. No. 1.7e-06; ive 0; Mismatches 0; Indels 20; Conservative Query Match Best Local Similarity Matches

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ADD93653 standard; protein; 431 AA 29-JAN-2004 (first entry) ADD93653; RESULT 5 ADD93653

Streptococcus mutans glucan binding protein-B.

Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen. Streptococcus mutans WO2003075845-A2. 

18-SEP-2003.

07-MAR-2002; 2002US-0363209P. 08-AUG-2002; 2002US-0402483P. 07-MAR-2003; 2003WO-US006962

Taubman MA; (FORS-) FORSYTH INST. Smith DJ, 2003-845091/78. GENBANK; AY046414

Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.

5; Page 8-9; 49pp; English. Claim The present sequence is the protein sequence of the glucan binding protein-B (GbpB) of Streptococcus mutans strain 5SM3. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions comprise major histocompatibilty complex (MHC) class II protein-binding GbpB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Dispitopic or multipeptopic polypeptides can be prepared synthetically or by recombinant bNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in passive immunisation.

Sequence 431 AA;

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Length 431; Score 93; DB 7; I Pred. No. 1.7e-06; 100.0%; Query Match Best Local Similarity

Matches

Š 요 ADX37272;

ADX372

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The invention relates to a composition comprising a fragment of a glucan binding protein-B (GbpB) and a biocompatible microparticle, where the fragment binds to a major histocompatibility complex (MHC) class II protein. The composition is useful for producing an antibody for immunizing mammala against dental caries. This sequence corresponds to a Streptococcus mutans GbpB protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
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microparticle; major histocompatibility complex; tooth disease.
                                                                immunogenicity; immune stimulation; glucan binding protein-B; microparticle; major histocompatibility complex; tooth disease.
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                                 Streptococcus mutant glucan binding protein B variant #2.
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100.0%; Pred. No. 1.7e-06;
iive 0; Mismatches 0;
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12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-0363209P.
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07-MAR-2003; 2003US-00383930
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21-APR-2005 (first entry)
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                                                                                                                       Streptococcus mutans
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(TAUB/) TAUBMAN M A.
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microparticle; major histocompatibility complex; tooth disease.
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                Streptococcus mutans
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(TAUB/) TAUBMAN M A.
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08-JAN-1999;
12-APR-1999;
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08-AUG-2002;
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10-FEB-2005

ADX37273

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RESULT 7 ADX37273

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The present invention relates to a computational method (M1) for identifying adhesin and adhesin-like proteins, by computing the sequence-based attributes of protein sequences using five attribute modules of a neural network software, training an artificial neural network (MNN) for each of the computed five attributes, and identifying the adhesin and adhesin adhesin and adhesin ad adhesin ad adhesin ad adhesin and adhesin ad adhesin ad adhesin ad adhesin ad adhesin ad adhesin ad adhesin ad adhesin ad adhesin ad adhesin ad adhesin ad adhesin ad adhesin ad adhesin ad adhesin ad adhesin ad adhesin 
    Computational method for identifying adhesin and adhesin like molecules, comprises computing sequence-based attributes of protein sequences using neural network software and training an artificial neural network.
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                                                                                               Claim 16; SEQ ID NO 210; 402pp; English
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08-AUG-2002; 2002US-0402483P.
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                                                                                                                                                                                                                                                                                                                                                                              New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing
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Pred. No. 1.7e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (COUL ) COUNCIL SCI & IND RES SOUTH AFRICA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; SEQ ID NO 33; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AEB91500 standard; protein; 431 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48 QQAAQAQVNTIQGQVSALQT 67
                                            13-APR-1998; 98US-0081550P.
08-JAN-1999; 99US-0115142P.
12-ARR-1999; 99US-0029049.
07-MAR-2002; 2002US-0363209P.
08-AUG-2002; 2002US-0402483P.
07-MAR-2003; 2003US-00383930.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
il Similarity 100.0%;
20; Conservative 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     mammals against dental caries.
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20-JUL-2004; 2004US-0589227P
    2004US-00797821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-FEB-2005; 2005WO-IN000037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                   Taubman MA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus mutans.
                                                                                                                                                                                                            SMITH D J.
TAUBMAN M A.
                                                                                                                                                                                                                                                                                                                                  WPI; 2005-151644/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2005-597835/61.
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Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 431 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2005076010-A2.
09-MAR-2004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-OCT-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-AUG-2005
                                                                                                                                                                                                                                                                                Smith DJ,
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(TAUB/)
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Gaps

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The present sequence is the protein sequence of the glucan binding protein. B (GbpB) of Streptococcus mutans strain 15JP2. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The compositions compositions and vaccines for dental caries. The compositions comprise major histocompatibility complex (WHC) class II protein-binding GbpB peptides, especially HLA-binding peptides, compositions are used in a claimed method of eliciting production of an antibody in a mammal. Dispitopic or multiepitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in
composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
                                                                                                                                                                                                                                                         Claim 5; Page 8; 49pp; English.
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100.0%; 100.0%; 20; Conservative Query Match Best Local Similarity Sequence 432 AA; 48 Matches

passive immunisation.

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Gaps ö

Length 432; 0; Indels

Score 93; DB 7; 1 Pred. No. 1.8e-06;

0; Mismatches

QQAAQAQVNTIQGQVSALQT 20 QOAAQAQVNTIQGQVSALQT 67 ઠે g

Streptococcus mutans glucan binding protein-B. ADD93652 standard; protein; 432 (first entry) 29-JAN-2004 ADD93652; RESULT 11

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07-MAR-2003; 2003WO-US006962 Streptococcus mutans WO2003075845-A2 18-SEP-2003 

Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.

07-MAR-2002; 2002US-0363209P.

(FORS-) FORSYTH INST.

Taubman MA; Smith DJ,

2003-845091/78. WPI; 2003-845091/7 GENBANK; AY046413. Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.

5; Page 8; 49pp; English. Claim

The present sequence is the protein sequence of the glucan binding protein-B (GbpB) of Streptococcus mutans strain 3SN1. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions commarise major histocompatibility complex (MHC) class II protein-binding GbpB peptides, especially HLA-binding peptides,

ő ö The invention relates to a composition comprising a fragment of a glucan binding protein-B (GbpB) and a biocompatible microparticle, where the fragment binds to a major histocompatibility complex (MHC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds to a Streptococcus mutans GbpB protein of the invention. New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries. covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Dispitopic or multispitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in passive immunisation. Gaps Gaps ö ; 0 immunogenicity; immune stimulation; glucan binding protein-B; microparticle; major histocompatibility complex; tooth disease. Length 432; Length 432; Indels Indels Streptococcus mutant glucan binding protein B variant #3. 100.0%; Score 93; DB 7; I 100.0%; Pred. No. 1.8e-06; Live 0; Mismatches 0; 100.0%; Score 93; DB 9; 100.0%; Pred. No. 1.8e-06; iive 0; Mismatches 0; Claim 3; SEQ ID NO 31; 73pp; English. ż 20 67 ADX37274 standard; protein; 432 ; 0 1 QQAAQAQVNTIQGQVSALQT 48 odaadadvintiocovsalot 08-JAN-1999; 99US-0115142P-12-APR-1999; 99US-00290049. 07-MAR-2002; 2002US-0363209P-08-AUG-2002; 2002US-0402483P-07-MAR-2003; 2003US-00383930. 09-MAR-2004; 2004US-00797821. 98US-0081550P (first entry) Local Similarity 100. Conservative Smith DJ, Taubman MA; Streptococcus mutans. (SMIT/) SMITH D J. (TAUB/) TAUBMAN M A. WPI; 2005-151644/16. Local Similarity ses 20; Conserv Sequence 432 AA; Sequence 432 AA; US2005031633-A1. 13-APR-1998; 08-JAN-1999; 21-APR-2005 10-FEB-2005 ADX37274; Query Match Query Match Best Loca Matches Best Loc Matches RESULT 12 ឧឧឧឧឧ g ð

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The present sequence is that of a peptide comprising amino acid residues 52-71 of the glucan binding protein-B (GbpB) of Streptococcus mutans 52-71 of the glucan binding protein-B (GbpB) of Streptococcus mutans strata AnD93649. The peptide binds to a major histocompatibility complex (MHC) class II protein. It was identified as a potential B cell epitope using a matrix-based algorithm for epitope prediction, which was used to search the primary amino acid sequence of GpbB for known MHC class II binding motifs. The peptide can be used in immunogenic compositions and subunit vaccines for dental caries. These comprise MHC class II protein-binding GbpB peptides covalently linked with peptide caubunits (preferably from the catalytic domain) of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Diepitopic or multiepitopic polypeptides can be raised against MHC class II binding fragments of GbpB can be used in passive immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                         Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
                                      Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
  Streptococcus mutans glucan binding protein-B peptide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunogenicity; immune stimulation; glucan binding protein-B;
microparticle; major histocompatibility complex; tooth disease.
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Pred. No. 4.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Prec. ... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADX37252 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 10; 49pp; English.
                                                                                                                                                                                              07-MAR-2003; 2003WO-US006962
                                                                                                                                                                                                                                   07-MAR-2002; 2002US-0363209P.
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                                                                             Streptococcus mutans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 AA;
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                                                                                                                                                                                                                                                                                                                                   Smith DJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New composition comprising a fragment of a glucan binding protein-B (GpB) that binds to MRC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
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                                                                                                                                                                                                                                                                                          immunogenicity; immune stimulation; glucan binding protein-B;
microparticle; major histocompatibility complex; tooth disease
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                                                                                                                                                                                                                                                     Streptococcus mutant glucan binding protein B variant #4.
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                                                                                                                                   ADX37275 standard; protein; 432 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADD93629 standard; peptide; 20 AA.
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                                QQAAQAQVNTIQGQVSALQT 67
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12-ARR-1999; 99US-00290049.
07-MAR-2002; 2002US-0363209P.
08-AUG-2002; 2002US-0402483P.
07-MAR-2003; 2003US-00383930.
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                                                                                                                                                                                                                                                                                                                                                        Streptococcus mutans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMITH D J.
TAUBMAN M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2005-151644/16.
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Matches 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-APR-1998;
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                                  48
                                                                                                                                                                          ADX37275;
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Search completed: January 25, 2006, 19:01:44 Job time : 68.2 secs

1 QAQVNTIQGQVSALQT 16

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5 OAQVNTIQGOVSALOT 20

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0; Gaps

Query Match 80.6%; Score 75; DB 9; Length 20; Best Local Similarity 100.0%; Pred. No. 4.5e-05; Matches 16; Conservative 0; Mismatches 0; Indels

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

January 25, 2006, 18:48:55; Search time 9.1 Seconds (without alignments) 211.465 Million cell updates/sec

1 QQAAQAQVNTIQGQVSALQT 20 US-10-797-821-8 93 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# STIMMARIES

		de			SUMMAKIES	
Result		Query				
No.	Score	Match	Length	8 ¦	ID	Description
-	57	61.3	392	7	G95258	secreted 45 kg pro
7	57	61.3	392	~	B98124	Btress
m	57	61.3	507	7	S05542	tical pr
4	48	51.6	825	~	S62042	probable membrane
Ŋ	48	51.6	2541	~	S11661	talin - mouse
9	46	49.5	259	~	G82865	conjugal tranšfer
7	46	49.5	454	~	AC0498	probable thiophene
80	46	49.5	456	N	E86903	hypothetical prote
6	46	49.5	461	7	7400ND	secreted 45K prote
10	46	49.5	1379	7	T13718	ρ
11	46	49.5	2427	7	T16613	
12	45	48.4	445	~	B40590	Ø
13	45	48.4	562	N	875308	DNA ligase (EČ 6.5
14	45	48.4	734	N	AH2359	Ģ
15	44	47.3	125	~	S74966	
16	44	47.3	393	~	S64733	retrovirus-related
17	44	47.3	434	~	AH1993	hypothetical prote
18	44	47.3	472	~	808509	cruciferin precurs
19	44	47.3		~	B35540	cruciferin 2/3 pre
20	43.5	46.8	7	Н	860735	splicing factor SF
21	43	46.2		7	A38085	S-layer glycoprote
22	43	46.2		~	T00931	hypothetical prote
23	43	46.2	454	N	C86055	hypothetical prote
24	43	46.2	454	7	AE0957	thiophene and fura
25	43	46.2	454	0	A98209	hypothetical prote
56	43	46.2	454	7	C65173	_
27	43	46.2	827	~	A37849	S-layer protein -
28	43	46.2	1474	~	T20488	hypothetical prote
29	42	45.2	112	7	S26221	cruciferin (clone

cruciferin (clone	hypothetical prote	hypothetical prote	hypothetical prote	Rabin3 - rat	cruciferin BnC2 -	conserved hypothet	probable ClpA/B-ty	conserved hypothet	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	gene 26 protein -	immunodominant typ
S26222	A72108	B86514	AD2555	I57546	\$25091	B75310	G83635	A10868	G90992	B85838	H64977	C81359	G84396	S34956	B42804
8	~	N	N	N	N	~	~	~	~	N	N	~	~	~	7
233	390	390	439	460	496	528	905	90	8	90	90	142	154	233	522
45.2	45.2	45.2	45.2	45.2	45.2	45.2	45.2	44.1	44.1	44.1	44.1	44.1	44.1	44.1	44.1
42	42	42	42	42	42	42	42	41	41	41	41	41	41	41	41
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

	RESULT 1
	G95258
	secreted 45 kd protein [imported] - Streptococcus pneumoniae (strain TIGR4)
	C; Species: Streptococcus pneumoniae
	C;Date: 03-Aug-2001 #sequence revision 03-Aug-2001 #text change 09-Jul-2004
_	C;Accession: G95258
_	R; Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heir
_	on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
	nson, T.; Hickey, B.K.; Holt, I.E.
	Science 293, 498-506, 2001

Science 2.91, 498-506, Z001
Ajauthors: Loftus, B.J.; Z001
A; Aithors: Loftus, B.J.; Morrison, A; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A; Reference number: A95000; MUD:21357209; PMID:11463916
A; Accession: G95258
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-392 <KUR>
A; Residues: 1-392 <KUR>
A; Residues: 1-392 <KUR>
A; Crosser-references: UNIPROT: Q97N55; UNIPROT: Q8DMY4; UNIPARC: UPI0000051B81; GB: AE005672; C; Genetics:

C;Genetics: A;Gene: SP2216

Length 392; 4; Indels Score 57; DB 2; Pred. No. 0.14; Query Match 61.3%; Score 57; DB Best Local Similarity 68.4%; Pred. No. 0.14 Matches 13; Conservative 2; Mismatches

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A;Gene: gsp-781

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A;Accession: S11661
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-251 <REE>
A;Cross-references: UNIPROT:P26039; UNIPARC:UPI00000273F0; EMBL:X56123; NID:g54257; PIDN
C;Keywords: cytoskeleton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conjugal transfer protein XFa0039 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Species: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: G82865
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC0498
probable thiophene and furan oxidation protein thdF [imported] - Yersinia pestis (strai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AC0498
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
Il, M.; Rucherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
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                                                                                                                                                                                                                                                                                          Length 2541;
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A,Title: Sequence and domain structure of talin.
A,Reference number: $11661; MUID:91015390; PMID:2120593
                                                                                                                                                                                                                                                                                             2
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Pred. No. 5.8;
1; Mismatches
                                                                                                                                                                                                                                                                                          30;
                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                   Query Match
51.6%; Score 48;
Best Local Similarity 64.7%; Pred. No. ...
Matches 11; Conservative 2; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 ÖKLÖLÖATTAĞĞÖMQALÖ 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1003 AAKASVPTIQDQASAMQ 1019
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Matches 10; Conservative
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A;Note: plasmid pXF5.1
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S62042
probable membrane protein YPL032c - yeast (Saccharomyces cerevisiae)
NiAlternate names: hypothetical protein P7102.17
C;Species: Saccharomyces cerevisiae
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: S62042
R;Dietrich, F.S.; Allen, E.; Araujo, R.; Aparicio, A.; Carpenter, J.; Churlet, Lin, A.; Lin, D.; Marathe, R.; Mirtipati, S.; Namath, A.; Oefner, P.; Petel, F.X.; submitted to the EMBL Data Library, December 1995
A;Reference number: S62026
A;Residues: 1825 and A;Residues: 1-825 and A
                                                                                                                                                                                                                                                                                                                                                          hypothetical protein, 54K - Enterococcus faecium
C;Species: Enterococcus faecium
C;Species: Enterococcus faecium
C;Species: Enterococcus faecium
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
E;Puerst, P.; Moesch, H.U.; Solioz, M.
Nucleic Acids Res. 17, 6724, 1989
A;Futle: A protein of unusual composition from Enterococcus faecium.
A;Reference number: S05542; MUID:89385998; PMID:2780297
A;Recession: S05542
A;Molecule: L507 <FUE>
A;Residues: 1-507 <FUE>
A;Residues: 1-507 <FUE>
A;Residues: 1-507 <FUE>
A;Rose-references: UNIPROT:P13692; UNIPARC:UPI000016F6FC; GB:X16421; EMBL:M26048; NID:gA;Note: the authors translated the codon CGT for residues 221 and 223 as Lys
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C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S11661
R;Rese, D.J.G.; Ades, S.E.; Singer, S.J.; Hynes, R.O.
Nature 347, 685-689, 1990
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Pred. No. 9.2;
6; Mismatches 5; Indels
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61.3%; Score 57; DB 2; Length 392; 68.4%; Pred. No. 0.14; ive 2; Mismatches 4; Indels
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C;Keywords: transmembrane protein
F;243-259/Domain: transmembrane #status predicted <TVM>
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39 QASAQSQIEALEGQVSAINT 58
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                                                                                                                                    1 OCAACACMITICGOVSALO 19
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Similarity 42.1%;
8; Conservative 6
Query Match
Best Local Similarity 68.4°
Matches 13; Conservative
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Best Local Similarity
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Deflux gene protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T13718
R;Xu, X.Z.; Wes, P.D.; Chen, H.; Li, H.S.; Yu, M.; Morgan, S.; Liu, Y.; Montell, C.
B;Xu, Chem. 273, 31297, 1998
A;Title: Retinal targets for calmodulin include proteins implicated in synaptic transmi:
A;Reference number: Z17709; MUID:99030403; PMID:9813038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: UNIPROT: Q9TX11; UNIPARC: UP10000084062; EMBL: Y17919; NID: 93893102; P.
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A;Experimental source: strain Bristol N2; clone K10B3
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A;Introns: 68/2; 96/3; 138/3; 665/3; 1052/3; 1104/3; 1173/2; 1995/2; 2187/3; 2235/2; 233
C;Superfamily: spectrin alpha chain; calmodulin repeat homology; SH3 homology; spectrin/
C;Keywords: EF hand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  flagellar distal capping protein homolog lafB - Vibrio parahaemolyticus CiSpecies: Vibrio parahaemolyticus CiSpecies: Vibrio parahaemolyticus CiDate: 12-May-1994 #sequence_revision 12-May-1994 #text_change 09-Jul-2004 CiAccession: B40590 R;McCarter, L.L.; Wright, M.E. A;Deater, L.L.; Wright, M.E. A;Title: Identification of genes encoding components of the swarmer cell flagellar motox A;Reference number: A40590; MUID:93273702; PMID:8501040
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Cibate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
Cibacession: Ti6613
RiGattung, S.
submitted to the EMBL Data Library, February 1996
A;Description: The sequence of C. elegans cosmid K10B3.
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F;2050-2155/Domain: spectrin/dystrophin repeat homology <SPR>
F;2277-2309/Domain: calmodulin repeat homology <EFH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein K10B3.10 - Caenorhabditis elegans
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Pred. No. 60;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: T13718
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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Pred. No. 33;
6; Mismatches
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1051 RSSQQAQITTLQSQVQSLE 1069
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A;Cross-references: UNIPROT:Q21408;
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Similarity 42.1%;
8; Conservative 6
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Best Local Similarity 52.6%;
Matches 10; Conservative
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E86503
By Protein usp45 [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: B86503
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Tille: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: E86903
A;Residues: 1-456 <STO>
A;Residues: 1-456 <STO>
A;Cross-references: UNIPROT:Q9CDJ1; UNIPARC:UPI00000C6BFC; GB:AE005176; FID:g12725296; F
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: usp45
A; Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A; Reference number: AB0001; MUD:21470413; PMID:11586360

A; Accession: AC0498

A; Status: preliminary

A; Residus: preliminary

A; Residus: 1-454 <KUR>
A; Residues: 1-454 <KUR>
A; Cross=references: UNIPROT:Q8Z9UZ; UNIPARC:UP1000013746C; GB:AL590842; PIDN:CAC93552.1;
C; Genetics:
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C;Species: Lactococcus lactis
C;Species: Lactococcus lactis
C;Date: 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: JN0097
R;van Asseldonk, M.; Rutten, G.; Oteman, M.; Siezen, R.J.; de Vos, W.M.; Simons, G.
Gene 95, 155-160, 1990
A;Title: Cloning of usp45, a gene encoding a secreted protein from Lactococcus lactis A;Reference number: JN0097; MUID:91071599; PMID:2123812
A;Accession: JN0097
A;Accession: JN0097
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Pred. No.
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Best Local Similarity 56.2%;
Matches 9; Conservative
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Matches 9; Conserv
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Search completed: January 25, 2006, 19:15:19 Job time : 10.1 secs
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DNA ligase (EC 6.5.1.-) s111583 - Synechocystis sp. (strain PCC 6803)

Nylternate names: protein s11583

C;Species: Synechocystis sp.

C;Species: Synechocystis sp.

A;Variety: PCC 6803

C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C;Accession: S75308

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, B.; Nakamura, Y.; Miyajima, N.;

C;Ki;Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: S75308
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-562 «KAN»
A;Cross-references: UNIPROT:P73196; UNIPARC:UPT00000D33EE; EMBL:D90904; GB:AB001339; NIE
C;Genetics:
A;Gene: 1ig
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A;Accession: AH2559
A;Accession: AH2559
A;Accession: Apper: DNA
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A;Residues: 1774 <KUR>
A;Cross-references: UNIPROT:Q8YMX7; UNIPARC:UPI00000CEB17; GB:BA000019; PIDN:BAB76131.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: al14432
hypothetical protein all4432 [imported] - Nostoc sp. (strain PCC 7120) C; Species: Nostoc sp. PCC 7120 C; Species: Nostoc sp. PCC 7120 C; Species: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004 C; Accession: AH3359 R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.;
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2; Mismatches 6; Indels
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C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: 874966
R;Raneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-125 <KAN>
A;Cross-references: UNIPROT:P72987; UNIPARC:UPI0000CCC65; EMBL:D90902; GB:AB001339; NIC
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
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Pred. No. 5.8;
2; Mismatches 3; Indels
                            IndelB
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                               3;
Best Local Similarity 47.1%; Pred. No. 25; Matches 8; Conservative 6; Mismatches
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229 AQAQLNDVKGRLEQLRT 245
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Best Local Similarity 66.7%;
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200.719 Million cell updates/sec
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Q9upx3
Q80tm2
                    GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                                     2166443 seqs, 705528306 residues
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05MZ12_STRMU
07MQ7_STRP8
08P318_STRP8
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09MZ4_STRMU
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Maximum Match 100%
Listing first 45 summaries
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93
1 QQAAQAQVNTIQGQVSALQT 20
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oryza sativ
neurospora
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rhodopseudo
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                                          sus scrofa
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"Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates.";

Infect. Immun. 69:6931-6941(2001).

EMBL, AY046414, AAX94504.1; -; Genomic_DNA.

InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.

PRINTS: PR05257; CHAP; 1.

PROSTTS: PR01825; SIBAPROTEIN.

PROSTTS: PR01825; SIBAPROTEIN.

SEQUENCE 431 AA; 44650 MW; 05D38D8D8BC4609F CRC64;
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0981g5
0911x4
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053nw8
078348
078348
09phg8
06md00
08ppa1
04ugx8
06ngy2
06ngy2
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STRAIN=58M3;
MEDLINE=21481971; PubMed=11598068;
DOI=10.11287A1.69.11.6931-6941.2001;
Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus mutans.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-PAR-2004 (TrEMBLrel. 26, Last annotation update)
Glucan-binding protein B.
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Last sequence update)
Last annotation update)
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100.0%; Pred. No. 2.3e-06;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                               431 AA
041.081_9BURK
0981.65_RHILO
0991.X4_PIG
04WYV3_ASPFU
0531WB_ORYSA
055876_9BACT
056876_9BACT
09PPGB_XYLPA
06MD0_PARUW
06PPA1_XANAC
04UQXB_XANCP
06N9H2_RHOPA
06N9H2_RHOPA
                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
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D (938V3 STRMU PRELIMINARY;
AC (938V3;
DT (01-DEC-2001 (TrEWBLrel: 19, Cr
DT (01-DEC-2004 (TrEWBLrel: 26, La
DT (01-MAR-2004 (TrEWBLrel: 26, La
DE Glucan-binding protein B.
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ID Q938VO_STRMU

AC Q938VO_CONTRMUNARY;

AC 01-DEC-2001 (TrEMBLrel. 19,

DT 01-DEC-2001 (TrEMBLrel. 19,

DT 01-DEC-2001 (TrEMBLrel. 19,

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DT 01-MAR-2004 (TrEMBLrel. 19,

CS STREPCOCCCUS MUTANS.

NOCLEOTIDE SEQUENCE.

RA JIN S., DUNCAN M.J., Taubmar RT 'Cloning of the gbpB gene fr 'Cloning of the gbpB gene fr 'Cloning of the gbpB gene fr 'Cloning of the gbpB gene fr 'Cloning of the gbpB gene fr 'Cloning of the gbpB gene fr 'Cloning of the STRAIN-SAN3;

RX MEDLINE-214617; Pubmed=11!

RX DOI=10.1128/1A1.69.11.6931-6931

RY Cloning of the Streptococcy protein B and analysis of granter Cloning of the Streptococcy protein B and analysis of granter Cloning of the Streptococcy protein B and analysis of Granter Pro; IPRO07921; CHAP.

RH INTERPOC; IPRO09148; SibA.

DR RININS; PRO1852; CHAP; 1.

SEQUENCE 431 AA; 44650 M
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Query Match
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MEDLINE=21153-617; PubMed=11254612;

DOI=10.1128/IAI.65-4.2493-2561.2001;

Chia J.S., Lee Y.Y., Huang P.T., Chen J.Y.;

"Identification of stress-responsive genes in Streptococcus mutans by differential display reverse transcription-PCR.";

Infect. Immun. 69:2493-2501(2001).
                                                                                                                                                                                                      "Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates."; Infect. Immun. 69:6931-6941(2001).

EMBL, AY046410, AXV84500.1; -; Genomic_DNA.

Interpro; IPR007921; CHAP.

Interpro; IPR009148; SibA.
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Chia J.S., Chang L.Y., Shun C.T., Chang Y.Y., Chen J.Y.;
"A 60-kilodalton immunodominant glycoprotein is essential for cell
wall integrity and the maintenance of cell shape in Streptococcus
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Immunodominant glycoprotein IDG-60 (Glucan-binding protein
                                                                                                                                                                                                                                                                                                                                                      Length 431;
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            Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                  Jin S., Duncan M.J., Taubman M.A., Smith D.J.; "Cloning of the gbpB gene from Streptococcus mutans."; J. Dent. Res. 79:224-224(2000).
                                                                                                                                                                                                                                                                                                                              44620 MW; 464FE3B563FB7E51 CRC64;
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Pred. No. 2.3e-06;
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100.0%; Pred. No. ...
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MEDLINE=21481977; PubMed=11598074;
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                                                                                                                                              STRAIN=SJ32;
MEDLINE=21481971; PubMed=11598068;
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PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
SEQUENCE 431 AA; 44650 MW;
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Q9AG98;
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Matches 20, Conservative
  Streptococcus mutans.
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                         Streptococcus.
NCBI_TaxID=1309;
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Duncan M.J.;
"Cloning of the Streptococcus mutans gene encoding glucan binding
protein B and analysis of genetic diversity and protein production in
clinical isolates.";
Infect. Immun. 69:6931-6941(2001).
EMBL; AF336445; AAK08104.1; -; Genomic_DNA.
EMBL; AY046411; AAK94501.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
FinterPro; IPR009148; SibA.
Pfam; PP05257; CHAP.
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STRAIN=UALS9 / ATCC 700610 / Serotype c;
STRAIN=UALS9 / ATCC 700610 / Serotype c;
MEDLINE=22295063; PubMed=12397186; DOI=10.1073/pnas.172501299;
Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Ajdic D.J., McShan W.M., Tian R., Kenton S., Jia H.G., Lin S.P.,
Qian Y., Li S., Zhu H., Najar F.Z., Lai H., White J., Roe B.A.,
Ferretti J.J.;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Putative secreted antigen GbpB/SagA; putative peptidoglycan
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Pred. No. 2.3e-06;
; Mismatches 0; Indels
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DOI=10.1128/IAI.69.11.6931-6941.2001;
Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
Chia J.-S., Chang L.-Y., Lee Y.-Y., Chen J.-Y.; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
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Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002).
EMEL: AR014855; AAN57811.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
Pfam; PF05257; CHAP; 1.
PRINTS; PR01852; SIBARROTEIN.
PROSITE; PS65011; CHAP; 1.
Complete proteome.
SEQUENCE 431 AA; 44620 MW; 2DICA685248CCD3E CRC64;
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                                                                                                                   STRAIN=3VF4;
Jin S., Duncan M.J., Taubman M.A., Smith D.J.;
"Cloning of the gbpB gene from Streptococcus mutans.";
J. Dent. Res. 79:224-224(2000).
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Pred. No. 2.3e-06;
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PROSITE; PS50911; CHAP; 1.
SEQUENCE 431 AA; 44592 MW;
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Duncan M.J.;

"Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates.";

Infect. Immun. 69:6931-6941(2001).

EMBL; AY046412; AA494502.1; -; Genomic_DNA.

InterPro; IPR007921; CHAP.

InterPro; IPR009148; SibA.

Pfam; PF05257; CHAP; 1.
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Borges F., Layec S., Thibessard A., Fernandez A., Gintz B., Hols P.,
Borges F., Layec S., Thibessard N.,
Decaris B., Leblond-Bourget N.,
T., Cse, a Chimeric and Variable Gene, Encodes an Extracellular Protein
Involved in Cellular Segregation in Streptococcus thermophilus.";
J. Bacteriol. 187:2737-2746(2005).
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Nat. Biotechnol. 22:1554-1558 (2004).
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Bolotin A., Quinquis B., Renault P., Sorokin A., Ehrlich S.D.,
Kulakauskas S., Lapidus A., Golteman E., Mazur M., Pusch G.D.,
Fonstein M., Overbeek R., Kyprides N., Purnelle B., Prozzi D.,
Ngui K., Masuy D., Hancy P., Burteau S., Boutry M., Delcour J.,
Goffeau A., Hols P.;
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 93; DB 2; Length 432;
Pred. No. 2.3e-06;
                                                                                                             Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
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Pred. No. 0.027;
2; Mismatches 3; Indels
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Glucan binding protein (PosB).
Name=posB; OrderedLocusNames=stu0022;
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100.0%; Score 93; DE
Best Local Similarity 100.0%; Pred. No. 2.3
Matches 20; Conservative 0; Mismatches
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EMBL; CP000023; AAV59752.1; -; Genomic_DNA.

EMBL; AY730643; AAW82375.1; -; Genomic_DNA.

Interpro; IPR007921; CHAP.

Interpro; IPR009148; SibA.

PF05257; CHAP: 1.
                                       MEDLINE=21481971; PubMed=11598068;
DOI=10.1128/IAI.69.11.6931-6941.2001;
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PROSITE; PSS0911; CHAP; 1.
SEQUENCE 432 AA; 44648 MW;
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PROSITE; PS50911; CHAP; 1.
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QSM6K4;
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Best Local Similarity 75.0°
Matches 15, Conservative
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NUCLEOTIDE SEQUENCE.
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   Gaps
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Pred. No. 2.3e-06;
Mismatches 0; Indels
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DOI=10.1128/IAI.69.11.6931-6941.2001;
Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
   Indels
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Bacteria, Pirmicutes, Lactobacillales, Streptococcaceae,
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Jin S., Duncan M.J., Taubman M.A., Smith D.J.;
"Cloning of the gbp8 gene from Streptococcus mutans.";
J. Dent. Res. 79:224-224(2000).
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Jin S., Duncan M.J., Taubman M.A., Smith D.J.;
"Cloning of the gbpB gene from Streptococcus mutans.";
J. Dent. Res. 79:224-224 (2000).
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Glucan-binding protein B.
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01-DEC-2001 (TYEWBLrel. 19, Last sequence update)
01-MAR-2004 (TYEMBLrel. 26, Last annotation update)
Glucan-binding protein B.
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EMBL; AX046413; AAK94503.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
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PRINTS; PR01852; SIBAPROTEIN.
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Q938V1;
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20; Conservative
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NCBI_TaxID=1309;
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Gaps

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Length 398;

DB 2;

0.92;

Score 58; Pred. No. 0

62.4%;

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398 AA; 42028 MW; 5DCEDA78CB863B60 CRC64;
PRINTS; PRO1852; SIBAPROTEIN. PROSITE; PS50911; CHAP; 1. Complete proteome. SEQUENCE 398 AA; 42028 MW;
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Matches 12; Conservative
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PubMed=15272401; DOI=10.1086/422697;
PubMed=15272401; DOI=10.1086/422697;
Banks D.J., Porcella S.F., Barbian K.D., Beres S.B., Philips L.E.,
Voyich J.M., Deleo F.R., Martin J.M., Somerville G.A., Musser J.M.;
"Progress toward characterization of the group A Streptococcus
"Progress complete genome sequence of a macrolide-resistant serotype
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Nat. Biotechnol. 22:1554-1558(2004).
EMBL; CD000024; AAV61641.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR00918; SibA.
                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLBORIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
PubMed=15543133; DOI=10.1038/nbt1034;
Bolotin A., Quinquis B., Renault P., Sorokin A., Ehrlich S.D.,
Kulakauskas S., Lapidus A., Goltsman E., Mazur M., Pusch G.D.,
Fonstein M., Overbeek R., Kyprides N., Purnelle B., Prozzi D.,
Ngui K., Masuy D., Hancy F., Burteau S., Boutry M., Delcour J.,
Goffeau A., Hols P.;
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                Streptococcus thermophilus (strain CNRZ 1066).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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01-FBB-2005 (TrEMBLrel. 29, Last sequence update)
01-FBB-2005 (TrEMBLrel. 29, Last annotation update)
Glucan binding protein.
Name=pcsB, OrderedLocusNames=str0022;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Secreted protein.
OrderedLocusNames=M6_Spy0017;
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EMBL; CP000003; ART86122.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR001948; SLDA.
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PROSITE; PS50911; CHAP; 1.
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Q5XEL1 STRP6 PRELIMINARY;
Q5XEL1;
                                                                                                                                                    QSM212_STRT1 PRELIMINARY;
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NCBI_TaxID=299768;
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Q5M212
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STRAIN=SF370 / ATCC 700294 / Serotype M1;
STRAIN=SF370 / ATCC 700294 / Serotype M1;
MEDLINE=21192684; PubMed=11296265; DOI=10.1073/pnas.071559398;
MEDLINE=21192684; PubMed=11296265; DOI—10.1073/pnas.071559398;
Perretti J.J., McShan W.M., Adidic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.E.;
"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
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"Identification and characterization of a novel secreted protein from group A streptococcus.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AR319999; AAL73158.1; -; Genomic_DNA.
InterPro; IPR009121; CHAP.
InterPro; IPR009148; SibA.
Pfam; PF05257; CHAP:
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Pred. No. 0.92;
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae;
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O7CNO7_STRP8 PRELIMINARY; PRT; 398 AA.
O7CNO7;
O5CNO7;
O5-JUL-2004 (TrEMBLrel. 27, Created)
O5-JUL-2004 (TrEMBLrel. 27, Last sequence update)
O5-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative secreted protein.
OrderedLocusNames=spyMl8 0020;
Streptococcus pyogenes (serotype Ml8).
                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
                                                                                                                                                                                                                                                                              398 AA
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45 QKAAQNQVSALQAQVSSLQS 64
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OrderedLocusNames=SPy0019;
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Pfam; PF05257; CHAP; 1.
PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
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                                                                                                                                           Query Match
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MEDLINE=22683278; PubMed=12799345; DOI=10.1101/gr.1096703;
Makagawa I., Kurokawa K., Yamaashita A., Nakata M., Tomiyagu Y.,
Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
Hayashi H., Hattori M., Hamada S.;
"Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
intage-scale genomic rearrangement in invasive strains and new insights
into phage evolution.";
                                                                                                                                                       Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S., Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.P., Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q., Kapur V., Daly J.A., Veasy L.G., Musser J.M.; Rome sequence and comparative microarray analysis of serotype MI8 group A Streptococcus strains associated with acute rheumatic fever
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                                                                                                                 STRAIN=MGAS8232 / Serotype M18;
MEDLINE=21927593; Pubmed=11917108; DOI=10.1073/pnas.062526099;
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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InterPro; IPR009212; -; Genomic_DNA.
InterPro; IPR00921; CHAP.
InterPro; IPR009148; SibA.
                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673 (2002).
EMBL, AR009955; AAL56849.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
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PROSITE; PSS0911; CHAP; 1.
Complete proteome.
SEQUENCE 398 AA, 42028 MW;
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Q8P318; Q7CFL7;
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Best Local Similarity 60.0°
Matches 12, Conservative
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                                             NCBI TaxID=301451;
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"Genome of the bacterium Streptococcus pneumoniae strain R6.";
                                                                          62.4%; Score 58; DB 2; Length 398; 60.0%; Pred. No. 0.92; ive 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 57; DB 2; Length 392;
Pred. No. 1.3;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=gsp-781; OrderedLocusNames=spr2021;
Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                       398 AA; 42028 MW; 5DCEDA78CB863B60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        392 AA; 41697 MW; B5A5A860FAEA77DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
General stress protein GSP-781.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                         392 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Bacteriol. 183:5709-5717(2001).
EMBL, ARONGS66; AALON823.1; -; Genomic_DNA.
PIR; B98124; B98124.
PIR; G95258; G95258.
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45 QKAAQNQVSALQAQVSSLQS 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS, PR01852; SIBAPROTEIN.
PROSITE, PS50911; CHAP; 1.
Complete proteome.
SEQUENCE 392 AA; 41697 MW:
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InterPro; IPR009148; SibA.
                                                                                                                                                                                                                                                                                                                                                                                   QBDMY4_STRR6 PRELIMINARY;
Q8DMY4;
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Q97N55;
                                                                                                    Local Similarity 60.0 tes 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
Complete proteome. SEQUENCE 398 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=171101;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                              MEDINE-21357209; PubMed=11463916; DOI=10.1126/science.1061217; MEDINE=21357209; PubMed=11463916; DOI=10.1126/science.1061217; MEDINE=21357209; PubMed=11463916; DOI=10.1126/science.1061217; Peterson S.N., Heidelberg J.F., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M.L., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtzapple B.K., Khouri H.M., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Feldblyum T.V., Angiuoli S.V., Dickinson T., Hickey B.K., Holt I.B., Loftus B.J., Yang F., Smith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.; "Complete genome sequence of a virulent isolate of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P54 protein precursor.
Enterococcus faecium (Streptococcus faecium).
Bacteria, Pirmicutes, Lactobacillales, Enterococcaceae, Enterococcus.
NCBI_TaxID=1352;
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NUCLEOTIDE SEQUENCE [GENOMIC DNA].

MUCLEOTIDE 99385998; PubMed=2780297;

Fuerst P., Moesch H.-U., Solioz M.;

Fuerst P., Moesch H.-U., Solioz M.;

Nucleic Acids Res. 17:6724-6724(1989).

-! SUBCELLULAR LOCATION: Attrached to the cell wall.

-! SINCELLULAR ELOCATION: Attrached to the cell wall.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.3%; Score 57; DB 2; Length 392; 68.4%; Pred. No. 1.3; tive 2; Mismatches 4; Indels
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        392 AA; 41697 MW; B5A5A860FAEA77DD CRC64;
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PIR; S05542; S05542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1990 (Rel. 13, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 516 AA.
                                                                                                                                                                                                                                                                                         Ecience 293:498-506(2001).

EMBL; AE007509; AAK76264.1; -; Genomic_DNA.
PIR; B98124; B98124.

PIR; G95258; G95258.

TIGR; SP2216; -.
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P54 protein.
Potential.
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Pfam; PP00877; NLPC P60; 1.
Cell wall; Signal.
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PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS050911; CHAP; 1.
Complete proteome.
SEQUENCE 392 AA; 41697 MW;
                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
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Best Local Similarity 68...
Lag 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                    NUCLEOTIDE SEQUENCE.
                   Streptococcus.
NCBI_TaxID=1313;
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P13692;
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Gaps
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                             61.3%; Score 57; DB 1; Length 516; 50.0%; Pred. No. 1.7;
                                                                 Indels
516 AA; 54596 MW; 402ECAA439846D26 CRC64;
                                                                 6; Mismatches
                                                Best Local Similarity 50.0 Matches 10; Conservative
 SEQUENCE
                                Query Match
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1 QQAAQAQVNTIQGQVSALQT 20 셤

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| :||:|: ::||||: | 48 QASAQSQIEALEGQVSAINT 67

Search completed: January 25, 2006, 19:13:40 Job time : 71.3 secs

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Sequence 51; Appl
Sequence 51, Appl
Sequence 609, Ap
Sequence 6472, Ap
Sequence 10850, A
Sequence 10850, A
Sequence 20035, A
Sequence 20035, A
Sequence 201, App
Sequence 201, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7380, Ap
10542, A
46, Appl
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Sequence 47, Appl
Sequence 2, Appli
Sequence 51, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51, Appl
51, Appl
51, Appl
5095, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 67, Appl
                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                     January 25, 2006, 18:50:05 ; Search time 16.6 Seconds (without alignments) 99.609 Million cell updates/sec
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.: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*

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:: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

:: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

:: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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S-08-885-291-51

S-09-496-672-51

S-09-107-532A-5095

S-09-543-611A-5472

S-09-543-611A-5472

S-09-543-611A-5472

S-09-252-991A-20035

S-09-252-991A-20035

S-09-270-767-4545

S-09-198-452A-201
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5-09-543-681A-7380
5-09-902-540-10542
5-09-562-737-46.
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3-09-562-737-41
3-09-562-737-47
3-08-186-222-2
                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-562-737-42
US-09-562-737-50
                                                                                                                                                            572060 segs, 82675679 residues
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Maximum Match 100%
Listing first 45 summaries
                                    OM protein - protein search, using sw model
                                                                                         US-10-797-821-8
93
1 QQAAQAQVNTIQGQVSALQT 20
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Gapop 10.0 , Gapext 0.5
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Maximum DB
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No.
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US-09-68-110-4374

1 Sequence 4374, Application US/09583110

2 Sequence 4374, Application US/09583110

3 Patent No. 6699703

4 GENERAL INFORMATION:

3 APPLICANT:

4 ITILE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

5 ITILE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

7 ITILE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

7 ITILE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

7 ITILE OF INVENTION: Number: US/09/583,110

7 CURRENT APPLICATION NUMBER: US 60/085,131

7 PRIOR PILING DATE: 1998-06-30

7 PRIOR FILING DATE: 1998-05-12

7 PRIOR FILING DATE: 1997-07-02

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Sequence 12740, A Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 32563, A Sequence 47780, A Sequence 3373, Ap Sequence 43237, A Sequence 13, Appl Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 30645, A Sequence 2, Appli Sequence 2, Appli Sequence 30645, A Sequence 2, Appli Sequence 2, Appli Sequence 30645, A Sequence 30645, A Sequence 30645, A Sequence 2, Appli
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| Sequence 67, Application US/09222938A
| Sequence 67, Application US/09222938A
| Patent No. 6437108
| Patent No. 6437108
| APPLICANT: INFORMATION: Philip
| APPLICANT: Pritz, Chrisian
| APPLICANT: Murphy, Christopher
| APPLICANT: Guzman, Luz-Maria
| TITLE OF INVENTION: ESSENTAL BACTERIAL GENES AND THEIR USE
| TITLE OF INVENTION: ESSENTAL BACTERIAL GENES AND THEIR USE
| CURRENT PRILIG DATE: 1998-12-30
| NUMBER OF SEQ ID NOS: 102
| SOFTWARE: PastSEQ for Windows Version 3.0
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US-09-489-039A-12740
US-09-572-191-2
US-09-723-262-2
US-09-723-219-2
US-09-723-219-2
US-09-700-767-32563
US-09-700-767-47780
US-09-583-110-3373
US-09-107-433-3863
US-09-902-540-16445
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48 QGEAQKQVDQIQEQVSAIQ 66
       Query Match
Best Local Similarity
Matches 13; Conserv
       US-09-222-938A-67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.8%; Score 50; DB 2; Length 1024; 70.6%; Pred. No. 6.9; tive 1; Mismatches 4; Indels
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Patent No. 6428967

GENERAL INFORMATION

APPLICANT: Herz, Joachim

APPLICANT: Gotthardt, Michael

TITLE OF INVENTION: LDL Receptor Signaling Pathways

FILE REFERENCE: UTSW0708

CURRENT APPLICATION NUMBER: US/09/562,737

CURRENT PILING DATE: 2000-05-01

NUMBER OF SEQ ID NOS: 132

SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
US-09-562-737-47
Squence 47, Application US/09562737
Patent No. 6428967
GENERAL INFORMATION:
APPLICANT: Herz. Joachim
APPLICANT: Gotthardt, Michael
TITLE OF INVENTION: LD. Receptor Signaling Pathways
FILE REFERENCE: UTSW0708
CURRENT APPLICATION NUMBER: US/09/562,737
                                                                                                     GENERAL INCOMPATION:
APPLICANT: Herz, Joachim
APPLICANT: Herz, Joachim
APPLICANT: Getthardt, Michael
APPLICANT: GOTHARDT, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REFERENCE: UTSW0708
CURRENT APPLICATION NUMBER: US/09/562,737
CURRENT FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SOFTWARE: PatentIn Ver. 2.1
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Pred. No. 15;
2; Mismatches
                                                              Sequence 45, Application US/09562737 Patent No. 6428967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1003 AAKASVPTIQDQASAMQ 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 || | | | || || || || || || || || 1003 AATASVPTIQDQVSAMQ 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 AAQAQVNTIQGQVSALQ 19
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TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 51.6%;
Best Local Similarity 64.7%;
Matches 11; Conservative ;
                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                            SEQ ID NO 45
LENGTH: 1024
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US-09-562-737-41
                                           US-09-562-737-45
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Matches
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                                                                                                                                                                                                                                                                                       RESULT 3
US-09-107-433-3230
US-09-107-433-3230
; Sequence 3230, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; TITLE OF INVENTION: NEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                       Query Match 61.3%; Score 57; DB 2; Length 392; Best Local Similarity 68.4%; Pred. No. 0.15; Matches 13; Conservative 2; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: GENOME THERAPEUTICS CORPORATION STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: CD/ROM SO9660
COMPUTER: CUNKNOWN>
OPERATING SYSTEM: cUnknown>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...399
SEQUENCE DESCRIPTION: SEQ ID NO: 3230:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 893-8277
INFORMATION FOR SEQ ID NO: 3230:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/ 085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 399 amino acids TYPE: amino acid
                                                                                                                                                                                                        48 QQEAQKQVDQIQEQVSAIQ 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55 QQEAQKQVDQIQEQVSAIQ 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-107-433-3230
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US-08-816-693A-51
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                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: Synthetic COTHER INFORMATION: Sequence US-09-562-737-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/186,222
                                                                                                                                                                                                                                                                                                                                                                              KESULT 7
US-08-186-222-2
; Sequence 2, Application US/08186222
; Patent No. 5559007
; GENERAL INFORMATION:
; APPLICANT: Suri, Bruno
; TITLE OF INVENTION: Bacterial Vectors
; NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSES: ADDRESS:
ADDRESSES: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STREET: New York
COUNTRY: USA
ZIF: 10532
COMPUTER PERSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/672,205
FILING DATE: 19-MAR-1991
APPLICATION NUMBER: GB 9006400.7
FILING DATE: 22-MAR-1990
ATTORNEY/AGENT INPORMATION:
NAME: Villamicar, John
REGISTATION NUMBER: 30,598
REFERENCE/DOCKET NUMBER: 4-17994/A
TELECOMMUNICATION INPORMATION:
CURRENT FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 47
LENGTH: 1024
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                   3 AAQAQVNTIQGQVSALQ 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 461 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (914)347-5769
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 461 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Indels
Sequence 51, Application US/08816693A; Sequence 51, Application US/08816693A; Patent No. 2874241; GENERAL INFORMATION:
APPLICANT: Takahashi, Joseph S; APPLICANT: Turek, Fred W
APPLICANT: Pinto, Lawrence H
ITILE OF INVENTION: Clock Gene and Gene Product; NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rockey, Milnamow & Katz STREET: Two Prudential Plaza, Suite 4700; CITY: Chicago
CITY: USA
                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRATT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,693A
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Sequence 51, Application US/08885291A

Sequence 51, Application US/08885291A

Sequence 51, Application US/08885291A

GENERAL INFORMATION:

APPLICANT: Takahashi, Joseph S.

APPLICANT: Takahashi, Joseph S.

TITLE OF INVENTION: CLOCK GENE AND GENE PRODUCT

FILE REFERENCE: 0290-5

CURRENT APPLICATION NUMBER: US/08/885, 291A

CURRENT FILING DATE: 1997-03-13

SOFTHARE: PATENTH: 1997-03-13

SOFTHARE: PatentIn Ver. 2.0

SEQ ID NO 51

THENTH: 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5874241chrup, Thomas
REGISTRATION NUMBER: 33,268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     545 QRAAQPQLVQLQGQISTQVT 564
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TELEPHONE: 312-616-5400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 747 amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 50.0%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Mus musculus
US-08-885-291-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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Sequence 5472, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709-1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
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US-09-562-737-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 43, Application US/09562737
; Patent No. 642867
; GERREAL INFORMATION:
APPLICANT: Herz, Joachim
; APPLICANT: Getthardt, Michael
; TITLE OF INVENTION: LDL Receptor Signaling Pathways
; TITLE REFERENCE: UTSW0708
; CURRENT FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 43
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-8277
INFORMATION FOR SEQ ID NO: 5095:
SEQUENCE CHARACTERISTICS:
LENGTH: 525 amino acids
TYPEL amino acid
TOPELOCY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 47.6%; Pred. No. 18;
Matches 10; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                          ) NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...525
; SEQUENCE DESCRIPTION: SEQ ID NO: 5095:
US-09-107-532A-5095
                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48 QQADAQSQIDALESQVSEINT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QOA-AQAQVNTIQGQVSALQT 20
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 62.5
Matches 10; Conservative
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US-09-543-681A-5472
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Patent No. 6583275
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A DOUCETTO ACID ANINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES AND THÜRAPEUTICS
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THÜRAPEUTICS
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                         DB 2; Length 747;
22;
                                                                        6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                 Sequence 51, Application US/09496672
Patent No. 6291429
GENERAL INFORMATION:
APPLICANT: Takahashi, Joseph S.
APPLICANT: Takahashi, Joseph S.
APPLICANT: Turek, Fred W.
TITLE OF INVENTION: CLOCK GENE AND GENE PRODUCT;
FILE REFERENCE: 0.290-5;
CURRENT APPLICATION NUMBER: US/09/496,672
CURRENT FILING DATE: 1097-06-30;
PRIOR FILING DATE: 1997-06-30;
PRIOR FILING DATE: 1997-03-13;
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin Ver. 2.0
SSOFTWARE: Patentin Ver. 2.0
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MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: CD/ROM ISO9660
COMPUTER: COPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                        4; Mismatches
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FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                            Score 46;
Pred. No.
                                                                                                                                              |:||| |: :|||: |
545 QRAAQPQLVQLQGQISTQVT 564
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545 QRAAQPQLVQLQGQISTQVT 564
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STATE: Massachusetts
COUNTRY: USA
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                            50.08;
                         Query Match
Best Local Similarity 50.0°
Matches 10; Conservative
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ORGANISM: Mus musculus
US-09-496-672-51
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US-09-107-532A-5095
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US-09-496-672-51
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Sequence 10850, Application US/09949016

Patent No. 6812339

GENERAL INPORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

SEQ ID NOS: 207012

SOFTWARE: PASESEQ for Windows Version 4.0

LENGTH: 773
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| Sequence 10762, Application US/09489039A
| Sequence 10762, Application US/09489039A
| Sequence 10762, Application US/09489039A
| Sequence 10762, Application Editor Inc. 6610836
| GENERAL INFORMATION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
| TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
| FILE REFERENCE: 2709.2004001
| CURRENT APPLICATION NUMBER: US/09/489,039A
| CURRENT FILING DATE: 2000-01-27
| PRIOR APPLICATION NUMBER: US 6/117,747
| PRIOR FILING DATE: 1999-01-29
| NUMBER OF SEQ ID NOS: 14342
| LENGTH: 231
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                                                                                                                                                                                                                Query Match 47.3%; Score 44; DB 2; Length 94; Best Local Similarity 45.0%; Pred. No. 4.2; Matches 9; Conservative 6; Mismatches 5; Indels
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PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 6344
SEQ ID NO 5472
LENGTH: 94
                                                                                                     ; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5472
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Search completed: January 25, 2006, 19:18:14 Job time : 16.6 secs

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RESULT 2
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33, Appl
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67, Appl
                                                                                               January 25, 2006, 19:13:51; Search time 60 Seconds (without alignments) 139.276 Million cell updates/sec
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(cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd
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US-10-797-821-8
US-10-383-930-29
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US-10-211-962-41
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US-10-719-993-535
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                                                                                                                                                                                                                                                                                            1867569 seqs, 417829326 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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Match Length DB
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No.
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28 48 51.6 2541 5 US-10-719-993-536 Sequence 536, App 29 48 51.6 2541 5 US-10-287-436A-460 Sequence 1259, Ap 31 47 50.5 214 5 US-10-287-436A-460 Sequence 1259, Ap 32 47 50.5 218 5 US-10-287-436A-129 Sequence 1259, Ap 32 47 50.5 378 5 US-10-820-155-28 Sequence 28, Appl 34 46 49.5 378 5 US-10-820-155-62 Sequence 28, Appl 35 46 49.5 378 6 US-10-029-386-3377 Sequence 29, Appl 36 49.5 354 4 US-10-28-122A-78518 Sequence 26, Appl 37 46 49.5 1379 6 US-110-282-122A-78518 Sequence 78518, Appl 37 46 49.5 1379 6 US-11-097-143-261 Sequence 6734, Ap 39 45.5 48.4 1024 4 US-10-282-122A-59037 Sequence 6734, Ap 40 45 48.4 1024 4 US-10-28-122A-568 Sequence 6734, Ap 41 44 47.3 502 4 US-10-393-176 Sequence 176, Appl 44 47.3 502 4 US-10-437-963-176 Sequence 125588, Appl 45 48.4 1024 4 US-10-28-223-176 Sequence 125588, Appl 45 48.4 1024 4 US-10-28-23-176 Sequence 6722, Ap 44 47.3 502 4 US-10-437-963-125588 Sequence 125588, Appl 45 45 46.8 70 3 US-09-864-761-43799 Sequence 125588, Appl 45 45 46.8 70 3 US-09-864-761-43799
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#### ALIGNMENTS

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Sequence 8, Application US/1079821
; Publication No. US20050031633A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Daniel J.
; APPLICANT: Taubman, Martin A.
; TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens
; TITLE REFERENCE: 25669-020
; CURRENT APPLICATION NUMBER: US/10/797, 821
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: 60/363,209
; PRIOR FILING DATE: 2002-03-07
; PRIOR FILING DATE: 2002-03-07
; PRIOR FILING DATE: 2002-03-07
; PRIOR FILING DATE: 2002-08-08
; PRIOR FILING DATE: 2002-08-08
; PRIOR PLILNG DATE: 2002-08-08
; PRIOR PLILNG DATE: 2002-08-08

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; SEQ ID NO 30
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-10-383-930-30
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Matches 20; Conservative
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; Publication No. US20040127400A1
; Publication No. US20040127400A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Daniel J
; APPLICANT: Smith, Daniel J
; TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
; FILE REFERENCE: 25669-018
; CURRENT APPLICATION NUMBER: US/10/383,930
; CURRENT FILING DATE: 2003-03-07
; PRIOR FILING DATE: 2003-03-07
; PRIOR PILING DATE: 2002-03-07
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
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100.0%; Score 93; DB 4; I
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 20; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 7.6e-08;
Matches 20; Conservative 0; Mismatches 0;
PRIOR FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: 60/081,550
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR PILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.2
SEQ ID NO 8
LENGTH: 20
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; OTHER INFORMATION: GbpB peptide
US-10-797-821-8
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; ORGANISM: Streptococcus mutans
US-10-383-930-29
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ORGANISM: Artificial
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US-10-383-930-29
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APPLICANT: Smith, Daniel J.
APPLICANT: Smith, Daniel J.
APPLICANT: Smith, Daniel J.
APPLICANT: Smith, Daniel J.
TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens;
FILE REFERENCE: 25669-020
CURRENT APPLICATION NUMBER: US/10/797,821
CURRENT FILING DATE: 2004-03-09;
PRIOR PELING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: 10/383,930
PRIOR PELING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: 60/462,483
PRIOR PELING DATE: 2002-08-08
PRIOR PELING DATE: 1999-04-12
PRIOR PELING DATE: 1999-04-12
PRIOR PELING DATE: 1999-04-13
PRIOR PELING DATE: 1999-04-13
PRIOR PELING DATE: 1999-01-08
NUMBER: 60/115,142
PRIOR PELING DATE: 1999-01-08
NUMBER: PALOR NUMBER: 60/115,142
PRIOR PELING DATE: 1999-01-08
NUMBER: PALOR NUMBER: 60/115,142
PRIOR PELING DATE: 1999-01-08
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PRIOR PELING DATE: 1999-01-08
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NUMBER: PALOR NUMBER: 60/115,142
PRIOR PELING DATE: 1999-01-08
NUMBER: PALOR NUMBER: 60/115,142
PRIOR PELING DATE: 1999-01-08
NUMBER: PALOR NUMBER: 60/115,142
PRIOR PELING DATE: 1990-01-08
NUMBER: PALOR NUMBER: 60/115,142
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APPLICANT: Taubman, Martin A
TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
FILE REFERENCE: 25669-018
CURRENT PELIKO DATE: 2003-03-07
FRIOR PPLICATION NUMBER: 60/402,483
FRIOR APPLICATION NUMBER: 60/402,483
FRIOR APPLICATION NUMBER: 60/363,209
FRIOR APPLICATION NUMBER: 60/363,209
FRIOR APPLICATION NUMBER: 60/363,209
FRIOR APPLICATION NUMBER: 60/363,209
FRIOR APPLICATION NUMBER: 41
SOGTWARE: PAGNIT VETSION 3.2
SEQ ID NOS: 41
SOGTWARE: PAGNIT VETSION 3.2
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       Length 431;
                                                                           Indels
Score 93; DB 4; 1 Pred. No. 2.3e-06;
   Query Match
100.0%; Score 93; DB
Best Local Similarity 100.0%; Pred. No. 2.3
Matches 20; Conservative 0; Mismatches
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; Publication No. US20040127400A1
; GENERAL INFORMATION:
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; Publication No. US20050031633A1
; GENERAL INFORMATION:
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US-10-383-930-33
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US-10-383-930-31
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## APPLICANT: Smith, Daniel J.

## APPLICANT: Smith, Daniel J.

## APPLICANT: Taubman, Martin A.

## TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens

## TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens

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## TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens

## TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens

## TITLE OF INVENTION NUMBER: 10/383,930

## PRIOR FILING DATE: 2002-08-08

## PRIOR FILING DATE: 1999-04-12

## PRIOR PELICATION NUMBER: 60/081,550

## PRIOR PELICATION NUMBER: 60/081,550

## PRIOR PELING DATE: 1999-04-13

## PRIOR FILING DATE: 1999-01-08

## NUMBER OF SEQ ID NOS: 45

## SOFTWARE: PatentIn Version 3.2

## ILENGTH: 431

## TITLE OF TIT
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; Publication No. US20050031633A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Daniel J.
; APPLICANT: Taubman, Martin A.
; TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens; TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens; TITLE OF INVENTION NUMBER: US/10/797,821
; CURRENT PELICATION NUMBER: US/209
; PRIOR APPLICATION NUMBER: 10/333,209
; PRIOR APPLICATION NUMBER: 60/402,483
; PRIOR APPLICATION NUMBER: 60/402,483
; PRIOR FILING DATE: 2002-03-07
; PRIOR FILING DATE: 2002-03-07
; PRIOR FILING DATE: 1999-04-12
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100.0%; Score 93; DB 5; I
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 20; Conservative 0; Mismatches 0;
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; Sequence 30, Application US/10797821
; Sequence 10, Application US/107821
; GENERAL INFORMATION:
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                                     TYPE: PRT; ORGANISM: Streptococcus mutans US-10-797-821-29
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LENGTH: 431
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; Publication No. US20040127400A1
; General INFORMATION:
; APPLICANT: Smith, Daniel J
; APPLICANT: Taubman, Martin A
; TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
; FILE REPERENCE: 25669-018
; CURRENT APPLICATION NUMBER: US/10/383,930
; CURRENT FILING DATE: 2003-03-07
; PRIOR PLILNG DATE: 2003-08-08
; PRIOR PLLING DATE: 2002-08-08
; PRIOR PLLING DATE: 2002-08-08
; RIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin version 3.2
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; Sequence 32, Application US/10383930
; Publication No. US20040127400A1
; GENERAL INFORMATION.
    APPLICANT: Smith, Daniel J
    APPLICANT: Taubman, Martin A
    TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
    FILE REFERENCE: 25669-018
; CURRENT APPLICATION NUMBER: US/10/383,930
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: 60/402,483
PRIOR PILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/363,209
; PRIOR APPLICATION NUMBER: 60/363,209
; RIUNG DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin Version 3.2
; SEQ ID NOS: 41
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PRIOR APPLICATION NUMBER: 60/081,550
PRIOR FILING DATE: 1998-04-13
PRIOR PRILING DATE: 1999-04-13
PRIOR PLING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.2
SEQ ID NO 33
LENGTH: 431
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; ORGANISM: Streptococcus mutans
US-10-383-930-31
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US-10-797-821-33
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Matches 20; Conserv
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RESULT 13
US-10-383-930-9
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                                                                                                                                                                                                    | Sequence 32, Application US/10797821
| Sequence 32, Application No. US20050031633A1
| GENERAL INFORMATION:
| APPLICANT: Smith, Daniel J.
| APPLICANT: Taubman, Martin A.
| TITLE OF INVENTION:
| TITLE OF INVENTION:
| CURRENT FILING DATE: 25669-020
| CURRENT FILING DATE: 2004-03-09
| PRIOR PILING DATE: 2003-03-09
| PRIOR PILING DATE: 2003-03-07
| PRIOR PILING DATE: 2003-03-07
| PRIOR PILING DATE: 2003-03-07
| PRIOR PILING DATE: 2003-03-07
| PRIOR PILING DATE: 2003-03-07
| PRIOR PILING DATE: 2004-03-08-08
| PRIOR FILING DATE: 2004-04-12
| PRIOR FILING DATE: 2004-04-12
| PRIOR FILING DATE: 2004-04-12
| PRIOR PILING DATE: 1999-04-12
| PRIOR PILING DATE: 1999-04-12
| PRIOR PILING DATE: 1998-04-12
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Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 20; Conservative 0; Mismatches 0;
                                          Query Match
100.0%; Score 93; DB 4; I
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 20; Conservative 0; Mismatches 0;
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                                                                                                                            48 QQAAQAQVNTIQGQVSALQT 67
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; ORGANISM: Streptococcus mutans US-10-383-930-32
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US-10-797-821-32
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US-10-797-821-31
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Sequence 9, Application US/10797821
; Sequence 9, Application US/10797821
; Canderdon No. US20050031633A1
; GENERAL INFORMATION:
APPLICANT: Smith, Daniel J.
APPLICANT: Taubman, Martin A.
TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens
FILE REFERENCE: 25669-020
CURRENT APPLICATION NUMBER: US/10/797,821
CURRENT FILING DATE: 2004-03-09
PRIOR APPLICATION NUMBER: 10/383,930
PRIOR APPLICATION NUMBER: 60/363,209
PRIOR PILING DATE: 2002-03-07
PRIOR PILING DATE: 2002-03-07
PRIOR PILING DATE: 2002-03-07
PRIOR PILING DATE: 2002-04-03-09
PRIOR PILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: 60/363,209
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Publication No. US20040127400A1;
GENERAL INFORMATION:
APPLICANT: Smith, Daniel J
ITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
FILE REPERRENCE: 2569-018;
CURRENT APPLICATION NUMBER: US/10/383,930
CURRENT FILING DATE: 2003-03-07;
PRIOR PILING DATE: 2002-08-08;
PRIOR FILING DATE: 2002-08-08;
PRIOR FILING DATE: 2002-08-08;
PRIOR FILING DATE: 2002-08-08;
PRIOR FILING DATE: 2002-08-09;
PRIOR FILING DATE: 2002-08-09
                                                                                                                                                                                                                                                                                                                Length 432;
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                                                                                                                                                                                                                                                                                                             Score 93; DB 5; I
Pred. No. 2.3e-06;
                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 93; DE
Best Local Similarity 100.0%; Pred. No. 2.3
Matches 20; Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.2
SEQ ID NO 32
LENGTH: 432
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US-10-797-821-32
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SOFTWARE: PatentIn version 3.2
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US-10-474-792-600
; Sequence 600, Application US/10474792
; Publication No. US20040236072A1
; GENERAL INFORMATION:
; APPLICANT: Olmsted, Stephen
; APPLICANT: Agursky, Robert
; APPLICANT: Minter, Lourie
; TITE OF INVENTION: SURFACE PROTEINS OF STREPTOCCCCUS PYOGENES
; TITLE OF INVENTION SURFACE PROTEINS OF STREPTOCCCUS PYOGENES
; TILLE REFERENCE: AM 100399
; CURRENT APPLICATION NUMBER: US/10/474,792
; CURRENT APPLICATION NUMBER: US/10/474,792
; NUMBER OF SEQ ID NOS: 674
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 600
; SEQ ID NO 600
; TYPE: RT
; ORGANISM: Streptococcus pyogenes
US-10-474-792-600
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80.6%; Score 75; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6e-05;
Matches 16; Conservative 0; Mismatches 0; Indels
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 45
; SGOTWARE: Patentin version 3.2
; SGO ID NO 9
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial
; PERATURE:
; OTHER INFORMATION: GDPB peptide
US-10-797-821-9
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Search completed: January 25, 2006, 20:10:04 Job time : 61 secs

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Sequence 252, App
Sequence 62, Appl
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1: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd.
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US-10-508-263-14
US-10-508-263-14
US-11-132-142-8
US-11-069-834-60
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Maximum Match 100%
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Sequence 210, Application US/11052554A

Sequence 210, Application US/11052554A

Publication No. US2005028866A1

GENERAL INFORMATION:

APPLICANT: Sachdeva, et al.

TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE

TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL

FILE REPERENCES: 3063340359A

CURRENT FILING DATE: 2005-02-07

PRIOR FILING DATE: 2004-07-20

PRIOR FILING DATE: 2004-02-06

NUMBER OF SEQ ID NOS: 763

SOFTWARE: Patentin version 3.3

SEQ ID NO 2.10
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Publication No. US20050288866A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC FOTENTIAL
FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT PILING DATE: 2004-07-20
PRIOR PILING DATE: 2004-07-20
FRIOR FILING DATE: 2004-07-20
FRIOR FILING DATE: 2004-07-20
FRIOR FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
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US-10-875-800-1
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US-10-10-875-800-2
US-11-043-590-13
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US-10-508-263-68
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ORGANISM: Streptococcus mutans UA159
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Matches 20; Conservative
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       \begin{array}{c} \mathbf{n} \\ \mathbf{
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US-10-508-263-14
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Sequence 64, Application US/10508263

Sequence 64, Application US/10508263

Publication No. US200520260754A1

GENERAL INFORMATION:

APPLICANT: BASF Plant Science GmbH

TITLE OF INVENTION: Constructs and methods for regulating gene expression FILLE REFERENCE: 53262-20085.00

CURRENT APPLICATION NUMBER: US/10/508,263

CURRENT FILING DATE: 2004-09-20

NUMBER OF SEQ ID NOS: 126

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 64

LENGTH: 472
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 62, Application US/10508263
Publication No. US20050260754A1
GENERAL INFORMATION:
APPLICANT BASF Plant Science GmbH
TITLE OF INVENTION: Constructs and methods for regulating gene expression
FILE REFERENCE: 53262-20085.00
CURRENT APPLICANTION NUMBER: US/10/508,263
CURRENT PILING DATE: 2004-09-20
NUMBER OF SEQ ID NOS: 126
SOFTWARE: Patentin Ver. 2.1
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47.3%; Score 44; DB 6; Length 472;
Best Local Similarity 50.0%; Pred. No. 4.8;
Matches 8; Conservative 4; Mismatches 4; Indels
                                                                                                                                                     Query Match 62.4%; Score 58; DB 7; Length 398; Best Local Similarity 60.0%; Pred. No. 0.02; Matches 12; Conservative 5; Mismatches 3; Indels
                                                                                        ORGANISM: Streptococcus pyogenes MGAS8232
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US-10-508-263-12
; Sequence 12, Application US/10508263
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 252
LENGTH: 398
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US-11-052-554A-252
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LENGTH: 472
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Publication No. US20050260754A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Constructs and methods for regulating gene expression
TITLE OF INVENTION: Constructs and methods for regulating gene expression
TITLE REFRENCE: 52362-20085.00
CURRENT PILING DATE: 2004-09-20
NUMBER OF SEQ ID NOS: 126
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 14
ILENGTH: 496
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Sequence 10, Application US/2050260754A1

Publication No. US20050260754A1

GENERAL INFORMATION:

APPLICANT: BASF Plant Science GmbH

TITLE OF INVENTION: Constructs and methods for regulating gene expression

FILE REFERENCE: 53262-20085.00

CURRENT APPLICATION NUMBER: US/10/508,263

CURRENT FILING DATE: 2004-09-20

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 10.
Publication No. US20050260754Al
GENERAL INFORMATION:
APPLICANT: BASF Plant Science GmbH
TITLE OF INVENTION: Constructs and methods for regulating gene expression
FILE REFERENCE: 53262-20085.00
CURRENT APPLICATION NUMBER: US/10/508,263
CURRENT APPLICATION NUMBER: US/10/508,263
NUMBER OF SEQ ID NOS: 126
SOFTWARE: PATENTN Ver. 2.1
SEQ ID NO 12
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Best Local Similarity 43.8%; Pred. No. 11;
Matches 7; Conservative 5; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                    Length 488;
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Pred. No. 5;
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Best Local Similarity 50.0°
Matches 8; Conservative
                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Brassica napus
US-10-508-263-12
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US-10-508-263-10
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ORGANISM: Brassica napus
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Publication No. US20050276811A1 GENERAL INFORMATION:
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Matches 7; Conservative
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ORGANISM: Homo sapiens
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US-10-508-263-18
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Publication No. US20050276818A1
GENERAL INFORMATION:
APPLICANT: The Burnham Institute
APPLICANT: Sikora, Sergey
APPLICANT: Godzik, Adam
TITLE OF INVENTION: UNCHRACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
TITLE OF INVENTION: UNCHRACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
TITLE OF INVENTION: CYCLIC-AMP-DEPENDENT KINASE AND A TARGET FOR SARS THERAPY
FILE REPERENCE: 8014-011-US
CURRENT APPLICATION NUMBER: US/11/132,142
CURRENT FILING DATE: 2005-05-17
PRIOR FILING DATE: 2004-05-17
PRIOR FILING DATE: 2004-05-17
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Best Local Similarity 45.0%; Pred. No. 41;
Matches 9; Conservative 2; Mismatches 9; Indels
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45.2%; Score 42; DB 7; Length 515;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 11; Conservative 4; Mismatches 3; Indels
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Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON BARIA Rita
APPLICANT: FOXTAM Maria Rita
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 6112
LENGTH: 1122
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136 EQAAQANLHRVTQQARVAAI 157
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US-10-467-657-6112
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.3
SEQ ID NO 8
LENGTH: 515
TYPE: PRT
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US-11-132-142-8
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US-11-069-834-60
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Sequence 66, Application US/10508263

Sequence 66, Application US/10508263

Publication No. US20050260754A1

GENERAL INFORMATION:

APPLICANT: BASP Plant Science GmbH

TITLE OF INVERTION: Constructs and methods for regulating gene expression

TITLE OF INVERTION: CONSTRUCTS and methods for regulating gene expression

CURRENT APPLICATION NUMBER: US/10/508,263

CURRENT FILING DATE: 2004-09-20

NUMBER OF SEQ ID NOS: 126

SEQ ID NO 66
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Publication No. US20050260754A1
GENERAL INFORMATION:
TITLE OF INVENTION: Constructs and methods for regulating gene expression
FILE REFERENCE: 53262-20085.00
CURRENT APPLICATION NUMBER: US/10/508,263
CURRENT PILING DATE: 2004-09-20
NUMBER OF SEQ ID NOS: 126
SEQ ID NO 18
SEQ ID NO 18
LENGTH: 509
LENGTH: 509
TYPE: PRT
ORGANISM: Brassica napus
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APPLICANT: CARROLL, MICHAEL C.
APPLICANT: MOORE JR., FRANCIS D.
APPLICANT: MCORE JR., FRANCIS D.
TITLE OF INVENTION: NATUREL IGM ANTIBODIES AND INHIBITORS THEREOF
TILE REFERENCE: CRA-002.01
CURRENT APPLICATION NUMBER: US/11/069,834
CURRENT FILING DATE: 2005-03-01
PRIOR APPLICATION NUMBER: 60/588,648
PRIOR APPLICATION NUMBER: 60/549,123
PRIOR PILING DATE: 2004-07-16
PRIOR APPLICATION NUMBER: 60/549,123
PRIOR PILING DATE: 2004-07-16
SOFTWARE: PALECHIN NUMBER: 60/549,123
SOFTWARE: PALECHIN VOIC: 3.3
SEQ ID NO 50
LENGTH: 1995
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Pred. No. 31;
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Pred. No. 1.2e+02;
8; Mismatches 3; Indels
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4; Mismatches
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1245 ALEAEVSELRAELSSLQT 1262
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; ORGANISM: Arabidopsis thaliana
US-10-508-263-66
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Best Local Similarity 38.9%;
Matches 7; Conservative
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Gaps

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41.9%;
Query Match
Best Local Similarity 53.33
Matches 8; Conservative
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| Sequence 23, Application US/10857780
| Sequence 23, Application US/10857780
| Sequence 23, Application No. US20050272043A1
| GENERAL INFORMATION:
| APPLICANT: ROTH, RICHARD B. |
| APPLICANT: RAWERER, STEFAN M. |
| APPLICANT: RELEAND, RIKARD BENTS |
| APPLICANT: RENELAND, RIKARD HENRY |
| APPLICANT: RENELAND, RIKARD BENTS |
| APPLICANT: TREED OF TOTAL-WRIGHTSON, CAROLYN R. |
| APPLICANT: RENELAND, RIKARD RENTS |
| APPLICANT: RENERANCE: SEQ-4069-CP |
| TITLE OF INVENTION: THEREOF |
| FILE REFERENCE: SEQ-4069-CP |
| FILE REFERENCE: SEQ-4069-CP |
| CURRENT APPLICATION NUMBER: 10/723,681 |
| PRIOR FILING DATE: 2003-01-24 |
| PRIOR FILING DATE: 2003-07-24 |
| PRIOR FILING DATE: 2003-07-24 |
| PRIOR FILING DATE: 2003-11-25 |
| NUMBER OF SEQ ID NOS: 4962 |
| COSTAMARE: PATENTIN VERSION 3.2
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US-10-821-234-889

i Sequence 889, Application US/10821234

j Publication No. US20050255114A1

GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
TITLE OF INVENTION: Methods
FILE REFERENCE: 823.4
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Pred. No. 38;
4; Mismatches 2; Indels
                                             41.9%; Score 39; DB 6; Length 509; 50.0%; Pred. No. 35;
                                                                                          4; Indels
                                                                                        4; Mismatches
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CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: PL_SEQ_genes Version 1.0
SEQ ID NO 889
LENGTH: 544
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447 ANAMVSTLAGRISALR 462
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Best Local Similarity 57.1%;
Matches 8; Conservative
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417 AQLSEIQTQISALE 430
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                      Query Match
Best Local Similarity 50.00
-hea 8; Conservative
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US-10-821-234-889
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US-10-857-780-23
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LENGTH: 2101
TYPE: PRT
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41.9%; Score 39; DB 7; Length 3674;
Best Local Similarity 44.4%; Pred. No. 3.5e+02;
Matches 8; Conservative 3; Mismatches 7; Indels
Score 39; DB 6; Length 2101;
Pred, No. 1.8e+02;
3; Mismatches 4; Indels
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TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILER REFRENCE: 785CIP4CN
CURRENT APPLICATION NUMBER: US/11/000,463
CURRENT FILING DATE: 2004-11-29
PRIOR APPLICATION WUMBER: UC/1291,265
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR FILING DATE: 2002-11-08
PRIOR FILING DATE: 2001-01-25
PRIOR FILING DATE: 2001-01-25
PRIOR FILING DATE: 2001-01-25
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-77
PRIOR PILING DATE: 2000-00-03
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR PILING DATE: 2000-09-03
PRIOR PILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-05
PRIOR FILING DATE: 2000-09-15
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 454
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Chen, Rui-hong
Qian, Xiaohong B.
Wang, Zhiwei
Wehrman, Tom
Zhang, Jie
Zhou, Ping
Cao, Yi-Cheng
                                                                                                                2 QAAQAQVNTIQGQVS 16
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
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ORGANISM: Homo sapiens
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5.1.6	Compugen	
GenCore version 5.1.6	- 2006	
GenCore	(c) 1993	
	Copyright	

OM protein - protein search, using sw model

Run on:

January 25, 2006, 18:48:24; Search time 68.2 Seconds (without alignments) 128.850 Million cell updates/sec

US-10-797-821-9 94

1 QAQVNTIQGQVSALQTQQAE 20 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

2443163 seqs, 439378781 residues Searched:

Total number of hits satisfying chosen parameters:

2443163

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp2005s:* A Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp2000s:*
3: geneseqp2001s:* geneseqp2002s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Add93629 Streptoco	Adx37252 Streptoco	Add93649 Streptoco	Add93650 Streptoco	Add93653 Streptoco	Adx37272 Streptoco	Adx37273 Streptoco	Adx37276 Streptoco	Aeb91500 Microbial	Add93651 Streptoco		Adx37274 Streptoco	Adx37275 Streptoco	Add93628 Streptoco	Adx37251 Streptoco	Add93622 Streptoco	Adx37245 Streptoco	Abp29684 Streptoco		Adv88392 Streptoco	Adv81808 Streptoco	Adv79645 Streptoco	Aay22579 Bacterial	Abu02747 S. pneumo
SUMMARIES	e e	ADD93629	ADX37252	ADD93649	ADD93650	ADD93653	ADX37272	ADX37273	ADX37276	AEB91500	ADD93651	ADD93652	ADX37274	ADX37275	ADD93628	ADX37251	ADD93622	ADX37245	ABP29684	ADU69524	ADV88392	ADV81808	ADV79645	AAY22579	ABU02747
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do	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	79.8	79.8	69.1	69.1	62.8	62.8	62.8	62.8	62.8	55.3	55.3
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25 26	0 0 B G G	31 33 33	4 5 6 4 5 6	33 38 39	4 4 4 0 1 2	43 44 5

## ALIGNMENTS

RESULT 1

Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen. Streptococcus mutans glucan binding protein-B peptide fragment. ADD93629 standard; peptide; 20 AA. (first entry) Streptococcus mutans. WO2003075845-A2 29-JAN-2004 18-SEP-2003. ADD93629; ADD93629 

07-MAR-2003; 2003WO-US006962. 07-MAR-2002; 2002US-0363209P. 08-AUG-2002; 2002US-0402483P. Taubman MA; (FORS-) FORSYTH INST. Smith DJ,

WPI; 2003-845091/78.

Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.

Claim 11; Page 10; 49pp; English.

The present sequence is that of a peptide comprising amino acid residues 52-71 of the glucan binding protein-B (GbpB) of Streptococcus mutans strain SK32 ADD93649. The peptide binds to a major histocompatibility complex (MHC) class II protein. It was identified as a potential B cell epitope using a matrix-based algorithm for epitope prediction, which was used to search the primary amino acid sequence of GbpB for known MHC class II binding motifs. The peptide can be used in immunogenic compositions and subunit vaccines for dental caries. These comprise MHC class II protein-binding GbpB peptides covalently linked with peptide subunits (preferably from the catalytic domain) of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Diepitopic or multiepitopic polypeptides can be

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Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
                                                                                                                                        Streptococcus mutans glucan binding protein-B.
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289. .308
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/note= "HLA-binding peptide"
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/note= "HLA-binding peptide"
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'note= "HLA-binding peptide"
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/note= "HLA-binding peptide"
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'note= "HLA-binding peptide"
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..e= "HLA-binding p
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194. .213
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'note= "HLA-binding
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'note= "HLA-binding
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                                                           ADD93649 standard; protein; 431 AA.
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08-AUG-2002; 2002US-0402483F.
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                                                                                                                                                                                                 Streptococcus mutans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a composition comprising a fragment of a glucan binding protein-B (GbpB) and a biocompatible microparticle, where the fragment binds to a major histocompatibility complex (MHC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds to a Streptococcus mutans GbpB-derived peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
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prepared synthetically or by recombinant DNA technology. Antibodies raised against MTC class II binding fragments of GbpB can be used in passive immunisation.
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                                                                                                                                                                                                                                                                                                                                                immunogenicity; immune stimulation; glucan binding protein-B; microparticle; major histocompatibility complex; tooth disease.
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                                                                                    100.0%; Score 94; DB 7; Length 20; 100.0%; Pred. No. 1.8e-08; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                        Streptococcus mutant glucan binding protein B peptide #9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; SEQ ID NO 9; 73pp; English.
                                                                                                                                                                                                                                       ADX37252 standard; peptide; 20 AA
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08-JAN-1999; 99US-0115142P.
12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-03632099.
08-AUG-2002; 2002US-0462483P.
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                                                                                                                                                                                                                                                                                            (first entry)
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Best Local Similarity 100.0
Matches 20; Conservative
                                                                       Query Match
Best Local Similarity 100...
20; Conservative
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(TAUB/) TAUBMAN M A.
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                                                                                                               protein-B (GDDB) of Streptococcus mutans strain SK32. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions comprise major histocompatibility complex (MHC) class II protein-binding GbpB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The antibody in a mammal. Diepitopic or multiepitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in
                                Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                      sequence is the protein sequence of the glucan binding
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                                                                               Claim 6; Page 7; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                       passive immunisation
WPI; 2003-845091/78.
GENBANK; AY046410.
                                                                                                                                                                                                                                                              Sequence 431 AA;
                                                                                                      present
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(FORS-) FORSYTH INST.
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                                                         Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
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Streptococcus mutans glucan binding protein-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Page 8; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                      07-MAR-2002; 2002US-0363209P.
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                                                                                                                   Streptococcus mutans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-845091/78.
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Smith DJ,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein-B (GbpB) of Streptococcus mutans strain 5SM3. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The includes a number of mumunogenic compositions and vaccines for dental caries. The compositions comprise major histocompatibility complex (MHC) class II protein-binding GbpB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Dispitopic or multiphtopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in
caries. The compositions comprise major histocompatibility complex (MHC) class II protein-binding GDpB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Dispitopic or multieptupic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GDpB can be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
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Pred. No. 7e-07;
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Pred. No. 7e-07;
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                                                                                                                                                                                                                                                         20; Conservative
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Best Local Similarity
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Matches

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The invention relates to a composition comprising a fragment of a glucan binding protein-B (GbpB) and a biocompatible microparticle, where the fragment binds to a major histocompatibility complex (MRC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds to a Streptococcus mutans GbpB protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental cartes.
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microparticle; major histocompatibility complex; tooth disease.
                                                                    immunogenicity; immune stimulation; glucan binding protein-B;
microparticle; major histocompatibility complex; tooth disease.
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                                    Streptococcus mutant glucan binding protein B variant #2.
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12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-0363209P.
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21-APR-2005 (first entry)
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                                                                                                                             Streptococcus mutans
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(TAUB/) TAUBMAN M A.
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nes 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunizing mammals against dental caries. This sequence corresponds to Streptococcus mutans GbpB protein of the invention.
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microparticle; major histocompatibility complex; tooth disease.
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Pred. No. 7e-07;
Mismatches 0; Indels
   Indels
                                                                                                                                                                                                                                                                            Streptococcus mutant glucan binding protein B variant #1
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   0; Mismatches
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08-JAN-1999; 99US-011542P.
12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-0363209P.
08-AUG-2002; 2002US-0402483P.
07-MAR-2003; 2003US-00383930.
                                                            QAQVNTIQGQVSALQTQQAE
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Best Local Similarity 100.
Matches 20; Conservative
     Conservative
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(TAUB/) TAUBMAN M A.
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10-FEB-2005

ADX37273;

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RESULT 7 ADX37273

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The present invention relates to a computational method (M1) for identifying adhesin and adhesin-like proteins, by computing the sequence-based attributes of protein sequences using five attribute modules of a neural network software, training an artificial neural network (ANN) for each of the computed five attributes, and identifying the adhesin and adhesin-like proteins an adhesin and adhesin-like proteins, having 274 fully defined 162-encoding adhesin and adhesin-like proteins, having 274 fully defined 62-encoding adhesin and adhesin-like proteins, having 105 hypothetical genes encoding adhesin and adhesin-like proteins, having 105 hypothetical genes encoding adhesin and adhesin-like proteins, having 105 hypothetical adhesin-like proteins, having 105 fully defined 53-3716 base pair (SEQ ID NO: 12-279); a set of 105 hypothetical adhesin-like proteins, having 105 fully defined 106-5291 base pair (SEQ ID NO: 12-279); a set of 105 hypothetical adhesin-like proteins, having 105 fully defined 106-5291 base pair (SEQ ID NO: 280-384) sequences; and a fully connected multilayer feed forward ANN (I) based on (M1). (M1) is useful for identifying and short-liking proteins of therapeutic potential. And identifying and short-liking proteins for further testing in development of new vaccine formulations to eliminate diseases caused by various pathogenic organisms. (M1) is capanisms, and from bacteria belonging to a wide chitantly related organisms, and from bacteria belonging to a wide chitantly related organisms, and from bacteria belonging to a wide chitantly related organisms, and from bacteria belonging to a wide chitantly related organisms, and from bacteria belonging to a wide contains. The present sequence is a microbial pathogen adhesin
Computational method for identifying adhesin and adhesin like molecules, comprises computing sequence-based attributes of protein sequences using neural network software and training an artificial neural network.
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100.0%; Pred. No. 7e-07;
tive 0; Mismatches 0; Indels
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                                                                                              Claim 16; SEQ ID NO 210; 402pp; English
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GENBANK; AY046412.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein sequence
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a composition comprising a fragment of a glucan binding protein-B (GbpB) and a biocompatible microparticle, where the fragment binds to a major histocompatibility complex (MHC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds to a Streptococcus mutans GbpB protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                         New composition comprising a fragment of a glucan binding protein-B (dpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental carles.
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Pred. No. 7e-07;
; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; SEQ ID NO 33; 73pp; English.
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                                         990S-0081550P.
990S-0115142P.
990S-00290049.
2002US-0363209P.
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09-MAR-2004; 2004US-00797821
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20-JUL-2004; 2004US-0589227P
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Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                               Smith DJ, Taubman MA;
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                                                                                                                                                                                                         (SMIT/) SMITH D J.
(TAUB/) TAUBMAN M A.
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08-AUG-2002;
                                           13-APR-1998;
08-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-AUG-2005
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The present sequence is the protein sequence of the glucan binding protein—B (GDpB) of Streptococcus mutans strain 15JP2. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions comprise major histocompatibility complex (MHC) class II protein-binding GDpB peptides, especially HLA-binding peptides, covalently linked with peptides subunits of a glucosyltransferase. The antibods in a claimed method of eliciting production of an antibody in a mammal. Dispitopic or multiepitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GDpB can be used in
                Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
                                                                                                                         Claim 5; Page 8; 49pp;
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English.

passive immunisation.

Score 94; DB 7; Length 432; Pred. No. 7e-07; Mismatches 20 52 QAQVNTIQGOVSALQTQQAE 71 ö 100.0%; 1 OACVNTIOCOVSALOTOCAE Ouery Match
Best Local Similarity luv...
Local 20; Conservative Sequence 432 AA;

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ADD93652 standard; protein; 432 AA ADD93652; 

(first entry) 29-JAN-2004

Streptococcus mutans glucan binding protein-B.

Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immundgen.

Streptococcus mutans

WO2003075845-A2.

18-SEP-2003

07-MAR-2003; 2003WO-US006962

Smith DJ, Taubman MA;

WPI; 2005-151644/16.

07-MAR-2002; 2002US-0363209P 08-AUG-2002; 2002US-0402483P

(FORS-) FORSYTH INST.

Taubman MA; Smith DJ,

WPI; 2003-845091/78. GENBANK; AY046413.

Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein. The present sequence is the protein sequence of the glucan binding protein-B (GbpB) of Streptococcus mutans strain 3SN1. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions comprise major histocompatibility complex (MHC) class II protein-binding GbpB peptides, especially HLA-binding peptides, Claim 5; Page 8; 49pp; English.

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covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Dispitopic or multispitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in passive immunisation.
                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                           immunogenicity; immune stimulation; glucan binding protein-B;
microparticle; major histocompatibility complex; tooth disease.
                                                                                                       100.0%; Score 94; DB 7; Length 432; 100.0%; Pred. No. 7e-07; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                     Streptococcus mutant glucan binding protein B variant #3
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08-JAN-1999; 99US-0115142P.
12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-0363209P.
08-AUG-2002; 2002US-0402433P.
07-MAR-2003; 2003US-00383930.
                                                                                                                                                                    52 QAQVNTIQGQVSALQTQQAE
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                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                 Streptococcus mutans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SMIT/) SMITH D J.
(TAUB/) TAUBMAN M A.
                                                                                                                  Local Similarity
les 20; Conserv
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                                                                                   Sequence 432 AA;
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Matches
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Gaps ö

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ö The invention relates to a composition comprising a fragment of a glucan binding protein-B (GbpB) and a biocompatible microparticle, where the fragment binds to a major histocompatibility complex (MRIC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds to a Streptococcus mutans GbpB protein of the invention. New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MfC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental cartes. Gaps o; Query Match 100.0%; Score 94; DB 9; Length 432; Best Local Similarity 100.0%; Pred. No. 7e-07; Matches 20; Conservative 0; Mismatches 0; Indels Claim 3; SEQ ID NO 31; 73pp; English. Sequence 432 AA;

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The present sequence is that of a peptide comprising amino acid residues 48-67 of the glucan binding protein-B (GbpB) of Streptococcus mutans carrain SK32 ADD93649. The peptide binds to a major histocompatibility complex (MHC) class II protein. It was identified as a potential B cell septice used to search the primary amino acid sequence of GbpB for known MHC class II binding motifs. The peptide can be used in immunoganic compositions and subunit vaccines for dental caries. These comprise MHC class II protein-binding GbpB peptides covalently linked with peptide subunits (preferably from the catalytic domain) of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Displication of mantibody in a mammal. Displication of mantibody in a mammal. Displication of prepared synthetically or by recombinant DNA technology. Antibodies can be prepared against MHC class II binding fragments of GbpB can be used in
                                                                                                                                                                                                                                                                                                                         Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
                              Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
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   Streptococcus mutans glucan binding protein-B peptide fragment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunogenicity; immune stimulation; glucan binding protein-B;
microparticle; major histocompatibility complex; tooth disease.
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Pred. No. 2.6e-05;
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Matches 16; Conservative
                                                                                                                                                                                                                                                               Taubman MA;
                                                             Streptococcus mutans
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ADX37251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New composition comprising a fragment of a glucan binding protein-B dibbB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
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                                                                                                                                                                                                                             immunogenicity; immune stimulation; glucan binding protein-B;
microparticle; major histocompatibility complex; tooth disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 94; DB 9; Length 432; 100.0%; Pred. No. 7e-07; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                 Streptococcus mutant glucan binding protein B variant #4.
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                           52 QAQVINTIQGOVSALOTODAE 71
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                                                                                                    ADX37275 standard; protein; 432
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08-7AN-1999; 99US-0115142P.
12-APR-1999; 99US-0020049.
07-VARR-2002; 2002US-0363209P.
08-AUG-2002; 2002US-0402483P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Taubman MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SMIT/) SMITH D J.
(TAUB/) TAUBMAN M A.
                                                                                                                                                                                                                                                                             Streptococcus mutans
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Best Local Si
Matches 20
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                                                                                                                                    ADX37275;
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The invention relates to a composition comprising a fragment of a glucan binding protein-B (GbpB) and a biocompatible microparticle, where the fragment binds to a major histocompatibility complex (MRIC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds to a Streptococcus mutans GbpB-derived peptide of the invention.
                                                                                                                                                                                                                                                                                New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.8%; Score 75; DB 9; Length 20; 100.0%; Pred. No. 2.6e-05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                               Claim 4; SEQ ID NO 8; 73pp; English.
                               13-APR-1998; 98US-0081550P.
08-JAN-1999; 99US-0115142P.
12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-03632209P.
08-AUG-2002; 2002US-04602483P.
07-MAR-2003; 2003US-00383930.
09-MAR-2004; 2004US-00797821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 79.8°
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                 Taubman MA;
                                                                                                                                                           (SMIT/) SMITH D J.
(TAUB/) TAUBMAN M A.
                                                                                                                                                                                                                                                      WPI; 2005-151644/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 AA;
                                                                                                                                                                                                                 Smith DJ,
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Gaps ö

Search completed: January 25, 2006, 19:01:45 Job time : 69.2 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

January 25, 2006, 18:48:55; Search time 9.1 Seconds (without alignments) 211.465 Million cell updates/sec

US-10-797-821-9 94

1 QAQVNTIQGQVSALQTQQAE 20 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		مِن			COLEGE	
Result	0100	Query	Query	2	£	1000
	2000	ייייייייייייייייייייייייייייייייייייייי	nangen	9 ;		Description
7	55	58.5	142	7	C81359	ica
0		55.3	392	~	G95258	1 45 k
m	52	55.3	392	7	B98124	stress
4	51	54.3	456	~	E86903	ical þr
Ŋ	49	52.1	507	~	S05542	hypothetical prote
ø	47	50.0	461	~	7000J	secreted 45K prote
7	46	48.9	113	~	G91038	hypothetical prote
89	46	48.9	113	~	A85883	hypothetical prote
σ	46	48.9	307	~	B83167	hypothetical prote
10	46	48.9	734	7	AH2359	hypothetical prote
11	46	48.9	768	~	S71477	homeotic protein,
12	46	48.9	813	7	T46242	kinesin-like prote
13	45	47.9	220	7	H83558	
14	45	47.9	1008	~	AE2304	_
15	45	47.9	1379	~	T13718	pollux gene protei
16	45		3165	~	\$15010	~
17	44	46.8	134	-	AWHUB	natriuretic peptid
18	44	46.8	825	~	S62042	probable membrane
19	44	46.8	925	7	T00334	hypothetical prote
20	44	46.8	2541	~	S11661	talin - mouse
21	43	45.7	259	~	G82865	conjugal transfer
22	43	45.7	520	~	JS0291	intermediate filam
23	43	45.7	539	~	A28549	M24 protein precur
24	43	45.7	546	~	AC2368	hypothetical prote
25	43	45.7	561	~	A31994	u
56	43	45.7	575	~	AF2374	hypothetical prote
27	43	45.7	823	7	A36378	
28	43	45.7	1550	N	S60228	glutamate synthase
53	42	44.7	280	7	AE2026	hypothetical prote

hypothetical prote	hypothetical prote	flagellar distal c	cytokeratin 15 - m	endopeptidase Clp	synaptonemal compl	hypothetical prote	hypothetical prote	H+-transporting tw	hypothetical prote	H+-exporting ATPas	probable glutamate	site-specific reco	keratin, 59K type	keratin, epidermal	merlin protein - m
AE2137	AD2555	B40590	149595	876197	S49461	819501	G83099	836962	D97131	T52300	T06210	T44094	KRMSE1	\$07330	154368
~	N	N	N	0	N	~	N	~	~	N	0	N	Н	N	0
396	439	445	452	872	993	190	157	159	187	375	435	542	269	570	591
44.7	44.7	44.7	44.7	44.7	44.7	44.1	43.6	43.6	43.6	43.6	43.6	43.6	43.6	43.6	43.6
42	42	42	42	42	42	41.5	41	41	41	41	41	41	41	41	41
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

```
hypothetical protein Cj0859c [imported] - Campylobacter jejuni (strain NCTC 11168)
C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Species: JarAar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: C81359
R;Parkhill, J; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilli, C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000
A;Reference number: A81250; MUD:20150912; PMID:10688204
A;Reference number: A81250; MUD:20150912; PMID:10688204
A;Reference number: A81250; MUD:20150912; PMID:10688204
A;Residues: 1-142 <ARP.
A;Residues: 1-142 <ARR.
A;Residues: 1-142 <ARR.
A;Residues: 1-142 <ARR.
A;Reperimental source: serotype 02, strain NCTC 11168
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A;Gene: Cj0859c C;Superfamily: Campylobacter jejuni hypothetical protein Cj0859c

; 58.5%; Score 55; DB 2; Length 142; ilarity 61.1%; Pred. No. 0.13; Conservative 3; Mismatches 4; Indels Query Match
Best Local Similarity

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Gaps

|| :||| |: ||:||| 125 AQASTIQAQIQELQSQQA 142 2 AQVNTIQGQVSALQTQQA 19 ઠે 셤

Gispecies: Streptococcus pneumoniae
C;Species: O3-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: G55258
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heir
On, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Reference number: A95000; MUID:21357209; PMID:11463916

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-392 <KUR>

A;Cross-references: UNIPROT:097N55; UNIPROT:Q8DMY4; UNIPARC:UPI0000051B81; GB:AE005672; A;Experimental source: strain TIGR4

C, Genetics: A, Gene: SP2216

EMBL:MZ6048; NID:g as Lys

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Gaps

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hypothetical protein EC83279 [imported] - Escherichia coli (strain O157:H7, substrain R] C;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004 C;Accession: G91038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-113 <HAY>
A;Cross-references: UNIPROT:QBXBN1; UNIPARC:UPI0000DD058A; GB:BA000007; PIDN:BAB36702.1
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Lactococcus lactis
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: JN0097
R;van Asseldonk, M.; Rutten, G.; Oteman, M.; Siezen, R.J.; de Vos, W.M.; Simons, G.
Gene 95, 155-160, 1990
A;Ticle: Cloning of usp45, a gene encoding a secreted protein from Lactococcus lactis A;Reference number: JN0097; MUID:91071599; PMID:2123812
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and A;Reference number: A99629; MUID:21156231; PMID:11288796
                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-507 <FUE>
A;Cross-references: UNIPROT:P13692; UNIPARC:UPI000016F6FC; GB:X16421;
A;Note: the authors translated the codon CGT for residues 221 and 223
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R;Fuerst, P.; Moesch, H.U.; Solioz, M.
Nucleic Acids Res. 17, 6724, 1989
A;Title: A protein of unusual composition from Enterococcus faecium.
A;Reference number: S05542; MUID:89385998; PMID:2780297
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Pred. No. 2.9;
5; Mismatches 6; Indels
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8.8;
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Pred. No. 4.6;
6; Mismatches
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Pred. No. 8.8;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                     Query Match 52.1%; Score 49; Best Local Similarity 47.1%; Pred. No. 'Matches 8; Conservative 6; Mismatch
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Best Local Similarity 50.0%;
Matches 9; Conservative
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Best Local Similarity 45.03
Matches 9; Conservative
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B98124
general stress protein GSP-781 [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: B98124
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E
R;Hoskins, J.A.; Alborn Jr., W.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAbren, S.; M
Y, P.; Sun, P.M.; Winkler, M.E.
J, Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-392 <KUR>
A;Residues: 1-392 <KUR>
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
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C;Species: Enterococcus faecium
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: S05542
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1.2;
                 Length 392;
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          Score 52; DB 2;
Pred. No. 1.2;
4; Mismatches
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6; Mismatches
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Pred. No.
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Pred. No.
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52 QKQVDQIQEQVSAIQAEQS 70
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52 QKQVDQIQEQVSAIQAEQS 70
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Best Local Similarity 52.6%;
Matches 10; Conservative
                 Query Match 55.3%;
Best Local Similarity 57.9%;
Matches 11; Conservative '
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Best Local Similarity 57.9%;
Matches 11; Conservative
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6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                          230 QAQLNDVKGRLEQLRTQ 246
                                                                                                                                                                                                      48.98;
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52.6%;
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Matches 10, Conservative
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Best Local Similarity
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Matches 9; Conserv
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A, Molecule type:
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Cipate: 15-56p-2000 #sequence_revision 15-5ep-2000 #text_change 09-Jul-2004
Cipate: 15-56p-2000 #sequence_revision 15-5ep-2000 #text_change 09-Jul-2004
Cipate: 15-56p-2000
Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; flickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Jature 406, 959-964, 2000
A; Title: Complete genome sequence of Pseudomomas aeruginosa PA01, an opportunistic pathoral A; Reference number: A82950; MUID:20437337; PMID:10984043
A; Reference number: A82950; MUID:20437337; PMID:10984043
A; Reference number: A82950; MUID:20437337; PMID:10984043
A; Reference number: A82950; MUID:20437337; PMID:10984043
A; Reference number: BNA
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                                           R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, B DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Status: preliminary
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C.Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AH2359
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Pred. No. 8.3;
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Local Similarity 52.6%;
hes 10; Conservative 3
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nes 9; Conservative
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Best Local S
Matches 9
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Best Local !
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A;Residues: 1-734 <KUR>
A;Residues: 1-734 <KUR>
A;Cross-references: UNIPROT: QSYNX7; UNIPARC: UP10000CCEB17; GB: BA000019; PIDN: BAB76131.1,
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all4432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: S71477
R;Nadeau, J.A.; Zhang, X.; Li, J.; O'Neill, S.D.
Rbubitted to the EMBL Data Library, August 1995
A;Description: Molecular characterization of ovule development: Isolation of stage- and A;Reference number: S71477
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A;Residues: 1-768 <NRD>
A;COSE-references: UNIPROT:Q40988; UNIPARC:UPI00000A5978; EMBL:U34743; NID:g1173621; P1
A;COSE-references: UNIPROT:Q40988; UNIPARC:UPI00000A5978; EMBL:U34743; NID:g1173621; P1
A;Experimental source: hybrid SM9108; tissue type ovule
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;90-146/Domain: homeobox homology <HOX>
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A;Note: T9C5.240
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T46242
R;Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Lemcke, submitted to the Protein Sequence Database, December 1999
A;Reference number: 223026
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C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 05-Oct-2004
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A;Experimental source: cultivar Columbia; BAC clone T9C5
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                                                                                                                                                                                                            Length 734;
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Pred. No. 22;
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                                                                                                                                                                                                            Score 46; DB 2;
Pred. No. 21;
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Search completed: January 25, 2006, 19:15:19
Job time: 9.1 secs
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C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Species: Ja-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T13718
R;Xu, X.Z.; Wes, P.D.; Chen, H.; Li, H.S.; Yu, M.; Morgan, S.; Liu, Y.; Montell, C.
A; Biol. Chem. 273, 31297, 1998
A;Title: Retinal targets for calmodulin include proteins implicated in synaptic transmis
A;Reference number: Z17709; MUID:99030403; PMID:9813038
A;Accession: T13718
A;Accession: T13718
A;Accession: T13718
A;Molecule type: mRNA
                                                                                                                                C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Jozcesion: H83558
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bx adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
A; Lory, S.; Olson, M.V.
A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A;Reference number: A62950; MUID:20437337; PMID:10984043
A;Reference number: A62950; MUID:20437337; PMID:10984043
A;Residues: 1-220 <STO>
A;Residues: 1-220 <STO>
A;Cross-references: UNIPROT:Q91SM9; UNIPARC:UPIO0000C5108; GB:AE004505; GB:AE004091; NIC
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUD:21595285; PMID:11759840
A;Reference number: AB1807; MUD:21595285; PMID:11759840
A;Reference number: AB1807; MUD:2159285; PMID:11759840
A;Residues: DNA
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A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
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hypothetical protein PA0697 [imported] - Pseudomonas aeruginosa (strain PAO1)
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Pred. No. 8.5;
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47.9%; Score 45; DB 3
Best Local Similarity 45.0%; Pred. No. 8.5;
Matches 9; Conservative 6; Mismatches
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A; Residues: 1-1379 <XUX>
A; Cross-references: UNIPROT: Q9TY11; UNIPARC: UPI0000084062; EMBL: Y17919; NID: g3893102; P1 Cydentetics:
A; Gente: pollux
A; Cross-references: FlyBase: FBgn0004879
Query Match
Best Local Similarity 53.3%; Pred. No. 59;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Matches 8; Conservative 4; Mismatches 0; Gaps 0;

Qy 1 QAQVNTIQGQVSALQ 15
Db 1055 QAQITTLQSQVQSLE 1069
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Duncan M.J.;

Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates.";

Infect. Immun. 69:6931-6941(2001).

EMBL; ANO46441; ARV94504.1; -; Genomic_DNA.

InterPro; IPR009148; SibA.

PRINTS; PR01852; SIBAPROTEIN.

PROSITE; PR05091; CHAP; 1.

SEQUENCE 431 AA; 44650 MW; 05D38D8D8BC4609F CRC64;
 Q4nc44
Q6d503
Q6d503
Q5n8y9
Q63n34
Q82188
Q881q6
Q88b1
Q9bxh3
Q65vx9
Q65vx9
Q4kke2
Q64ypx
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Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
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Last sequence update)
Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DRC-2004 (TrEMBLrel. 26, Last annotation update)
Glucan-binding protein B.
Streptococous mutans.
                                                                                                                                                                                                                                                                                                                                                                           431 AA
Q4NC44_9MICC
Q6D503_BRWCT
Q5D8Y9_ORYSA
USP45_IACLC
Q63N34_BRPS
Q82188_STRAW
Q83K83_SHIFL
Q8XRN1_ECO57
Q9HXH3_PSEAE
Q65VX9_MANSM
Q40KXZ_PSEEF
Q68VX7_ANASP
Q40988_3ASPA
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MEDLINE=21481971; PubMed=11598068;
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Q938V3,
Q1-DEC-2001 (TEMBLEE). 19, C:
Q1-DEC-2001 (TEMBLEE). 19, L:
Q1-MAR-2004 (TEMBLEE). 26, Lis
Glucan-binding protein B.
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Q84ec7
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              GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                    2166443 seqs, 705528306 residues
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Chia J.-S., Chang L.-Y., Lee Y.-Y., Chen J.-Y.; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=gbpB; OrderedLocusNames=SMU.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                      MEDLINE=21481971; PubMed=11598068;
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PROSITE; PS50911; CHAP; 1.
SEQUENCE 431 AA; 44592 MW
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PRINYS; PRO1852; CHAP; 1.
PROSTIE; PSO911; CHAP; 1.
COMPLETE PRO18091; CHAP; 1.
SEQUENCE 431 AA; 44620 MW;
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Best Local Similarır,
Watches 20; Conservative
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Best Local Similarity
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"Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates.";
Infect. Immun. 69:6931-6941(2001).
EMBL; AXO46410; AX694500.1; -; Genomic_DNA.
InterPro; IPR007921; GHAB.
InterPro; IPR009148; SibA.
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MEDLINES-1153617; PubMed=11254612;

DOI=10.1128/IA1.69.4.2493-2501.2001;

Chia J.S., Lee Y.Y., Huang P.T., Chen J.Y.;

"Identification of stress-responsive genes in Streptococcus mutans by differential display reverse transcription-PCR.";

Infect. Immun. 69:2493-2501(2001).
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MEDLINE=21481977; PubMed=11598074;
DOI=10.1128/IAI.691.1.6987-6998.2001;
Chia J.S., Chang L.Y., Shun C.T., Chang Y.Y., Chen J.Y.;
"A 60-kilodalton immunodominant glycoprotein is essential for cell wall integrity and the maintenance of cell shape in Streptococcus
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 29, Last annotation update)
Immunodominant glycoprotein IDG-60 (Glucan-binding protein B)
                                                                                                                                                                                                                                                                                    DOI=10.1128/IAI.69.11.6931-6941.2001;
Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 431;
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                    Bacteria, Firmicutes, Lactobacillales, Streptococcaceae, Streptococcus.
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Bacteria, Firmicutes, Lactobacillales; Streptococcaceae,
                                                                                                                                       Jin S., Duncan M.J., Taubman M.A., Smith D.J.; "Cloning of the gbpB gene from Streptococcus mutans."; J. Dent. Res. 79:224-224 (2000).
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44620 MW; 464FB3B563FB7E51 CRC64;
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100.0%; Score 94; DB 2; L
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 20; Conservative 0; Mismatches 0;
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PRINTS; PR01822; SIBARROTEIN.
PROSITE; PS50911; CHAP; 1.
SEQUENCE 431 AA; 44620 MW;
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Q9AG98;
            Streptococcus mutans.
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                                                               NCBI_TaxID=1309;
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Duncan M.J.;
"Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates.";
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Putative secreted antigen GbpB/SagA; putative peptidoglycan
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Pred. No. 2.1e-06;
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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STRAIN=3VF4;
Jin S., Duncan M.J., Taubman M.A., Smith D.J.;
Jin S., Duncan M.J., Taubman M.A., Smith D.J.;
"Cloning of the gbpB gene from Streptococcus mutans.";
J. Dent. Res. 79:224-224 (2000).
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EMBL; AE014855; AANS7811.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
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Pred. No. 2.1e-06;
; Mismatches 0;
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EMBL; AF338445; AAK08104.1; -; Genomic_DNA.

EMBL; AY046411; AAK94501.1; -; Genomic_DNA.

Interpro; IPR007921; CHAP.

Interpro; IPR009148; SLDA.

PF05257; CHAP: 1.
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Gaps

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Matches

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Duncan M.J.;
Duncan M.J.;
Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates.";
Infect. Immun. 69:6931-6941(2001).
EMBL; ANO46412; ANO46420.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
PRINTS; PRO1652; SIBAPROTEIN.
PROSITE; PRO5051; CHAP; 1.
SEQUENCE 432 AA; 44648 MW; E769B2504AEESOB9 CRC64;
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Bolotin A., Quinquis B., Renault P., Sorokin A., Ehrlich S.D.,
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 94; DB 2; Length 432; 100.0%; Pred. No. 2.1e-06; live 0; Mismatches 0; Indels
                          MEDLINE=21481971; Pubmed=11598068;
DOI=10.1128/IAI.69.11.6931-6941.2001;
Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
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Peruzzi F., Piggot P.J., Daneo-Moore L.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U78607; AD000288.1; -; Genomic_DNA.
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SEQUENCE 211 AA; 22803 MW; 4ACE331159CFAFC6 CRC64;
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Glucan binding protein (PosB).
Name=pcsB; OrderedLocusNames=stu0022;
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Best Local Similarity 100.
Matches 15; Conservative
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"Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates.";
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DOI=10.1128/IAI.69.11.6931-6941.2001;
Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Jin S., Duncan M.J., Taubman M.A., Smith D.J.;
"Cloning of the gdpB gene from Streptococcus mutans.";
J. Dent. Res. 79:224-224(2000).
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PROSITE; PSS0911; CHAP; 1.
SEQUENCE 432 AA; 44652 MW; 3F88ECB9A1F3BE4F CRC64;
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01-DEC-2001 (TrEMBirel. 19, Last sequence update)
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BMBL; AV046413; AAK94503.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009146; SibA.
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Borges F., Layec S., Thibessard A., Fernandez A., Gintz B., Hols P.,
Decaris B., Leblond-Bourget N.;
Lese, a Chimeric and Variable Gene, Encodes an Extracellular Protein
Involved in Cellular Segregation in Streptococcus thermophilus.";
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EMBL, CORONG23, AAVS9752.1; -; Genomic_DNA.

EMBL, AV730643; AAW82375.1; -; Genomic_DNA.

InterPro; IPR009148; SibA.
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PubMed-15543133; DOI=10.1038/nbt1034;
Bolotin A., Quinquis B., Renault P., Sorokin A., Ehrlich S.D.,
Kulakauskas S., Lapidus A., Golteman E., Mazur M., Pusch G.D.,
Fonstein M., Woerbeek R., Kyprides N., Purnelle B., Prozzi D.,
Ngui K., Masuy D., Hancy F., Burteau S., Boutry M., Delcour J.,
Goffeau A., Hols P.,
"Complete sequence and comparative genome analysis of the dairy
bacterium Streptococcus thermophilus.";
Nat. Biotechnol. 22:1554-1558 (2004).
BMBL, CP000024; AAV61641.1; -; Genomic_DNA.
InterPro; IPR007921, GHAP.
Kulakauskas S., Lapidus A., Goltsman B., Mazur M., Fusch G.D., Fonstein M., Overbeek R., Kyprides N., Purnelle B., Prozzi D., Ngui K., Masuy D., Hancy F., Burteau S., Boutry M., Delcour J., Goffeau A., Hols P., "Complete sequence and comparative genome analysis of the dairy bacterium Streptococcus thermophilus.";
Nat. Biotechnol. 22:1554-1558(2004).
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Glucan binding protein.
Name-posB: OrderedLocusNames=str0022;
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Q5M212 STRT1 PRELIMINARY;
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MEDLINE=2222988; PubMed=12200547; DOI=10.1073/pnas.182380799;
MEDLINE=22222988; PubMed=12200547; DOI=10.1073/pnas.182380799;
Madignain V., Cieelbewicz M.J., Elefon J.A., Peterson S.N., Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D., Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R., Lewis M.R., Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M., Tacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D., Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
                                                                                                                                                                                                                                                                                                                                                                 Chhatwal G.S.;
"Identification and molecular analysis of PcsB, a protein required for "Identification and molecular streptococcus.";
J. Barteriol. 183:1175-1183 (2001).
EMBL; AJ277292; CAC28144.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR003148; SibA.
PF05257; CHAP:
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Reinscheid D.J., Gottschalk B., Schubert A., Bikmanns B.J.,
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                     Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 25 Potential.
26 447 PcsB protein.
447 AA, 46681 MW, F4DB14B0A5F962C8 CRC64;
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                             Last sequence update)
Last annotation update)
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447 AA
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Name=pscB; OrderedLocusNames=SAG0017;
                                        Created)
PRT;
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PROSITE; PS50911; CHAP; 1.
                                      01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-MAR-2004 (TrEMBLrel. 26,
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Q8E2H1;
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                                                                                                                                                   Streptococcus agalactiae.
                                                                                                        Poss protein precursor.
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                                                                                                                                                                                              Streptococcus.
NCBI_TaxID=1311;
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Campylobacter jejuni
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Best Local Similarity
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Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequence of Streptococcus agalactiae, a pathogen causing
emerging human pathogen, serotype V Streptococcus agalactiae.";
Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396 (2002).
EMBL; AE014192; AAM98925.1; -; Genomic_DNA.
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Pred. No. 0.84;
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
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Last annotation update)
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4; Mismatches
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EMBL; AL766843; CAD45661.1; -; Genomic_DNA.
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10-MAY-2005 (TrEMBLrel. 30, Last sequ
10-MAY-2005 (TrEMBLrel. 30, Last anno
Hypothetical protein.
OrderedLocusNames=C780946;
Campylobacter jejuni (strain RM1221).
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                                                                           InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
Pfam; PP05257; CHAP; 1.
PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
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PROSITE, PS50911; CHAP, 1.
Complete proteome.
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InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
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QSHUT7 CAMJR PRELIMINARY;
QSHUT7;
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QBETX9_STRA3 PRELIMINARY;
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Best Local Similarity 60.09
                                                                                                                                                                                                                                                                   Local Similarity 60.0
nes 12; Conservative
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PubMed=15660156; DOI=10.1371/journal.pbio.0030015;
Pouts D.E., Mongodin B.P., Mandrell R.E., Miller W.G., Rasko D.A.,
Ravel J., Brinkac L.M., DeBON R.T., Parker C.T., Daugherty S.C.,
Dodson R.J., Durkin A.S., Madupu R., Sullivan S.A., Shetty J.U.,
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Major structural differences and novel potential virulence mechanisms
from the genomes of multiple Campylobacter species.";
PLOS BIOL 3:72-85(2005).
EMBL: CP000025; AAW35283.1; -; Genomic_DNA.
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MEDLINE=20150912; PubMed=10688204; DOI=10.1038/35001088;
Barkhill J., Wren B.W., Mungall K.L., Ketley J.M., Churcher C.M.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Campylobacter jejuni
reveals hypervariable sequences.";
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Campylobacteraceae, Campylobacter.
NCBI_TaxID=197;
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Campylobacteraceae; Campylobacter.
NCBI_TaxID=195099;
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EMBL; AL139076; CAB73124.1; -; Genomic_DNA.
PIR; C81359; C81359.
Complete protein.
SEQUENCE 142 AA; 15545 MW; 982CF70B2F2FC073 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome; Hypothetical protein.
SEQUENCE 142 AA; 15570 MW; 1A2CE595CC5FD19D CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UJUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein Cj0859c.
OrderedLocusNames=Cj0859.3;
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QSLSX9_CHLAB PRELIMINARY; PRT; 366 AA.
QSLSX9_CHSB9-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
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Pred. No. 1.2;
3; Mismatches
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61.1%; Pred. No. 1.2;
ive 3; Mismatches
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125 AQASTIQAQIQELQSQQA 142
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NUCLEOTIDE SEQUENCE.
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Search completed: January 25, 2006, 19:13:41 Job time: 71.3 secs

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3 QVNTIQGQVSALQTQQAE 20 :||:||:||:||:|| 120 EVNRLQGEVSASQAQLAE 137

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VS-01-583-110-4374

i Sequence 4374, Application US/09583110

i Patent No. 6699703

i GRNERAL INFORMATION:

i APPLICANT: Lynn Doucette-Stamm et al.

i TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

i TITLE OF INVENTION: Preumoniae for Diagnostics and Therapeutics

i TITLE OF INVENTION: Preumoniae for Diagnostics and Therapeutics

i TITLE OF INVENTION: Preumoniae for Diagnostics and Therapeutics

i TITLE OF INVENTION: NUMBER: US/09/583,110

i CURRENT APPLICATION NUMBER: US 60/05.26

i PRIOR PILING DATE: 1998-06-30

i PRIOR PILING DATE: 1998-06-12

i PRIOR PILING DATE: 1998-05-12

i PRIOR FILING DATE: 1998-05-12

i RUMBER: OF SEQ ID NOS: 5322

i LENGTH: 392
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US-09-222-938A-67
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LENGTH: 210
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30, Appl
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2, Appli
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6, Appli
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                                                                                                                                                                          January 25, 2006, 18:50:05; Search time 16.6 Seconds (without alignments) 99.609 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                      GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd
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US-09-107-433-3230
US-08-110-433-3230
US-09-252-22
US-09-252-91A-22811
US-08-562-737-43
US-09-562-737-43
US-08-38-58-1
US-08-459-146-3
US-08-338-58-1
US-08-850-910A-48
US-08-850-910A-48
US-09-902-517-45
US-09-902-517-45
US-09-902-517-48
US-09-902-517-48
US-09-902-517-48
US-09-543-681A-5999
US-09-543-681A-5999
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JS-08-737-629-6
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-09-562-737-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                            OM protein - protein search, using sw model
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94
1 QAQVNTIQGQVSALQTQQAE 20
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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            Sequence 7412, Ap Sequence 24051, A Sequence 24051, A Sequence 29118, A Sequence 94, Appl Sequence 44, Appl Sequence 3473, A Sequence 24295, A Sequence 24295, A Sequence 24295, A Sequence 2973, Ap Sequence 2973, Ap
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                                                                                                                                                                                                                                                                                                     Sequence 67, Application US/09222938A
Patent No. 6437108
GENERAL INFORMATION:
APPLICANT: Youngman, Philip
APPLICANT: Murphy, Christan
APPLICANT: Murphy, Christopher
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 07334/060001
CURRENT APPLICATION NUMBER: US/09/222,938A
CURRENT FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 102
NUMBER OF SEQ ID NOS: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
US-09-252-991A-26233
US-09-228-322-7412
US-09-252-991A-24051
US-09-538-092-86
US-09-270-767-58615
US-09-370-767-58615
US-09-370-767-58615
US-09-370-767-43273
US-09-134-001C-3479
US-09-134-001C-3479
US-09-134-001C-2973
US-09-538-092-919
US-08-466-390-4
US-08-467-447-4
US-08-467-470-919
US-08-467-470-919
US-08-467-781-4
US-08-195-487-4
US-08-195-487-4
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Pred. No. 0.48;
4; Mismatches
                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QAQVNTIQGQVSALQTQQA 19
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52 QKQVDQIQEQVSAIQAEQS 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 55.3%;
I Similarity 57.9%;
11; Conservative
  Query Match
Best Local Similarity
Matches 11; Conserv
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Gaps
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Pred. No. 8.5;
6; Mismatches 3; Indels
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US-09-562-737-45

Sequence 45, Application US/09562737

Sequence 45, Application US/09562737

Sequence 45, Application US/09562737

GENERAL INFORMATION:

APPLICANT: Herz, Joachim
APPLICANT: Gotthardt, Michael
ITLE OF INVENTION: LDL Receptor Signaling Pathways
ITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REFERENCE: USW0708

CURRENT FILING DATE: 2000-05-01

NUMBER OF SEQ ID NOS: 132

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 45

LENGTH: 1024

TYPE: PRATURE:

CREATURE:

SEATURE:
                                                                                                                                                                                                                                                                                       ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/186,222
                                              Sequence 2, Application US/08186222;
Patent No. 5559007;
GENERAL INFORMATION:
APPLICANT: Suri, Bruno
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
NUMBER OF SEQUENCES:
ADDRESSEE: CIBA-GEIGY Corporation
STRRET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CIASSIFICATION: 435
CIASSIFICATION DATA:
APPLICATION UNDRER: US 07/672,205
FILING DATE: 19-WAR-1991
APPLICATION NUMBER: GB 9006400.7
FILING DATE: 22-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Villamizar, John
REGISTRATION NUMBER: 30,5998
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TELEPHONE: (914)785-7121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.0%;
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INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 461 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                          STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                           CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                  US-08-186-222-2
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                                                                       DB 2; Length 392;
1;
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                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: CD/ROW ISO9660
COMPUTER: CUNCHOWN:
OPERATING SYSTEM: CUNCHOWN:
SOFTWARE: CUNCHOWN:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085131
FILING DATE: MAY 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: MAY 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: MAY 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: MAY 12, 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...399
; SEQUENCE DESCRIPTION: SEQ ID NO: 3230:
US-09-107-433-3230
                                                                                                              4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Attniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
                                                                         Score 52;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 399 amino acids TYPE: amino acid
                                                                                                                                                                      | ||: || ||||: |:
52 QKQVDQIQEQVSAIQAEQS 70
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INFORMATION FOR SEQ ID NO: 3230:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                       55.3%;
nilarity 57.9%;
Conservative
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
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Best Local Similarity 57.9°
Matches 11; Conservative
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                                                                       Query Match
Best Local Similarity
Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                                              26 AQINILEGQQLPLQHQLAE 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas aeruginosa
      TELECOMMUNICATION INFORMATION:
                        TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 768 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                   48.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 45.v.
Best Local 9; Conservative
                                                                                                                                                                                                                                                                            10; Conservative
                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-560-398-2
                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
US-09-252-991A-29621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Pseudo
US-09-252-991A-29621
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                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                           Sequence 22811, Application US/09252991A

Batent No. 6551795
GENERAL INFORMATION:
FARLAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
ARRGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 22811

LENGTH: 722
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                                                                                                                              Gaps
i OTHER INFORMATION: Description of Artificial Sequence: Synthetic
i OTHER INFORMATION: Sequence
US-09-562-737-45
                                                                                                                              ö
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                                                                                   Score 47; DB 2; Length 1024;
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
48.9%; Score 46; DB 2; Length 722;
Best Local Similarity 52.6%; Pred. No. 21;
Matches 10; Conservative 3; Mismatches 6; Indels
                                                                                                                              5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-560-398-2
; Sequence 2, Application US/08560398
; Patent No. 59707082
; GENERAL INFORMATION:
APPLICANT: O'Neill, Sharman
APPLICANT: O'Neill, Sharman
TITLE OF INVENTION: Ovule-Specific Gene Expression
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: The PC-COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,398
FILING DATE: 17-NOV-1995
CLASSIFICATION: 435
ATTOMREY/AGENT INPORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REGISTRATION NUMBER: 34,774
                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         547 AOVPTVSGHASALRRTRAE 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 AQVNTIQGQVSALQTQQAE 20
                                                                                                                                                                                              1006 ASVPTIQDQVSAMQLSQ 1022
                                                                                                                                                                 2 AQVNTIQGOVSALQTQQ 18
                                                                                Query Match
Best Local Similarity 64.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                          RESULT 6
US-09-252-991A-22811
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Sequence 29617.

Sequence 29617.

Parent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 29621

LENGTH: 383
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                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
7 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
7 OTHER INFORMATION: Sequence
7 OTHER 105-737-43
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45.0%; Pred. No. 15;
ive 6; Mismatches 5; Indels
  Length 768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 43, Application US/09562737
Fatent No. 6428967
GENERAL INFORMATION:
APPLICANT: Herr, Joachim
TILE OF INVENTION: LDL Receptor Signaling Pathways
FILE REFERENCE: UNWHORDER: US/09/562,737
CURRENT FILING DATE: 2000-05-01
CURRENT FILING DATE: 2000-05-01
SOFTWARE: Patentin Ver. 2.1
SEQ. ID NO 43
Score 46; DB 1;
Pred. No. 23;
                                                3; Mismatches
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US-08-338-558-1
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                                             Gaps
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Query Match 47.9%; Score 45; DB 2; Length 1024; Best Local Similarity 55.6%; Pred. No. 48; Matches 10; Conservative 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 3
CARRESPONDENCE ADDRESS:
ADDRESSEE: George M. Gould, Esq., Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
CITY: New Jersey
COUNTRY: U.S.A.
                                                                                                                                                                                                                                            Sequence 3, Application US/08459146
Patent No. 5866405
GENERAL INFORMATION:
APPLICANT: Choi, Gil Ho
APPLICANT: Nues, Donald Lee
TITLE OF INVENTION: Genetically Engineered Transmissible
TITLE OF INVENTION: Hypovirulence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: POLYM:

COMPUTER: READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Ploppy disk

COMPUTER: PE-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,146

FILING DATE: 02-JUN-1995

CLASSIFICATION: DATA:

APPLICATION NUMBER: US 07/832,117

FILING DATE: 06-PEB-1992

ATTORNEY/AGRAT INFORMATION:

NAME: ROSEMAN. Catherine R

REGISTRATION NUMBER: 34,240

REFERENCE/DOCKET NUMBER: 35-6208

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION 1010 235-6308

TELEFAX: (201) 235-3500

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Endothia parasitica (Cryphonectria ORGANISM: parasitica) STRAIN: EP713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08459065
Patent No. 5882642
GENERAL INFORMATION:
APPLICANT: Chol, Gil Ho
                                                                                                                  3122 QAQVNELRAQNLALQSQ 3138
                                                                                         1 OADVNTIQGOVSALQTOO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QAQVNTIQGQVSALQTQ 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-459-065-3
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Patent No. 5786163
GENERAL INFORMATION:
APPLICANT: Hall, Christian
TITLE OF INVENTION: BNP ANTIBODY AND IMMUNOASSAY USING IT
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: Now York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 3165;
APPLICANT: Nuss, Donald Lee
TITLE OF INVENTION: Genetically Engineered Transmissible
TITLE OF INVENTION: Hypovirulence
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: George M. Gould, Esq., Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,065
FILING DATE: 02-010-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/832,117
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Endothia parasitica (Cryphonectria ORGANISM: parasitica) STRAIN: EP713 US-08-459-065-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
47.9%; Score 45; DB 1; 1
Best Local Similarity 58.8%; Pred. No. 1.8e+02;
Matches 10; Conservative 3; Mismatches 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Roseman, Catherine R
REGISTRATION NUMBER: 34,240
REFERENCE/DOCKET NUMBER: 8899
TELECOMUNICATION INFORMATION:
TELEFRONE: (201) 235-6208
TELEFAX: (201) 235-6208
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3122 QAQVNELRAQNLALQSQ 3138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                     CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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Sequence 48, Application US/08850910A
| Patent No. 5948761
| GENERAL INFORMATION:
| APPLICANT: STILHAMER, J.J.
| APPLICANT: STARBOROUGH, R.M.
| TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR
| TITLE OF INVENTION: PRODUCTION OF BRAIN NATRIUETIC PEPTIDE
| NUMBER OF SEQUENCES: 50
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: MORRISON & FORESTER, LLP
| STREET: 2000 Pennsylvania Avenue, NW, Suite 5500
| CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 134;
                                                                                                                                                                                                                                                                DB 1; Length 134;
                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: ...
ZOUG-1888
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASESEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,910A
FILING DATE: 05-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/477,226
FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 07/299,880
FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 07/206,470
FILING DATE: 14-JUN-1988
APPLICATION NUMBER: 07/206,470
FILING DATE: 31-MAY-1988
APPLICATION NUMBER: 07/206,383
FILING DATE: 31-MAY-1988
APPLICATION NUMBER: 07/206,383
FILING DATE: 31-MAY-1988
APPLICATION NUMBER: 27.006,383
FILING DATE: 31-MAY-1988
APPLICATION NUMBER: 27.006,383
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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50.0%; Pred. No. 6.3;
                                                                                                                                                                                                                                                             Query Match 46.8%; Score 44; DB Best Local Similarity 50.0%; Pred. No. 6.3; Matches 9; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            1 QAQVNTIQGQVSALQTQQ 18
                                                                                                                                                                                                                                                                                                                                                                                                            44 QEQRNHLQGKLSELQVEQ 61
                                     i TENGTH: 134 amino acids
i TYPE: amino acid
syraAndenNeSs: single
i MOLGOY: linear
i MOLECULE TYPE: protein
; PRAGMENT TYPE: internal
US-08-850-910A-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 amino acids
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           SEQUENCE CHARACTERISTICS
LENGTH: 134 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: si:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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US-08-550-910A-45

Sequence 45, Application US/08850910A

PRECENT No. 55447

GENERAL INFORMATION:
APPLICANT: SELIMANE, J.J.
APPLICANT: SELIMANE, J.J.
APPLICANT: SCARBOROUGH R.M.
TITLE OF INVENTION: RECOMEINANT TECHNIQUES FOR
TITLE OF INVENTION: RECOMEINANT TECHNIQUES FOR
TITLE OF INVENTION: RECOMEINANT TECHNIQUES FOR
TITLE OF INVENTION: RECOMEINANT TECHNIQUES FOR
TITLE OF INVENTION: RECOMEINANT TECHNIQUES FOR
TITLE OF INVENTION: RECOMEINANT TECHNIQUES FOR
TITLE OF INVENTION: RECOMEINANT TECHNIQUES FOR
TITLE OF INVENTION: RECOMEINES:
ADDRESSER: MORRISON & FOERSTER, ILP
STREET: 2000 Pennsylvania Avenue, NW, Suite 5500
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: HAM COMPALIADE
OPERATING SYSTEM: Windows
COMPUTER: TEM COMPALIADE
OPERATING SYSTEM: Windows
SOFTWARE: OF SAFE OF WINDOWS
CHING DATE: OF-MAY.1997
FILING DATE: OF-MAY.1997
FILING DATE: OF-MAY.1999
FILING DATE: 19-1AN-1988
APPLICATION NUMBER: 07/200,383
FILING DATE: 11-MAY-1988
APPLICATION NUMBER: 07/200,383
FILING DATE: 11-MAY-1988
APPLICATION NUMBER: 07/200,383
FILING DATE: 11-MAY-1988
APPLICATION NUMBER: 29,959
REFRERENCE/DATATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.8%; Score 44; DB 1; Length 76; 50.0%; Pred. No. 3.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 219002025212
TELECOMMUNICATION INFORMATION:
TELEPRONS: 202-897-1500
TELEPRAX: 202-897-1500
APPLICATION NUMBER: US/08/338,558
FILING DATE: 21-NOV-1994
CLASSIFTCATION: 436
ATTORNEY/AGENT INPORMATION:
NAME: Panucci, Allan A.
REGISTRATION NUMBER: 8080-010
REPERENCE/DOCKET NUMBER: 8080-010
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELERAX: 66141 PENNIE
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QAQVNTIQGQVSALQTQQ 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 QEQRNHLQGKLSELQVEQ 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 50.0
Matches 9; Conservative
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5; Indels

4; Mismatches

9; Conservative

Matches

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        Db
        44 QEQRAHLQGKLSELQVEQ 61

        BESULT 15
        4 QEQRAHLQGKLSELQVEQ 61

        15 GG-508-435A-2
        5 Sequence 2, Application US/09508435A

        15 Sequence 2, Application US/09508435A
        5 Sequence 2, Application US/09508435A

        15 Sequence 2, Application US/09508435A
        5 Sequence 2, Application US

        1 GENERAL INFORMATION:
        1 Sequence 2, Application US

        2 FILE REFERENCE:
        2000-0359A/JJF WMC/00177

        3 FILE REFERENCE:
        2000-03-12

        4 FILE REPRENCE:
        1 DO00-03-13

        5 FILE REPRENCE:
        2000-03-13

        6 FILE REPRENCE:
        1 DO00-03-13

        7 FILE REPRENCE:
        1 DO00-03-13

        8 FILE REPRENCE:
        1 DO00-03-13

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        8 SEQ ID NOS:
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        8 SEQ ID NOS:
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        2

        8 SEQ ID NOS:
        3

        8 SEQ ID NOS:
        4

        1 SOS-435A-2

        1 SEQ 13 SEQ ID NO
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Sequence 45, Appl Sequence 48, Appl Sequence 2, Appli Sequence 2, Appli Sequence 45, Appli

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APPLICANT: Smith, Daniel J.
APPLICANT: Taubman, Martin A.
APPLICANT: Taubman, Martin A.
TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens FILE REPERENCE: 25669-020
CURRENT APPLICATION NUMBER: US/10/797,821
CURRENT FILING DATE: 2004-03-09
PRIOR PPLICATION NUMBER: 60/363,209
PRIOR APPLICATION NUMBER: 60/363,209
PRIOR APPLICATION NUMBER: 60/363,209
PRIOR APPLICATION NUMBER: 60/363,209
PRIOR APPLICATION NUMBER: 60/402,483
PRIOR APPLICATION NUMBER: 09/402,483
PRIOR APPLICATION NUMBER: 09/402,483
                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/10383930
; Sequence 9, Application US/10383930
; Publication No. US20040127400A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Daniel J
; APPLICANT: Taubman, Martin A
; TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
; FILE REFERENCE: 25669-018
; CURRENT FILING DATE: 2003-03-07
; PRIOR PELING DATE: 2003-09-08
; PRIOR FILING DATE: 2002-08-08
; PRIOR FILING DATE: 2002-08-08
; PRIOR FILING DATE: 2002-08-08
; PRIOR PLING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin Version 3.2
; SEQ ID NO 9
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100.0%; Score 94; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 7e-08;
Matches 20; Conservative 0; Mismatches 0; Indels
US-10-282-122A-69274
US-11-097-143-261
US-10-359-028-9
US-10-419-059-1
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US-10-359-021-1
US-10-645-874-1
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US-10-827-919-1
US-10-938-760-1
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Publication No. US20050031633A1
GENERAL INFORMATION:
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   JS-10-383-930-9
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Sequence 33, Appl
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Sequence 31, Appl
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Sequence 32, Appl
Sequence 8, Appli
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Sequence 3230, Ap
Sequence 600, App
Sequence 10807, A
Sequence 45, Appl
Sequence 213685,
Sequence 164844,
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                                                                                               January 25, 2006, 19:13:51; Search time 60 Seconds (without alignments) 139.276 Million cell updates/sec
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'cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep: *

'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep: *

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'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep: *

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'cgn2_6/ptodata/1/pubpaa/USIO8_PUBCOMB.pep: *
                GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-10-797-821-9
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US-10-797-821-29
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Maximum Match 100%
Listing first 45 summaries
                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                       QAQVNTIQGQVSALQTQQAE 20
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Maximum DB seq length: 200000000
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Matches 20; Conserv
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US-10-383-930-33
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; Publication No. US20040127400A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Daniel J
; APPLICANT: Taubman, Martin A
; TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
; FILE REFERENCE: 25669-018
; CURRENT APPLICATION NUMBER: US/10/383,930
; CURRENT FILING DATE: 2003-03-07
; PRIOR FILING DATE: 2002-08-08
; PRIOR PLILOG DATE: 2002-09-08
; PRIOR PLILOG DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 29
; LINGTH: 431
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i Sequence 30, Application US/10383930

i Sequence 30, Application US/10383930

j Publication No. US20040127400A1

c GENERAL INFORMATION:

APPLICANT: Smith, Daniel J

APPLICANT: Taubman, Martin A

TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein

FILE REFERENCE: 25669-018

CURRENT APPLICATION NUMBER: US/10/383,930

CURRENT PILING DATE: 2003-03-07

PRIOR APPLICATION NUMBER: 60/402,483

PRIOR APPLICATION NUMBER: 60/363,209

PRIOR APPLICATION NUMBER: 60/363,209

PRIOR APPLICATION NUMBER: 40/363,209

NUMBER OF SEQ ID NOS: 41

SOFTWARE: PatentIn version 3.2
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Pred. No. 7e-08;
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Pred. No. 2.1e-06;
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100.0%; Score 94; DB
Best Local Similarity 100.0%; Pred. No. 7e-
Matches 20; Conservative 0; Mismatches
PRIOR FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: 60/081,550
PRIOR PILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR PILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.2
SEQ ID NO 9
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; OTHER INFORMATION: GbpB peptide
US-10-797-821-9
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US-10-383-930-29
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| Sequence 29, Application US/10797821
| Sequence 29, Application US20050031633A1
| Sequence 29, Application No. US20050031633A1
| GENERAL INFORMATION:
| APPLICANT: Smith, Daniel J.
| APPLICANT: Smith, Daniel J.
| TITLE OF INVERTION Glucan Binding Protein and Glycosyltransferase Immunogens
| TITLE OF INVERTION Glucan Binding Protein and Glycosyltransferase Immunogens
| FILE REFERENCE: 25669-020
| CURRENT APPLICATION NUMBER: US/10/797,821
| CURRENT PELING DATE: 2004-03-09
| PRIOR APPLICATION NUMBER: 60/363,209
| PRIOR FILING DATE: 2002-03-07
| PRIOR FILING DATE: 2002-08-08
| PRIOR FILING DATE: 1999-04-12
| PRIOR FILING DATE: 1999-04-12
| PRIOR FILING DATE: 1999-04-13
| PRIOR FILING DATE: 1999-04-13
| PRIOR FILING DATE: 1999-01-08
| NUMBER: PROPELICATION NUMBER: 60/081,550
| PRIOR FILING DATE: 1999-01-08
| NUMBER: PROPELICATION NUMBER: 60/115,142
| PRIOR FILING DATE: 1999-01-08
| NUMBER: PATENTING DATE: 1999-01-08
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; Sequence 33, Application US/10383930
; Publication No. US20040127400A1
; GENERAL INFORMATION:
    APPLICANT: Smith, Daniel J
    APPLICANT: Taubman, Martin A
    TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
    FILE REFERENCE: 25669-018
; CURRENT FILING DATE: 2003-03-07
; PRIOR PAPLICATION NUMBER: 60/402,483
; PRIOR PAPLICATION NUMBER: 60/363,209
; PRIOR PILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/363,209
; PRIOR APPLICATION NUMBER: 60/363,209
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
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                                                                                                                                        Score 94; DB 4; Length 431;
Pred. No. 2.1e-06;
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100.0%; Score 94; DB
Best Local Similarity 100.0%; Pred. No. 2.1
Matches 20; Conservative 0; Mismatches
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; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-10-383-930-30
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; ORGANISM: Streptococcus mutans
US-10-383-930-33
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PRIOR APPLICATION NUMBER: 60/081,550
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR FILING DATE: 1999-01-08
NUMBER: OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.2
SEQ ID NO 33
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Matches 20; Conservative
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Publication No. US20050031633A1

GENERAL INFORMATION:

APPLICANT: Buith, Daniel J.

APPLICANT: Taubman, Martin A.

TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens

TITLE OF INVENTION Glucan Binding Protein and Glycosyltransferase Immunogens

TITLE OF INVENTION NUMBER: US/10/797,821

CURRENT FILING DATE: 2004-03-09

PRIOR APPLICATION NUMBER: 60/363,209

PRIOR PELICATION NUMBER: 60/363,209

PRIOR PELICATION NUMBER: 60/402,483

PRIOR FILING DATE: 2002-08-08

PRIOR FILING DATE: 1999-04-12

PRIOR FILING DATE: 1999-04-12

PRIOR FILING DATE: 1999-04-13

PRIOR FILING DATE: 1998-04-13

SEQ ID NO 30

LENGTH: 431
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; Publication No. US20050031633A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Daniel J.
; APPLICANT: Taubman, Martin A.
; TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens
; FILE REFERENCE: 25669-020
; CURRENT APPLICATION NUMBER: US/10/797,821
; CURRENT FILING DATE: 2004-03-09
; PRIOR FILING DATE: 2003-03-07
; PRIOR FILING DATE: 2002-03-07
; PRIOR FILING DATE: 2002-03-07
; PRIOR PRILING DATE: 2002-03-07
; PRIOR PRILING DATE: 2002-03-07
; PRIOR FILING DATE: 2002-03-07
; PRIOR FILING DATE: 2002-03-07
; PRIOR FILING DATE: 10999-04-12
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                                                                                                                 100.0%; Score 94; DB 5; Length 431; 100.0%; Pred. No. 2.1e-06;
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                      TYPE: PRT; ORGANISM: Streptococcus mutans US-10-797-821-29
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                                                                                                                                     Best Local Similarity 100.
Matches 20; Conservative
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US-10-797-821-33
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  LENGTH: 431
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US-10-383-930-31
Squence 31, Application US/10383930
Squence 31, Application US/10383930
Squence 31, Application US/10383930
Squence 31, Application US/10383930
STILE APPLICANT: Smith, Daniel J
STILE APPLICANT: Taubman, Martin A
TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
STILE APPLICANTION: Immunogenicity of Glucan Binding Protein
STILE APPLICANTION: IMMUNER: US/10/383,930
CURRENT FILING DATE: 2003-03-07
SPRIOR FILING DATE: 2002-08-08
SPRIOR FILING DATE: 2002-08-08
SPRIOR FILING DATE: 2002-08-08
SPRIOR FILING DATE: 2002-08-08
SPRIOR FILING DATE: 2002-08-08
SUMMER OF SEQ ID NOS: 41
SOPTWARE: Patentin version 3.2
SSOILD NOS: 31
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## Sequence 32, Application US/10383930

## Sequence 32, Application US/10383930

## Sequence 32, Application William Sequence 32, Application No. US20040127400A1

## APPLICANT: Smith, Daniel J

## APPLICANT: Taubman, Martin A

## TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein FILE REPERBERS: 25669-018

## CURRENT APPLICATION NUMBER: US/10/383,930

## CURRENT PILING DATE: 2003-03-07

## PRIOR PILING DATE: 2002-08-08

## PRIOR PILING DATE: 2002-03-07

## NUMBER OF SEQ ID NOS: 41

## SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 94; DB 4; Length 432; Best Local Similarity 100.0%; Pred. No. 2.1e-06; Matches 20; Conservative 0; Mismatches 0; Indels
      Length 431;
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100.0%; Score 94; DB 5; I
100.0%; Pred. No. 2.1e-06;
iive 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: 60/115,142
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.2
SEQ ID NO 32
LENGTH: 432
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                                                                                                                                                                                      ; ORGANISM: Streptococcus mutans
US-10-797-821-32
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US-10-797-821-8
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US-10-383-930-8
                                                                                                                                                                TYPE: PRT
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Publication No. US20050031633A1

GENERAL INPORMATION:

APPLICANT: Smith, Daniel J.

APPLICANT: Taubman, Martin A.

TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens

FILE REFERENCE: 25669-020

CURRENT APPLICATION NUMBER: US/10/797,821

CURRENT PILING DATE: 2004-03-09

PRIOR APPLICATION NUMBER: 60/363,209

PRIOR FILING DATE: 2002-03-07

PRIOR FILING DATE: 2002-08-08

PRIOR FILING DATE: 2002-08-08

PRIOR PILING DATE: 2002-09-04

PRIOR PILING DATE: 1999-04-12

PRIOR FILING DATE: 1999-04-12
                                                                                                                                                                                                                                                                                                                                                                 ## Sequence 31, Application US/10797821
## Sequence 31, Application US/200503163341
## Sequence 31, Application No. US2005003163341
## Sequence 31, Application No. US2005003163341
## Sequence 31, Application No. US2005003163341
## APPLICANT: Smith, Daniel J.
## APPLICANT: Smith, Daniel J.
## TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens
## TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens
## TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens
## TITLE OF INVENTION: UNMBER: US/10/797, 821
## CURRENT PILING DATE: 2004-03-07
## PRIOR PELICATION NUMBER: 60/363,209
## PRIOR PELICATION NUMBER: 60/363,209
## PRIOR PELICATION NUMBER: 60/402,483
## PRIOR PELICATION NUMBER: 60/402,483
## PRIOR PELICATION NUMBER: 60/081,550
## PRIOR PELICATION NUMBER: 60/081,550
## PRIOR PILING DATE: 1998-04-13
## PRIOR PILING DATE: 1999-01-08
## NUMBER OF SEQ ID NOS: 45
## SOO TO NOS: 45
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100.0%; Score 94; DB 4; L
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 20; Conservative 0; Mismatches 0;
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; ORGANISM: Streptococcus mutans US-10-383-930-32
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US-10-797-821-31
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Sequence 8, Application US/10797821

| Publication No. US20050031633A1
| GENERAL INPORMATION:
| APPLICANT: Smith, Daniel J. |
| APPLICANT: Smith, Daniel J. |
| APPLICANT: Taubman, Martin A. |
| TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens |
| TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens |
| TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens |
| TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens |
| TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens |
| TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens |
| PRIOR APPLICATION NUMBER: 1004-03-09 |
| PRIOR FILING DATE: 2002-03-07 |
| PRIOR FILING DATE: 1999-04-12 |
| PRIOR APPLICATION NUMBER: 09/290,049 |
| PRIOR APPLICATION NUMBER: 06/081,550 |
| PRIOR APPLICATION NUMBER: 06/081,550 |
| PRIOR PILING DATE: 1998-04-13 |
| PRIOR APPLICATION NUMBER: 06/115,142
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Sequence 8, Application US/10383930

Publication No. US20040127400A1

GENERAL INFORMATION:

APPLICANT: Smith Daniel J

TITLE OF INVENTYON: Immunogenicity of Glucan Binding Protein

FITLE OF INVENTYON: Immunogenicity of Glucan Binding Protein

FILE REFERENCE: 25669-018

CURRENT APPLICATION NUMBER: US/10/383,930

CURRENT APPLICATION NUMBER: 60/402,483

PRIOR PLING DATE: 2002-08-08

PRIOR FILING DATE: 2002-03-07

PRIOR FILING DATE: 2002-03-07

NUMBER OF SEQ ID NOS: 41

SOFTWARE PATENTIN VERSION 3.2
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       Length 432;
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Query Match
100.0%; Score 94; DB 5; I
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 20; Conservative 0; Mismatches 0;
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US-10-383-930-2
; Sequence 2. Application US/10383930
; Publication No. US20040127400A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Daniel J
; APPLICANT: Taubman, Martin A
; TILLE OF INVENTION: Immunogenicity of Glucan Binding Protein
; FILE REFERENCE: 25669-018
; CURRENT FILING DATE: 2003-03-07
; PRIOR FILING DATE: 2003-03-07
; PRIOR PLILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/402,483
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2
; LEMOTH: 20
; TYPE: PRT
; ORGANISM: Streptccoccus mutans
US-10-383-930-2
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; OTHER INFORMATION: GbpB peptide
US-10-797-821-8
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.2
SEQ ID NO 8
LENGTH: 20
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ORGANISM: Artificial
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Search completed: January 25, 2006, 20:10:04 Job time : 60 secs

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RESULT 2
US-11-052-554A-252
US-11-052-554A-252
US-11-052-554A-252
Sequence 25. Application US/11052554A
Publication No. US2005028886A1
GENERAL INFORMATION:
APPLICANT'S Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT PILING DATE: 2006-02-07
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
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Matches 20; Conservative
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Sequence 10, Appl
Sequence 5304, Ap
Sequence 5, Appli
Sequence 2, Appli
Sequence 1, Appli
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Sequence 12, Appli
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                                                                                                                            January 25, 2006, 19:15:26 ; Search time 5.5 Seconds (without alignments) 39.378 Million cell updates/sec
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3: /cgn2_6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pep:*
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8: /cgn2_6/ptodata/2/pubpaa/USIO NEW PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-11-052-554A-252
US-11-147-109-10
US-10-467-657-5304
US-10-510-880-6
US-10-510-880-5
US-10-510-880-1
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US-10-834-889
                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                           75621 seqs, 10829074 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                        OM protein - protein search, using sw model
                                                                                                                                                                                                                          US-10-797-821-9
94
1 QAQVNTIQGQVSALQTQQAE 20
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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                                                                                                                                                                                                                                                                                                                        Scoring table:
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4, Appli
88, Appl
97, Appl
16, Appl
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Sequence 2
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Sequence
US-10-821-234-975
US-10-467-657-6112
US-10-467-657-6112
US-10-821-234-1285
US-11-052-54A-73
US-10-821-234-1286
US-11-077-550-64
US-11-077-550-122
US-11-077-550-122
US-11-077-550-128
US-11-077-550-128
US-11-077-550-128
US-11-077-550-128
US-11-077-550-128
US-11-077-550-128
US-11-077-550-128
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US-11-077-550-128
US-11-077-550-128
US-11-081-688-4
US-11-081-688-4
US-11-081-688-4
US-11-118-881-88
US-10-508-253-16
US-11-467-657-568
US-11-467-657-568
US-11-188-743-25
  1122
2228
2228
1325
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1448
173
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228
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# ALIGNMENTS

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## Sequence 210, Application US/11052554A

## Sequence 210, Application US/11052554A

## Sequence 210, Application US/11052554A

## Sequence 210, Application US/11052554A

## SEQUENCE 210, Application US/11052554A

## TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE

## TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE

## TITLE OF INVENTION: COMPUTATION OF THERAPEUTIC POTENTIAL

## CURRENT APPLICATION NUMBER: US/11/052,554A

## CURRENT PELING DATE: 2004-02-07

## PRIOR APPLICATION NUMBER: US 60/589,227

## PRIOR FILING DATE: 2004-07-20

## PRIOR FILING DATE: 2004-02-06

## NUMBER OF SEQ ID NOS: 763

## SOFTWARE: Patentin Version 3.3

## SEQ ID NO 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Streptococcus mutans UA159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 OAQVNTIQGQVSALQTQQAE 20
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ORGANISM: Homo sapiens
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US-10-977-334-2
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Publication No. US20050278805A1

GENERAL INFORMATION:

APPLICANT: Shen, Bo

TITLE OF INVENTION: Method of Increasing Seed Oil Content in TITLE OF INVENTION: Plants

FILE REFERENCE: 1409P

CURRENT FILING DATE: 2005-06-07

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 10

LENGTH: 768
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APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: FONTANA Maria Rita
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REPERENCE:
CURRENT PILING DATE: 2003-08-11
FRICA APPLICATION NUMBER: GB-0103424.8
FRICA APPLICATION NUMBER: GB-0103424.8
FRICA REPLICATION NUMBER: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWing9, version 1.04
SEQ ID NO 5304
LENGTH: 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 47.9%; Score 45; DB 6; Length 642; Best Local Similarity 35.0%; Pred. No. 5.2; Matches 7; Conservative 9; Mismatches 4; Indels
                                                                                                                                           Ouery Match 54.3%; Score 51; DB 7; Length 398; Best Local Similarity 55.6%; Pred. No. 0.32; Matches 10; Conservative 5; Mismatches 3; Indels
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                                                                                ) ORGANISM: Streptococcus pyogenes MGAS8232
US-11-052-554A-252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5304, Application US/10467657 Publication No. US20050260581A1 GENERAL INFORMATION:
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US-10-467-657-5304
                                                                                                                                                                                                                                1 QAQVNTIQGQVSALQTQQ 18
SOFTWARE: Patentin version 3.3 SEQ ID NO 252 LENGTH: 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Phalaenopsis sp.
US-11-147-109-10
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                                                               TYPE: PRT
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FUDIICACION NO. US20050244904A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: DIAGNOSTICS BASED ON SIGNAL PEPTIDE DETECTION

FILE REFERENCE: ISA-016.01

CURRENT PILLING DATE: 2004-10-29

PRIOR PILLING DATE: 2004-10-29

PRIOR PILLING DATE: 2004-02-06

PRIOR PILLING DATE: 2004-02-06

PRIOR PILLING DATE: 2003-10-29

NUMBER: OF SEQ ID NOS: 8

SOFTWARE: PALENTIN VET: 3.3

SEQ ID NO 2
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APPLICANT: Rehfeld, Jens Peter
APPLICANT: Received Jens Peter

APPLICANT: Reference Jens Peter

APPLICANT: Reference Jens Peter

TITLE OF INVENTION: Methods for determining levels of human
TITLE OF INVENTION: B-type natriuretic peptide precursors

TITLE OF INVENTION: B-type natriuretic peptide precursors

TITLE OF INVENTION: B-type natriuretic peptide precursors

CURRENT APPLICATION NUMBER: 105/10/510,880

CURRENT FILING DATE: 2004-10-08

PRIOR FILING DATE: 2003-04-11

PRIOR FILING DATE: 2002-04-11

PRIOR FILING DATE: 2002-04-11

NUMBER OF SEQ ID NOS: 7

NUMBER OF SEQ ID NOS: 7

SEQ ID NO 6
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| ::: : :::||:|||
573 QRELDALPDEIAALETEQAE 592
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US-10-510-880-5
; Sequence 5, Application US/10510880
                                                                                                                                        Sequence 6, Application US/10510880; Publication No. US20050244902A1; GENERAL INFORMATION:
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Best Local Similarity 50.0%;
Matches 9; Conservative
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Matches 9; Conservative
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RESULT 9
US-10-299-977-1
Sequence 1, Application US/10299977
Publication No. US20050287613A1
GENERAL INFORMATION:
APPLICANT: Jackowski, George
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     18 QEQRNHLQGKLSELQVEQ 35
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Best Local Similarity 50.0°
Matches 9; Conservative
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; ORGANISM: Homo sapiens
US-10-299-977-1
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; ORGANISM: Homo sapiens
US-10-510-880-1
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LENGTH: 134
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; Sequence 1, Application US/10875800
; Sequence 1, Application US/10875800
; Publication No. US20050255484A1
; GENERAL INFORMATION:
; APPLICANT: VALKIES, GUNARS
; APPLICANT: DAHLEN, UBER
; APPLICANT: EDECHLER, KEN
; TITLE OF INVENTION: DIAGNOSTIC MARKERS OF STROKE AND CEREBRAL INJURY APPLICANT: EUGHLORY OF USE THEREOF
; TITLE OF INVENTION: METHODS OF USE THEREOF
; TITLE OF INVENTION: METHODS OF USE THEREOF
; TITLE OF INVENTION: METHODS OF USE THEREOF
; TITLE OF INVENTION: METHODS OF USE THEREOF
; TITLE OF INVENTION WUMBER: US/10/714,078
; PRIOR FILING DATE: 2003-02-20
; PRIOR FILING DATE: 2003-02-20
; PRIOR FILING DATE: 2001-02-20
; PRIOR PILING DATE: 2001-08-20
; PRIOR FILING DATE: 2001-08-20
; PRIOR FILING DATE: 2001-08-20
; PRIOR FILING DATE: 2001-03
; PRIOR FILING DATE: 2001-03
; PRIOR FILING DATE: 2001-01-11-30
; PRIOR FILING DATE: 2001-02
; PRIOR FILING DATE: 2002-01-02
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                                             APPLICANT: Getze, Jens F.
APPLICANT: Getze, Jens Peter
APPLICANT: Righspospitalet
TITLE OF INVENTION: Methods for determining levels of human
TITLE OF INVENTION: Methods for determining levels of human
TITLE OF INVENTION: Methods for determining levels of human
TITLE OF INVENTION: Methods for determining levels of human
TITLE OF INVENTION: Methods for determining levels of human
TITLE OF INVENTION: METHOD METHOD ADDITION NUMBER: US/10/510,880
CURRENT APPLICATION NUMBER: PCT/DK03/00250
PRIOR PILING DATE: 2003-04-11
PRIOR FILING DATE: 2003-04-11
PRIOR FILING DATE: 2002-04-11
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44; DB 6; Length 108;
Pred. No. 0.97;
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Best Local Similarity 50.0%;
Matches 9; Conservative 4
Publication No. US20050244902A1
GENERAL INFORMATION:
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Best Local Similarity 50.0*
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE.
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-510-880-5
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APPLICANT: Kupchak, Peters
APPLICANT: Stanton, Eric
APPLICANT: Stanton, Eric
APPLICANT: Stanton, Eric
APPLICANT: Stanton, Eric
APPLICANT: Stanton, Eric
TILE OF INVENTION: Polyclonal-Polyclonal ELISA Assay For Detecting N-Terminus ProBNE
FILE REFERENCE: 2132.127
CURRENT APPLICATION NUMBER: US/10/299,977
CURRENT APPLICATION NUMBER: US/10/299,977
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
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Sequence 1, Application US/10510880

Publication No. US20050244902A1

SERNERAL INFORMATION:

APPLICANT: Rehfeld, Jens F.

APPLICANT: Righspospitalet

TITLE OF INVENTION: Methods for determining levels of human

TITLE OF INVENTION: B-type natriuretic peptide precursors

FILE REFERENCE: 271212000200

CURRENT APPLICATION WUMBER: US/10/510,880

CURRENT FILING DATE: 2004-10-08

PRIOR FILING DATE: 2003-04-11

PRIOR FILING DATE: 2003-04-11

PRIOR FILING DATE: 2002-04-11

NUMBER OF SEQ ID NOS: 7

SOFTWARE FRAEESEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44; DB 6; Length 108;
Pred. No. 0.97;
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; Publication No. US20050255484A1
; GENERAL INFORMATION:
; APPLICANT: VALKIRS, GUNARS
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APPLICANT: Wang, Zhiwel

APPLICANT: Zhang, Zhiwel

APPLICANT: Zhang, Jie

APPLICANT: Zhang, Jie

APPLICANT: Zhou, Fing

APPLICANT: Cao, Yi-Cheng

APPLICANT: Dramanc, Radoje T.

TITLE OF INVENTION: NOVel Nucleic Acids and Polypeptides

FILE REFERENCE: 785CIP4CN

CURRENT APPLICATION NUMBER: US/11/000,463

CURRENT APPLICATION NUMBER: 10/291,265

PRIOR FILING DATE: 2001-01-25

PRIOR FILING DATE: 2001-01-25

PRIOR PILING DATE: 2001-01-25

PRIOR PILING DATE: 2000-01-25

PRIOR FILING DATE: 2000-07-17

PRIOR FILING DATE: 2000-07-17

PRIOR FILING DATE: 2000-07-17

PRIOR FILING DATE: 2000-07-17

PRIOR APPLICATION NUMBER: 09/611,746

PRIOR FILING DATE: 2000-07-17

PRIOR APPLICATION NUMBER: 09/631,451

PRIOR PILING DATE: 2000-09-15

PRIOR PILING DATE: 2000-09-15
                                                                                                                                                                                                                                               46.8%; Score 44; DB 7; Length 162; 50.0%; Pred. No. 1.5;
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 454
CURRENT APPLICATION NUMBER: US/11/043,590
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 13
LENGTH: 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 454, Application US/11000463
Publication No. US20050266423A1
GENERAL INFORMATION:
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; Sequence 58, Application US/11069834
; Publication No. US20050276811A1
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Chen, Rul-hong
APPLICANT: Clan, Xiaohong B.
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US-11-000-463-454
                                                                                                                                                                    ORGANISM: Homo sapiens
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Matches 9; Conserv
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Best Local &
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APPLICANT: Compugen Ltd
TITLE COMPUGEN INVOIS Brain Natriuretic Peptide Variants and Methods of use there
FILE REFERENCE: 1847.1011
CURRENT APPLICATION NUMBER: US/11/043,590
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 12
           APPLICANT: DAHLEN, JEFF
APPLICANT: KIRCHICK, HOWARD
APPLICANT: KIRCHICK, HOWARD
APPLICANT: KIRCHICK, HOWARD
TITLE OF INVENTION: DIAGNOSTIC MARKERS OF STROKE AND CEREBRAL INJURY AND
TITLE OF INVENTION: DIAGNOSTIC MARKERS OF STROKE AND CEREBRAL INJURY AND
FILE REFERENCE: 071349-5408
CURRENT APPLICATION NUMBER: US/10/714,078
PRIOR PELLOR APPLICATION NUMBER: US/10/714,078
PRIOR FILING DATE: 2003-02-20
PRIOR FILING DATE: 2002-08-20
PRIOR FILING DATE: 2002-08-20
PRIOR PELLOR APPLICATION NUMBER: PCT/US02/26604
PRIOR APPLICATION NUMBER: 60/313,75
PRIOR PELLOR DATE: 2001-08-20
PRIOR PELLOR DATE: 2001-08-20
PRIOR PELLOR DATE: 2001-08-20
PRIOR PELLOR DATE: 2001-08-20
PRIOR PELLOR DATE: 2001-10-30
PRIOR PELLOR DATE: 2001-10-30
PRIOR PELLOR DATE: 2001-11-30
PRIOR PELLOR PELLOR DATE: 2001-11-30
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4; Mismatches
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Best Local Similarity 50.0%;
Matches 9; Conservative
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Matches 9; Conservative
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US-11-043-590-12
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ORGANISM: Homo sapiens
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GENERAL INFORMATION:

APPLICANT: CARROLL, MICHAEL C.
APPLICANT: MOORE JR., FRANCIS D.
APPLICANT: MECHYAN, HERBERT B.
TITLE OF INFERTION: NATURAL IGM ANTIBODIES AND INHIBITORS THEREOF
FILE REFERENCE: CRA-002.01
CURRENT APPLICATION NUMBER: 05/58,648
PRIOR PILING DATE: 2004-03-01
PRIOR APPLICATION NUMBER: 60/549,123
PRIOR FILING DATE: 2004-07-16
PRIOR APPLICATION NUMBER: 60/549,123
PRIOR PILING DATE: 2004-03-01
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PARENTIN Ver. 3.3
IENGTH: 1992
TYDE: RRT
TYDE: RRT
ORGANISM: MUS MUS WUSCULUS
US-11-069-834-58
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 GenCore version
Copyright (c) 1993 - 2006
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Maximum Match 100%
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Maximum DB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description :	Add93630 Streptoco	Adx37253 Streptoco	-	Add93650 Streptoco	Add93653 Streptoco		Adx37273 Streptoco	Adx37276 Streptoco	Aeb91500 Microbial	Add93651 Streptoco	Add93652 Streptoco	Adx37274 Streptoco	Adx37275 Streptoco	Abp25918 Streptoco	Abp29684 Streptoco	Adu69524 S agalact	Adv88392 Streptoco	Adv81808 Streptoco	Adv79645 Streptoco	Abp25919 Streptoco	Adr83884 S. pyogen	Aeb91542 Microbial	Aay22579 Bacterial	Abu02747 S. pneumo
SUMMARIES	ΩI	ADD93630	ADX37253	ADD93649	ADD93650	ADD93653	ADX37272	ADX37273	ADX37276	AEB91500	ADD93651	ADD93652	ADX37274	ADX37275	ABP25918	ABP29684	ADU69524	ADV88392	ADV81808	ADV79645	ABP25919	ADR83884	AEB91542	AAY22579	ABU02747
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de	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	89.1	89.1	89.1	89.1	89.1	89.1	9.69	9.69	9.69	53.3	53.3
	Score	92	92	92	92	92	92	92	92	92	92	92	92	92	82	82	82	82	82	82	64	64	64	49	49
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392 8 ADK47859 392 8 ADT50226 392 8 ADT50226 393 9 ADT50165 393 9 AEA58465 415 8 ADG76637 415 8 ADG76637 422 2 ABP31138 422 2 ABP43470 422 5 ABP43470 422 6 ABU13749 449 5 ABU38497 449 6 ABU38497 449 6 ABU38497 449 6 ABU38497 449 6 ABU38497 449 6 ABU38497 449 6 ABU38497 449 6 ABU38497 449 6 ABU38497 449 6 ABU38497 449 6 ABU38497 449 6 ABU38497 449 6 ABU38497	Adk47859 Streptoco Adt50227 S pneumon Adt50226 S pneumon Adt50165 S pneumon	Adr94595 Novel S. Aea58465 Streptoco Adg76637 Phospholi Abb71138 Drosophil		Abu88498 E. faecal Abu13749 Enterococ Ady39218 Novel Ent		Adv16734 E. faecal Ady39216 Novel Ent Adh87829 Enterococ
	ADK47859 ADT50227 ADT50226 ADT50165	ADR94595 AEA58465 ADG76637 ABB71138	ADS11023 AAY00251 ABP43470	ABU88498 ABU13749 ADY39218 AAY00250	ABP43469 ABU88497 ABU13748	ADV16734 ADY39216 ADH87829
	392 8 392 8 392 8	399 8 399 9 415 8 578 4	281 8 422 2 422 5	9000	, 0, 0, 0	449 9 449 9 450 7
	53.3 53.3 53.3	53.3 53.3 53.3	51.6 51.1 51.1	51.1	51.1 51.1 51.1	51.1 51.1 51.1
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	25 26 27 28	33 33 35 35 35	3 3 3 5 4 3	36 38 39	444	44 44 5

### ALIGNMENTS

Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein. Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen. Streptococcus mutans glucan binding protein-B peptide fragment. ADD93630 standard; peptide; 20 AA. 07-MAR-2003; 2003WO-US006962. 07-MAR-2002; 2002US-0363209P. 08-AUG-2002; 2002US-0402483P. (first entry) Taubman MA; Streptococcus mutans. (FORS-) FORSYTH INST. WPI; 2003-845091/78. WO2003075845-A2 29-JAN-2004 18-SEP-2003. Smith DJ, ADD93630; RESULT 1 ADD93630 

Claim 11; Page 10; 49pp; English.

The present sequence is that of a peptide comprising amino acid residues 88-107 of the glucan binding protein-B (GbpB) of Streptococcus mutans strain SX23 ADD93649. The peptide binds to a major histocompatibility complex (MHC) class II protein. It was identified as a potential B cell epitope using a matrix-based algorithm for epitope prediction, which was used to search the primary amino acid sequence of GbpB for known MHC class II binding motifs. The peptide can be used in immunogenic compositions and subunit vaccines for dental caries. These comprise MHC class II protein-binding GbpB peptides covalently linked with peptide subunits (preferably from the catalytic domain) of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Diepitopic or multiepitopic polypeptides can be

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Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
                                                                                                                                  Streptococcus mutans glucan binding protein-B.
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174. .193
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/note= "HLA-binding peptide"

    33. .52
    /note= "HLA-binding peptide"

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re= "HLA-binding peptide"
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e= "HLA-binding
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/note= "HLA-binding
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                                                    ADD93649 standard; protein; 431 AA.
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08-AUG-2002; 2002US-0402483P.
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/note= "HL
289. .308
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                                                                                                                                                                                        Streptococcus mutans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New composition comprising a fragment of a glucan binding protein-B (dppB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
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prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in
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                                                                                                                                                                                                                                                                                                                                     immunogenicity; immune stimulation; glucan binding protein-B; microparticle; major histocompatibility complex; tooth disease.
                                                                             Score 92; DB 7; Length 20; Pred. No. 1.3e-08;
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                                                                                                                                                                                                                                                                                                             Streptococcus mutant glucan binding protein B peptide #10.
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                                                                                                          0; Mismatches
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                                                                                                                                                                                                                               ADX37253 standard; peptide; 20 AA
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Best Local Similarity 100.0%;
Matches 20; Conservative 0;
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08-JAN-1999; 9US-0115142P.
12-APR-1999; 99US-020049.
07-MAR-2002; 2002US-0363209P.
08-AUG-2002; 2002US-0402483P.
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07-MAR-2003; 2003US-00383930.
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                              passive immunisation.
                                                                                                                                                                                                                                                                                                                                                                                Streptococcus mutans.
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(TAUB/) TAUBMAN M A.
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protein B (GDpB) of Streptococcus mutans strain SK32. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The includes a number of human leucocyte antigen (HLA)-binding epitopes. The caries. The compositions comprise major histocompatibility complex (MHC) class II protein-binding GDpB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Diepitopic or multiepitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GDpB can be used in
                                                        Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.
                                                                                                                                                                                                                     The present sequence is the protein sequence of the glucan binding
                                                                                                                                                                       Claim 6; Page 7; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  passive immunisation.
2003-845091/78.
                       GENBANK; AY046410
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Query Match
100.0%; Score 92; DB 7; I
Best Local Similarity 100.0%; Pred. No. 4.3e-07;
Matches 20; Conservative 0; Mismatches 0; QQIQTLSSKIVARNESLKQQ 107 1 QQIQTLSSKIVARNESLKQQ 20 ò

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ADD93650 standard; protein; 431 AA. 29-JAN-2004 ADD93650; RESULT 4 ADD93650

Streptococcus mutans glucan binding protein-B. (first entry) 

Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.

Streptococcus mutans.

WO2003075845-A2.

18-SEP-2003

07-MAR-2003; 2003WO-US006962

07-MAR-2002; 2002US-0363209P.

(FORS-) FORSYTH INST.

Taubman MA; Smith DJ,

WPI; 2003-845091/78. GENBANK; AY046411. Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein. Claim 5; Page 8; 49pp; English.

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caries. The compositions comprise major histocompatibility complex (MHC) class II protein-binding GbpB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Disptopic or multisptopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in
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Best Local Similarity
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ADD93653 standard; protein; 431 AA (first entry) 29-JAN-2004 ADD93653; RESULT 5 ADD93653 

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Gaps

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Length 431; Indels Streptococcus mutans glucan binding protein-B.

Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen. Streptococcus mutans

WO2003075845-A2.

18-SEP-2003

07-MAR-2003; 2003WO-US006962

07-MAR-2002; 2002US-0363209P.

(FORS-) FORSYTH INST

Taubman MA; Smith DJ,

2003-845091/78. GENBANK; AY046414. Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein.

5; Page 8-9; 49pp; English. Claim

The present sequence is the protein sequence of the glucan binding protein-B (GbpB) of Streptococcus mutans strain SSM3. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions comprise major histocompatibility complex (MHC) class II protein-binding GbpB peptides, especially HLA-binding peptides, covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of an antibody in a mammal. Dispitopic or multipatiopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in passive immunisation.

Sequence 431 AA;

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The present sequence is the protein sequence of the glucan binding protein-B (GbB) of Streptococcus mutans strain 3VF4. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. Invention provides immunogenic compositions and vaccines for dental invention

Score 92; DB 7; Length 431; Pred. No. 4.3e-07; 100.0%; Query Match Best Local Similarity

Matches

RESULT 6 ADX37272

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New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
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microparticle; major histocompatibility complex; tooth disease.
                                                              immunogenicity; immune stimulation; glucan binding protein-B; microparticle; major histocompatibility complex; tooth disease.
                             Streptococcus mutant glucan binding protein B variant #2.
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100.0%; Pred. No. 4.3e-07;
iive 0; Mismatches 0;
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12-APR-1999; 99US-00290049.
07-MAR-2002; 2002US-0363209P.
08-AUG-2002; 2003US-0405483P.
07-MAR-2003; 2003US-00383930.
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21-APR-2005 (first entry)
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                                                                                                                        Streptococcus mutans
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(TAUB/) TAUBMAN M A.
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nes 20; Conservative
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TAUBMAN M A.
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08-JAN-1999;
12-APR-1999;
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10-FEB-2005

ADX37273

RESULT 7 ADX37273

Best Loc Matches

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Length 431;

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The present invention relates to a computational method (M1) for identifying adhesin and adhesin-like proteins, by computing the sequence-based attributes of protein sequences using five attribute modules of a neural network software, training an artificial neural network (ANN) for each of the computed five attributes, and identifying the adhesin and adhesin-like proteins an artificial neural network (ANN) for each of the computed five attributes, and identifying the adhesin and adhesin-like proteins, having 274 fully defined 162-encoding adhesin and adhesin-like proteins, having 105 fully defined 306-18976 base pairs (SEQ ID NO: 385-658) sequences; a set of 105 hypothetical genes encoding adhesin and adhesin-like proteins, having 105 fully defined 306-18976 base pairs (SEQ ID NO: 12-79); a set of 105 hypothetical adhesin and adhesin-like proteins, having 105 fully defined 106-5291 base pair (SEQ ID NO: 12-79); a set of 105 hypothetical adhesin-like proteins, having 105 fully defined 106-5291 base pair (SEQ ID NO: 280-384) sequences; and a fully connected multilayer feed forward ANN (I) based on (M1). (M1) is useful for identifying and adhesin-like proteins, of therapeutic potential. And identifying and short-listing proteins for further testing in development of new vaccine formulations cueful for identifying putative adhesins that are important in drug discusses caused by various pathogenic organisms. (M1) is cueful for identifying putative adhesins that are important in drug distantly valuary and understant and uninary racet infections. (M1) identifies adhesins from distantly valuary and preventing therapeutics for whooping cough, pneumonia, and distantly valuary and uninary racet infections. (M1) identifies from the proteins and uninary racet infections. (M1) identifies in the proteins and uninary racet infections. (M1) identifies in the proteins and uninary racet infections. (M1) identifies in the proteins and uninary racet infections. (M1) identifies in the proteins and praventing the proteins and pravent
  Computational method for identifying adhesin and adhesin like molecules, comprises computing sequence-based attributes of protein sequences using neural network software and training an artificial neural network.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gastric ulcer and urinary tract infections. (MI) identilies aumerable distantly related organisms, and from bacteria belonging to a wide phylogenetic spectrum. (MI) is capable of predicting adhesive nature of unique proteins. The present sequence is a microbial pathogen adhesin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.
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100.0%; Pred. No. 4.3e-07;
iive 0; Mismatches 0;
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                                                                                                  Claim 16; SEQ ID NO 210; 402pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADD93651 standard; protein; 432 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus mutans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 431 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a composition comprising a fragment of a glucan binding protein-B (GbpB) and a biocompatible microparticle, where the fragment binds to a major histocompatibility complex (MHC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds to a Streptococcus mutans GbpB protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                     New composition comprising a fragment of a glucan binding protein-B (dppB) that binds to MiC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing mammals against dental caries.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; SEQ ID NO 33; 73pp; English.
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                                               98US-0081550P.
99US-0115142P.
99US-00290049.
2002US-0363209P.
09-MAR-2004; 2004US-00797821
                                                                                                                                                                      07-MAR-2003; 2003US-00383930
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2004US-0589227P
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                                                                                                                                                                                                                                                                                                Smith DJ, Taubman MA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus mutans.
                                                                                                                                                                                                                      (SMIT/) SMITH D J.
(TAUB/) TAUBMAN M A.
                                                                                                                                                                                                                                                                                                                                                     WPI; 2005-151644/16.
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                                             13-APR-1998;
08-JAN-1999;
12-APR-1999;
07-MAR-2002;
08-AUG-2002;
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20-JUL-2004;
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AEB91500
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The present sequence is the protein sequence of the glucan binding protein—B (GbpB) of Streptococcus mutans strain 15JP2. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions comprise major histocompatibility complex (WHC) class II protein-binding GbpB peptides, especially HLA-binding peptides, compositions are used in a claimed method of eliciting production of an antibody in a mammal. Dispitopic or multicipitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein. English. Claim 5; Page 8; 49pp; passive immunisation

100.0%; Score 92; DB 7; I 100.0%; Pred. No. 4.3e-07; 0; Mismatches 1 QQIQTLSSKIVARNESLKQQ 20 Local Similarity 100. Sequence 432 AA; Query Match Best Loc Matches 셤 8

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Gaps

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Length 432; Indels

QQIQTLSSKIVARNESLKQQ 107

ADD93652 standard; protein; 432 AA ADD93652; RESULT 11 

(first entry) 29-JAN-2004

Streptococcus mutans glucan binding protein-B.

Glucan binding protein-B; GbpB; vaccine; anticaries; epitope; immunogen.

Streptococcus mutans

WO2003075845-A2

18-SEP-2003

07-MAR-2003; 2003WO-US006962.

07-MAR-2002; 2002US-0363209P.

(FORS-) FORSYTH INST.

Taubman MA; Smith DJ,

WPI; 2003-845091/78. GENBANK; AY046413. Composition useful as vaccines for dental caries comprises a fragment of a glucan binding protein-B binding to a major histocompatibility complex class II protein. Claim 5; Page 8; 49pp; English.

The present sequence is the protein sequence of the glucan binding protein-B (GbpB) of Streptococcus mutans strain 3SN1. The sequence includes a number of human leucocyte antigen (HLA)-binding epitopes. The invention provides immunogenic compositions and vaccines for dental caries. The compositions comprise major histocompatiblity complex (MHC) class II protein-binding GbpB peptides, especially HLA-binding peptides,

ö ö The invention relates to a composition comprising a fragment of a glucan binding protein-B (GbpB) and a biocompatible microparticle, where the fragment binds to a major histocompatibility complex (MRIC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds to a Streptococcus mutans GbpB protein of the invention. New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing covalently linked with peptide subunits of a glucosyltransferase. The compositions are used in a claimed method of eliciting production of a antibody in a mammal. Diepitopic or multiepitopic polypeptides can be prepared synthetically or by recombinant DNA technology. Antibodies raised against MHC class II binding fragments of GbpB can be used in passive immunisation. Gaps immunogenicity; immune stimulation; glucan binding protein-B; microparticle; major histocompatibility complex; tooth disease. ö 100.0%; Score 92; DB 7; Length 432; 100.0%; Pred. No. 4.3e-07; Streptococcus mutant glucan binding protein B variant #3. Indels ö Mismatches Claim 3; SEQ ID NO 31; 73pp; English. ADX37274 standard; protein; 432 AA 88 QQIQTLSSKIVARNESLKQQ 107 1 QQIQTLSSKIVARNESLKQQ 20 ö 13-APR-1998; 98US-0081550P. 08-JAN-1999; 99US-0115142P. 12-APR-1999; 99US-00250049. 07-MAR-2002; 2002US-03623209P. 08-AUG-2002; 2002US-0402483P. 07-MAR-2003; 2003US-00383930. mammals against dental caries. 09-MAR-2004; 2004US-00797821 (first entry) 20; Conservative Taubman MA; Streptococcus mutans ΩĠ. WPI; 2005-151644/16. Local Similarity Sequence 432 AA; US2005031633-A1. (SMIT/) SMITH D TAUBMAN Sequence 432 AA; 21-APR-2005 10-FEB-2005. Smith DJ, ADX37274; Query Match (TAUB/) RESULT 12 ADX37274 Matches 8888888 8 셤

Gaps ö 100.0%; Score 92; DB 9; Length 432; 100.0%; Pred. No. 4.3e-07; ive 0; Mismatches 0; Indels Query Match Best Local Similarity 100.9

RESULT 13

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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus pyogenes), comprising one of 5481 sequences (S1), given in the specification. The proteins have entil bacterial and antiinflammatory activity. [1], nucleic acids encoding (1), ABN66044-ABN71526 and antibodies that bind (1) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (1) are used to detect Streptococcus in a biological sample. (1) is used to detect Streptococcus in a composition comprising (1) or a nucleic acid encoding (1), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (1) may be used to recombinantly produce (1) and may be used in gene therapy. Antibodies to (1) are used for affinity chromatography, immunoassays, and distinguishing/identifying
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
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                                         Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
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                                                           group A streptococcus; Streptococcus pyogenes; antibacterial; antinflammatory; infection; vaccine; meningitis; gene therapy.
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Pred. No. 2.1e-05;
3; Mismatches 0; Indels
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    Streptococcus polypeptide SEQ ID NO 1012.
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24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
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Best Local Similarity 85.0'
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(GENO-) INST GENOMIC RES.
                                                                                                                     Streptococcus agalactiae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a composition comprising a fragment of a glucan binding protein-B (GbpB) and a biocompatible microparticle, where the fragment binds to a major histocompatibility complex (MHC) class II protein. The composition is useful for producing an antibody for immunizing mammals against dental caries. This sequence corresponds to a Streptococcus mutans GbpB protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New composition comprising a fragment of a glucan binding protein-B (GbpB) that binds to MHC class II protein, and a biocompatible microparticle, useful for producing an antibody (claimed) for immunizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                              immunogenicity; immune stimulation; glucan binding protein-B;
microparticle; major histocompatibility complex; tooth disease.
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                                                                                                                                                                                                                                                         Streptococcus mutant glucan binding protein B variant #4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; SEQ ID NO 32; 73pp; English.
                                                                                                                                    ADX37275 standard; protein; 432 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP25918 standard; protein; 395 AA.
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QQIQTLSSKIVARNESLKQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mammals against dental caries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-JAN-1999; 99US-0115142P.
12-ARR-1999; 99US-00290049.
07-MAR-2002; 2002US-0363209P.
08-AUG-2002; 2002US-046483P.
07-MAR-2003; 2003US-00383930.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-MAR-2004; 2004US-00797821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0081550P
                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Taubman MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SMIT/) SMITH D J.
(TAUB/) TAUBMAN M A.
                                                                                                                                                                                                                                                                                                                                                          Streptococcus mutans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2005-151644/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                US2005031633-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-APR-1998;
08-JAN-1999;
12-APR-1999;
                                                                                                                                                                                                              21-APR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                       10-FBB-2005
                                                                                                                                                                           ADX37275;
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                                     88
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Best Loc Matches

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RESULT 14
ABP25918
1D ABP25
XX
AC ABP25
DT 02-JU

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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN7126 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
                                                                                                                                                                                                                                                                                                                                                                                              Telford J, Masignani V, Margarit Y RosI, Grandi G, Fraser C, Tettelin H;
group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 89.1%; Score 82; DB 5; Length 447; Best Local Similarity 85.0%; Pred. No. 2.4e-05; Matches 17; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 3965; 4525pp; English.
                                                                                                                                                                                                                                        27-OCT-2000; 2000GB-00026333.
24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
                                                                                                                                                                                               29-OCT-2001; 2001WO-GB004789
                                                                                                                                                                                                                                                                                                                              (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES.
                                                                  Streptococcus agalactiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-352536/38
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                                                                                                                                                      02-MAY-2002.
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1 QQIQTLSSKIVARNESLKQQ 20 ઠ

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Search completed: January 25, 2006, 19:01:45 Job time : 68.2 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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OM protein - protein search, using sw model

January 25, 2006, 18:48:55; Search time 9.1 Seconds (without alignments) 211.465 Million cell updates/sec Run on:

1 QQIQTLSSKIVARNESLKQQ 20 US-10-797-821-10 92 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing:

Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

ES		Description	secreted 45 kg pro	stresâ	CCS prot	epair	w	prophage pi3 prote	thermolabile hemol	_	hypothetical prote		hypothetical prote		ical	_	finge	ical p			hypothetical \$5.8K	clostripain-relate	hypothetical prote	Mad3 protein - mou	ATP-phosphoribosyl	probable HLH DNA	ggdef family prote	hypothetical prote	·	GGDEF family prote	100000
SUMMAKIES		ឧ	G95258	B98124	I58009	835993	T13030	D86801	H82485	D82743	H72670	G83436	T15278	T17272	T17484	E86340	T51853	G71403	C85155	S74941	JS0375	E72236	E82229	860005	E83089	T51265	C97512	T19857	T14909	AD2731	
		8	N	~	N	~	N	N	N	N	N	N	~	N	N	N	N	N	N	~	~	N	~	N	~	N	7	~	N	N	
		Length	392	392	1185	1186	1690	169	418	71	297	526	913	1780	4077	233	329	354	376	458	741	979	140	205	211	230	396	405	407	415	
	Query	Match	53.3	53.3	20.0	50.0	50.0	48.9	48.9	47.8	•	47.8	47.8	47.8	47.8	45.7	45.7	45.7	45.7	45.7	45.7	45.7	44.6	44.6	44.6	•	44.6	4	44.6	44.6	
		Score	49	49	46	46	46	45	45	44	44	44	44	44	44	42	42	42	42	42	42	42	41	41	41	41	41	41	41	41	
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AAA family ATPase Chaperonin hsp78p hypothetical prote	laminin beta-1 cha 240k tegument prot hypothetical prote hymothetical arote	radixin - mouse radixin - human radixin - pig	suppressor protein probable transcrip stress-inducible p	hypothetical prote hypothetical prote hypothetical prote
F90460 T40514 T05505	MMHUB1 WZBEZ4 T46322 T40378	A41129 A46127 S39805	S74519 B83393 C48583	S56256 G97129 T02106
000	H H 8 8		0 0 0	000
585 803 981	1786 2077 117	583 583 583	110 134 174	204 222 253
44.6 44.6 44.6	4 4 4 4 4 4 4 4 6 0 0 0	4 4 4	43.5 43.5 5.5	43.5 43.5
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30 32	33 33 45 55 55 55 55 55 55 55 55 55 55 55 55	33 38 39	4 4 4 0 1 2	4 4 4 6 4 7

# ALIGNMENTS

	KESULI 1
_	G95258
_	secreted 45 kd protein [imported] - Streptococcus pneumoniae (strain TIGR4)
	C;Species: Streptococcus pneumoniae
	C;Date: 03-Aug-2001 #sequence revision 03-Aug-2001 #text change 09-Jul-2004
	C,Accession: G95258
	R; Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Hei
	on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
	nson, T.; Hickey, B.K.; Holt, I.B.
-	Science 293, 498-506, 2001

Ajauthors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison Ajauthors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison Ajritle: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A; Mcession: G9528
A; Accession: G9528
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-39 < kCUR>
A; Cross-references: UNIPROT: Q97N55; UNIPROT: Q8DMY4; UNIPARC: UPI0000051B81; GB: AE005672; A; Gene: SP2216

Gaps ö Length 392; 4; Indels DB 2; Query Match 53.3%; Score 49; DB; Best Local Similarity 52.6%; Pred. No. 3.3; Matches 10; Conservative 5; Mismatches

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89 EITELSKNIVSRNQSLEKQ 107 2 QIQTLSSKIVARNESLKOQ 20 셤 ઠે

Gispecies: Streptococcus protein GSP-781 [imported] - Streptococcus pneumoniae (strain R6)
Cispecies: Streptococcus pneumoniae
Cispecies: Streptococcus pneumoniae
Cispecies: Streptococcus pneumoniae
Cispecies: Streptococcus pneumoniae
Cispecies: Streptococcus pneumoniae
Cispecies: Streptococcus pneumoniae Strain B93124
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; R;Hoskins, J.A.; Alborn Jr., W.; Lefkowitz, B.J.; Lu, J.; Matsushima, P.; McAhren, S.; S. J.; Bacteriol. 183, 5709-5717, 2001
A;Authors: Yi, Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R. A;Authors: Yi, Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R. A;Accession: B98124
A;Accession: B98124
A;Accession: B98124
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-392 <KUR>
A;Cross-references: UNIPROT:Q97N55; UNIPROT:Q8DMY4; UNIPARC:UPI0000051B81; GB:AE007317; C;Genetics:
A;Genetics:

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microtubule binding protein D-CLIP-190 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Accession. T13030
R;Lantz, V.A.; Miller, K.G.
J. Cell Biol. 140, 897-910, 1998
A;Titler A class VI unconventional myosin is associated with a homologue of a microtubul A;Reference number: Z17588; MUID:9412949; PMID:9472041
A;Accession: T13030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-1690 <LAN>
A;Cross-references: UNIPARC:UPI0000079B78; EMBL:AF041382; NID:g2773362; PID:g2773363; P.
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  maps
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A.Title: The human gene for xeroderma pigmentosum complementation group G (XPG) A.Reference number: 139304; MUID:94375034; PMID:8088806 A.Accession: 139304
                                                                    A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-88 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                             ; Score 46; DB 2
; Pred. No. 33;
7; Mismatches
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                                                                                                                                                                                                         A;Gene: GDB: ERCCS; ERCM2
A;Cross-references: GDB:120515; OMIM:133530
A;Introns: 13q33-13q33
A;Introns: 31st of introns is incomplete
C;Keywords: DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C,Genetics:
A,Cross-references: FlyBase:FBgn0020503
C,Keywords: cytoskeleton
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527 EQIATLQSELVSKDEALEK 545
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                                                                                                                                                                                                                                                                                                                                                                                                     50.0%;
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Best Local Similarity 40.03
Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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A; Residues: 1-95,753-889,1166-1186 <SCH>
A; Cross-reneces: UNIPARC.UPI000017COE2; EMBL:X69978
A; MacInnes, M.A.; Dickson, J.A.; Hernandez, R.R.; Learmonth, D.; Lin, G.Y.; Mudgett, J.S
Mol. Cell. Biol. 13, 6393-6402, 1993
A; Title: Human ERCCS CDNA-COSMId complementation for excision repair and bipartite amind
A; Reference number: A54439; MUID:94019313; PMID:8413238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-1186 <CLA.
A; Cross-references: UNIPROT: P28715; UNIPARC: UPI0000139014; EMBL: X69978; NID: 9298110; PLD
R; Scherly, D.; Nouspikel, T.; Corlet, J.; Ucla, C.; Bairoch, A.; Clarkson, S.G.
Rsture 353, 182-185, 1933
A; Title: Complementation of the DNA repair defect in xeroderma pigmentosum group G cells
A; Reference number: S33319; MUID: 93247645; PMID: 8483504
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-253, VV, 255-1103, DV, 1105-1186 <MAC>
A;Cross-references: UNIPARC:UPI000016A8AD; GB:L20046; NID:g306741; PIDN:AAC37533.1; PID:
A;Note: neither nucleotide sequence nor conceptual translation is complete
R;Samec, S.; Jones, T.A.; Corlet, J.; Scherly, D.; Sheer, D.; Wood, R.D.; Clarkson, S.G.
Genomics 21, 283-285, 1994
                                                                                                                                                                                                                                                                gene ERCCS protein - human

G.Speciaes: Homo sapiens (man)

C.Speciaes: Homo sapiens (man)

C.Speciaes: Homo sapiens (man)

C.Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000

C;Accession: IS8009

K;Shidoni, T.; Harada, Y.

Mutat. Res. 314, 167-175, 1994

A;Title: An ERCCS gene with homology to yeast RAD 2 is involved in group G xeroderma pig

A;Reference number: IS8009; MUID:94173288; PMID:7510366

A;Reference number: IS8009

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Molecule type: mRNA

A;Residues: 1-1185 <RES>

A;Cross-references: UNIPARC:UPI000016A8AC; GB:D16305; NID:g303606; PIDN:BAA03812.1; PID:C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA repair protein XPGC - human
NyAlternate names: xeroderma pigmentosum group G complementing factor; XP-G factor Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: 22-Nov-1993 #sequence revision 12-Apr-1996 #text_change 09-Jul-2004
Cisacession: 835993; 833319; A54439; I39304
Riclarkson, S.G.
Submitted to the EMBL Data Library, January 1993
AiReference number: 835993
AiReference number: 835993
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        Score 49; DB 2; Length 392;
Pred. No. 3.3;
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          Query Match 53.3%; Score 49; DB Best Local Similarity 52.6%; Pred. No. 3.3; Matches 10; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.0%; Score 46; 40.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Gene: GDB:ERCC5
A,Cross-references: GDB:120515; OMIM:133530
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A,Status: nucleic acid sequence not shown
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                                                                                                                                                   2 QIQTLSSKIVARNESLKQQ 20
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Best Local Similarity 40.09
Matches 8; Conservative
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C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #text_change 09-Jul-2004
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Date: 20-Aug-1999
A;Rawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takalawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Jin Res. 6 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: H72670
A;Status: preliminary
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: G39436
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; B. J., Lory, S.; Olson, M.V.
J. Lory, S.; Olson, M.V.
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A,Accession: G83436
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A;Cross-references: UNIPROT:Q91365; UNIPARC:UPI00000C5432; GB:AE004594; GB:AE004091; NI<sup>T</sup>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:Q9YDX9; UNIPARC:UPI00005DCB5; DDBJ:AP000060; NID:g5104188;
A;Experimental source: strain Kl
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein PA1660 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 44; DB 2; Length 526;
Pred. No. 30;
7; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein APE0790 - Aeropyrum pernix (strain K1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44; DB 2;
Pred. No. 16;
                                           Query Match
47.8%; Score 44; DB 2
Best Local Similarity 56.2%; Pred. No. 3.4;
Matches 9; Conservative 3; Mismatches
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C,Superfamily: uncharacterized conserved protein
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EQIETLSVELTCTNONLPOR 358
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                                                                                                                                                                                                  1 QQIQTLSSKIVARNES 16
                                                                                                                                                                                                                                              5 QQSQTTASRITARNSN 20
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Best Local Similarity 47.4
Matches 9; Conservative
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Best Local Similarity 40.0°
Matches 8; Conservative
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A; Residues: 1-297 < KAW>
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Ryanonymous, The Xylella fastidiosa Consortium of the Organization for Nycleotide Sequent Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A;Reference number: A82515; MUID:20365717; PMID:10910347

A;Reference number: A82515; MUID:20365717; PMID:10910347

A;Residues complete list of authors see reference number A59328 below

A;Residues preliminary

A;Residues: 1-71 < SIM

A;Residues: 1-71 < SIM

A;Residues: 1-71 < SIM

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A;Experimental source: serogroup O1; strain N16961; biotype Bl Tor
                                                                                                                                                                                                                                                                                                                                                                              thermolabile hemolysin VCA0218 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: H82485
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. R.R.; Mealanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
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Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
Accession: H82485
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48.9%; Score 45; DB 2; Length 418;
Best Local Similarity 40.0%; Pred. No. 16;
Matches 8; Conservative 6; Mismatches 6; Indels
                                           Indels
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C;Superfamily: phosphatidylcholine-sterol O-acyltransferase
                                           7;
47.4%; Pred. No. 5.9; ative 3; Mismatches
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                                                                                                               1 QQIQTLSSKIVARNESLKQ 19
                                           9; Conservative
Best Local Similarity
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-418 <HEI>
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C; Species: Amycolatopsis orientalis
C; Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 12-Jul-2004
C; Accession: T17484
R; Van Wageningen, A.; Kirkpatrick, P.; Williams, D.; Harris, B.; Kershaw, J.; Lennard, P. Chem. Biol. 3, 155-162, 1998
A; Title: Sequencing and analysis of genes involved in the biosynthesis of a vancomycin g
A; Reference number: 218804
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Residues: 1-4077 < VANA
A,Residues: 1-4077 < VANA
A,Residues: 1-4077 < VANA
A,Cross-references: UNIPROT: 052820; UNIPARC: UPI00001101F5; EMBL: AJ223999; NID:e1251240;
C,Superfamily: non-ribosomal peptide synthetase
C,Reywords: carrier protein; phosphopantecheine; phosphoprotein
F;501-2939/Domain: acetate-CoA ligase homology <ACLI>
F;201-2441/Domain: acetate-CoA ligase homology <ACLI>
F;3547-2554/Domain: acetate-CoA ligase homology <ACLI>
F;357-3956/Domain: acetate-CoA ligase homology <ACLI>
F;357-3956/Domain: acetate-CoA ligase homology <ACLI>
F;3877-3956/Domain: acetate-CoA ligase homology <ACLI>
F;3877-4039/Domain: acyl carrier protein homology <ACRI>
F;3877-4096/Binding site: phosphopantetheine (Ser) (covalent) #status predicted
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Nature 408, 816-820, 2000
A.; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.; Alathors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Rer, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A.; Rizzo, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A.; Rizzo, M.; Mu, D.; Yu, G.; Praser, C.M.; Venter, J.C.; Davis, R.W.
A.; Rizzo, M.; Mu, D.; Yu, G.; Praser, C.M.; Venter, J.C.; Davis, R.W.
A.; Rizzo, M.; Mu, D.; Yu, G.; Praser, C.M.; Venter, J.C.; Davis, R.W.
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A;Residues: 1-233 <STO>
A;Cross-references: UNIPARC:UPI000016D8F8; GB:AB005172; NID:g8886936; PIDN:AAF80622.1; <sup>(</sup>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein F2D10.32 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: E86340
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RING-H2 finger protein RHFla [imported] - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
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Pred. No. 26;
3; Mismatches 6; Indels
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                                                                         - Amycolatopsis orientalis
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Pred, No. 2.7e+02;
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1550 QRLRTAWNQVVARHESLR 1567
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Conservative
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                                                                             hypothetical protein PCZA363.4
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nes 8; Conserv
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1215-1261, E',1263-1418, S',1420-1608, K',1610-1780 <WES>
A;Crose-references: UNIPARC:UP1000016AD74; GB:L16782; NID:g292328; PIDN:AAC37542.1; PID:C;Genetics:
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A;Status: preliminary
A;Nolecule type: mRNA
A;Molecule type: mRNA
A;Kesidues: 575-1136, C, 1138-1608, K',1610-1780 <AAA>
A;Acsidues: 575-1136, C', 1138-1608, K',1610-1780 <AAA>
A;Esperimental source: adult testis; clone DKFZp4341152
A;Experimental source: adult testis; clone DKFZp4341152
A;Experimental source: Al S.A. 91, 714-718
A;Title: Cloning of cDNAs for M-phase phosphoproteins recognized by the MPM2 monoclonal
A;Reference number: A36881; MUID:94119956; PMID:8290587
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15279
R;Geisel, C; Wameley, P; Kramer, J.
Submitted to the EMBL Data Library, May 1997
A;Description: The sequence of C. elegans cosmid R155.
A;Reference number: Z18321
A;Accession: T15278
A;Accession: T15278
A;Accession: T15278
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A;Molecule type: mRNA
A;Residues: 1-1780 <POU>
A;Cross-references: UNIPROT:Q9UFR5; UNIPARC:UPI0000037D09; EMBL:AL117496
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K, Ansorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann,
submitted to the Protein Sequence Database, January 2000
A, Reference number: Z23028
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A;Map position: 3
A;Introns: 47/1; 68/1; 355/1; 719/1; 794/2; 864/1
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C, Keywords: phosphoprotein
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427 METLTSKFVALNEMVK 442
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C; Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C; Accession: T51853
F; Jensen, K.L.; Jespersen, H.M.; Skriver, K.
F; Jensen, K.B.; Jensen, K.L.; Jespersen, H.M.; Skriver, K.
FEBS Lett. 436, 283-7, 1998
A, Title: Widespread occurrence of a highly conserved RING-H2 zinc finger motif in the mc
A, Reference number: Z13771; MUID:98452956; PMID:9781696
A, Recession: T51853
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Residues: L-229 a, JENS
A, Residues: 1-329 a, JENS
A, Cross-references: UNIPROT:Q92743; UNIPRARC:UPI00000A8E52; EMBL:AP079181; PIDN:AAC69855.
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    Q4jf57 to Q59f27 to Q59f27 to Q59f27 to Q50f27                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus mutans.
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae, Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1] — WUCLEOTIDE SEQUENCE.
STRAIN-GS-5 Kuramitsu;
Peruzi F., Piggot P.J., Daneo-Moore L.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U7860'; AAD00288.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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211 AA; 22803 MW; 4ACB331159CFAFC6 CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Putative secreted protein (Fragment).
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Glucan-binding protein B.
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059PZ7_HUPAN
059PZ7_HUPAN
07XT48_DDROME
0190_DROME
091QY5_9VIRU
09MIED_9VIRU
09AZU7_9CAUD
09CRQ3_LACLA
056631_VIBCH
081GB0_DROME
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Q9ZAS7;
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(c) 1993 - 2006 Compugen Ltd.
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Listing first 45 summaries
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09VMT8_1
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2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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DOI=10.1128/IAI.69.4.2493-2261.2001,
Chia J.S., Lee Y.Y., Huang P.T., Chen J.Y.;
"Identification of stress-responsive genes in Streptococcus mutans by
differential display reverse transcription-PGR.";
Infect. Immun. 69:2493-2501(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein B and analysis of genetic diversity and protein production clinical isolates.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-21481977; PubMed-11598074; DO1-10.1128/TAL.69.11.6987.2001; DO1-10.1128/TAL.69.11.6987.6998.2001; Chia J.S., Chang L.Y., Shun C.T., Chang Y.Y., Chen J.Y.; a 60-kilodalten immunodominant glycoprotein is essential for cell wall integrity and the maintenance of cell shape in Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Juncan M.J.;
"Cloning of the Streptococcus mutans gene encoding glucan binding
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Immunodominant glycoprotein IDG-60 (Glucan-binding protein B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 92; DB 2; Length 431; 100.0%; Pred. No. 4e-06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=GS-5; Chang L.-Y., Lee Y.-Y., Chen J.-Y.; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                  Streptococcus mutans.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jin S., Duncan M.J., Taubman M.A., Smith D.J.; "Cloning of the gbpB gene from Streptococcus mutans."; J. Dent. Res. 79:224-224(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            431 AA; 44592 MW; 3EBE21FC5E47232E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
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EMBL; AF338445; AAK08104.1; -; Genomic_DNA.
EMBL; AF338445; AAK08104.1; -; Genomic_DNA.
InterPro; IPR07921; CHAP.
InterPro; IPR05148; SibA.
Pfam; PF0525; CHAP; 1.
PRINTS; PR01852; SIBAROTEIN.
PROSITE; PS50911; CHAP; 1.
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DOI=10.1128/IAI.69.11.6931-6941.2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Infect. Immun. 69:6987-6998(2001).
                                                                                                                                                                                                                                                      STRAIN=GS-5;
MEDLINE=21153617; PubMed=11254612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 QQIQTLSSKIVARNESLKQQ 107
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QBDWM3 STRMU
ID QBDWM3 STRMU PRELIMINARY;
OGDWM3;
DT 01-MAR-2003 (TrEMBLrel. 23, 6
DT 01-MAR-2003 (TrEMBLrel. 23, 3)
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Best Local Similarity 100.
Matches 20; Conservative
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NUCLEOTIDE SEQUENCE.
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  Duncan M.J.; "Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in
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                                                                                                                                                                                                                                                                                                                            Score 92; DB 2; Length 431;
Pred. No. 4e-06;
Mismatches 0; Indels
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DOI=10.1128/IAI.69.11.6931-6941.2001;
Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
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Pred. No. 4e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-SU32;
Jin S., Duncan M.J., Taubman M.A., Smith D.J.;
Jin S., Duncan M.J., Taubman M.A., Smith D.J.;
"Cloning of the gbpB gene from Streptococcus mutans.";
J. Dent. Res. 79:224-224 (2000).
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PRINTS; PR01852; SIBAROYEIN.
PROSITE; PS50911; CHAP; 1.
SEQUENCE 431 AA; 44620 MW; 464FE3B563FB7E51 CRC64;
                                                                                                                                                                                                                                                                             431 AA; 44650 MW; 05D38D8D8BC4609F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DRA-2004 (TrEMBLrel. 26, Last annotation update)
Glucan-binding protein B.
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EMBL; AX046410; AAK94500.1; -; Genomic_DNA.
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                                                                                          Infect. Immun. 69:6931-6941(2001).

EMBL; AY046414; AAK94504.1; -; Genomic_DNA.

InterPro; IPR001921; CHAP.

InterPro; IPR001948; SibA.

Pfan; PF05257; CHAP; 1.

PRINTS; PR01852; SIBAPROTEIN.

PROSITE; PSS0911; CHAP; 1.
                                                                                                                                                                                                                                                                                                                                                        l Similarity 100.0%; Pred. No. 4e-
20; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 QQIQTLSSKIVARNESLKQQ 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QQIQTLSSKIVARNESLKQQ 107
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InterPro; IPR009148; SibA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus mutans
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Matches 20; Conserv
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Best Local Similarity
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Q9AG98 ST
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NCBI_TaxID=1309;
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                                                                                                                                                                                                                                                                               STRAIN=15JP2;
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                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                  "Genome sequence of Streptococcus mutans UA159, a cariogenic dental
                                                                                                   MEDLINE-22295063; Pubmed=12397186; DOI=10.1073/pnas.172501299; Ajdic D.J., McShaw W.M., McLaughlin R.E., Savic G., Chang J., Carson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P., Qian Y., Li S., Zhu H., Najar F.Z., Lai H., White J., Roe B.A.,
                                                                                                                                                                                                                                                                                                                                                 ö
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Putative secreted antigen GbpB/SagA; putative peptidoglycan
                                                                                                                                                                                                                                                                                                                         Score 92; DB 2; Length 431;
Pred. No. 4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=3SN1;
MEDLINE=21481971; PubMed=11598068;
DOI=10.1128/IAI.69.11.6931-6941.2001;
Mattos-Graner R.O., Jin S., King W.F., Chen T., Smith D.J.,
                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus mutans.
Bacteria, Firmicutes; Lactobacillales, Streptococcaceae,
                                             Streptococcus mutans.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jin S., Duncan M.J., Taubman M.A., Smith D.J.; "Cloning of the gbpB gene from Streptococcus mutans."; J. Dent. Res. 79:224-224(2000).
                                                                                                                                                                                                                                                                                                   431 AA; 44620 MW; 2D1CA685248CCD3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       432 AA; 44652 MW; 3P88ECB9A1F3BE4F CRC64;
                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Glucan-binding protein B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Infect. Immun. 69:6931-6941(2001).

EMBL, AXO46413; AAK94503.1; -; Genomic_DNA.

InterPro; IPR007921; CHAP.

InterPro; IPR009148; SibA.

Pfam, PF05257, CHAP; 1.

PRINTS; PR01852; SIBARROTEIN.

PROSTER, PS50911; CHAP; 1.

SEQUENCE 432 AA; 44652 MW; 3F88ECB9A1F3BE4
                                                                                                                                                                                                                                                                                                                                                                                                                                                       432 AA.
                                                                                                                                                                                                                   EMBL; AE014855; AAN57811.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                       hydrolase.
Name=gbpB; OrderedLocusNames=SMU.22;
                                                                                                                                                                                                                                                                                                                                                                                  88 QQIQTLSSKIVARNESLKQQ 107
                                                                                                                                                                                                                                                                                                                                                                      1 QQIQTLSSKIVARNESLKQQ 20
                                                                                                                                                                                                                                                                 PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PS50911; CHAP; 1.
Complete proteome.
SEQUENCE 431 AA; 44620 MW;
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%;
Matches 20; Conservative 0
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Q938V1;
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STRAIN=3SN1;
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                                                                                NCBI_TaxID=1309;
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                                                                                                                                                                                              pathogen.'
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"Cloning of the Streptococcus mutans gene encoding glucan binding protein B and analysis of genetic diversity and protein production in clinical isolates.";
                                                              Gaps
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                  Length 432;
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                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jin S., Duncan M.J., Taubman M.A., Smith D.J.; "Cloning of the gbpB gene from Streptococcus mutans."; J. Dent. Res. 79:224-224(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44648 MW; E769B2504AEE50E9 CRC64;
                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
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Last annotation update)
                Score 92; DB 2; ] Pred. No. 4.1e-06;
100.0%; Scc...
100.0%; Pred. No. ....
0; Mismatches
                                                                                                                                                                                                                                                              432 AA
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InterPro; PR000921; CHAP.
InterPro; PR000948; SibA.
Pfam, PF05257; CHAP; 1.
PRINTS; PR01852; SIBAPROTEIN.
PROSTER: PS50911; CHAP; 1.
SEQUENCE 432 AA; 44648 MW; E769B2504AEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21481971; PubMed=11598068;
DOI=10.1128/IAI.69.11.6931-6941.2001;
                                                                                                                                                                                                                                                              PRT;
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MEDLINE=21101799; PubMed=11157929;
                                                                                                                                  88 QQIQTLSSKIVARNESLKQQ 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88 QQIQTLSSKIVARNESLKQQ 107
                                                                                                      1 QQIQTLSSKIVARNESLKQQ 20
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C9AKA4 STRAG
ID C95AKA4_STRAG PRELIMINARY;
AC Q9AKA4;
                                                                                                                                                                                                                                                           Q938V2_STRMU PRELIMINARY;
             Query Match
Best Local Similarity 100.
Matches 20, Conservative
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tes 20; Conservative
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NUCLEOTIDE SEQUENCE
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                                                                                                                                                                         NCBI_TaxID=216495;
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                                                                                                                                                               Streptococcus.
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                                                                                                         PcsB protein.
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                           STRA3
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MEDLINE-22222988; PubMed=12200547; DOI=10.1073/pnas.182380799;

MEDLINE-22222988; PubMed=12200547; DOI=10.1073/pnas.182380799;

Tettelin H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson S.N.,

Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,

Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,

DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,

Radune D., Fedorova N.B., Scanlan D., Khouri H.M., Mulligan S.,

Tacobini E.T., Brettoni C., Galli G., Marlani M., Vegni F., Maione D.,

Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
                                       "Identification and molecular analysis of PcsB, a protein required for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence and comparative genomic analysis of ar emerging human pathogen, serotype V Streptococcus agalactiae."; Proc. Natl. Acad. Sci. U.S.A. 99;12391-12396 (2002). EMBL; PAG14192; AAM98925.1; -; Genomic_DNA. TIGR: SAG0017; -. InterPro; IPR007921; CHAP.
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DOI=10.1128/JB.183.4.1175-1183.2001;
Reinscheid D.J., Gottschalk B., Schubert A., Eikmanns B.J.,
Chhatwal G.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 447;
                                                                                                                                                                                                                                  89.1%; Score 82; DB 2; Length 447; 85.0%; Pred. No. 0.00017;
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85.0%; Pred. No. 0.00017;
tive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                              0; Indels
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Streptococcus agalactiae (serotype V).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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46681 MW; F4DB14B0A5F962C8 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                   cell wall separation of group B streptococcus.";
J. Bacteriol. 183:1175-1183(2001).
EMBL, AJ77292; CAC20144.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR007914; SibA.
Pfam; PP05257; CHAP; I.
PRINTS; PR01852; SIBARROTEIN.
PROSITE; PS50911; CHAP; 1.
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PROSITE; PS50911; CHAP; 1.
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QBE2H1 STRAS PRELIMINARY;
QBE2H1;
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Best Local Similarity 85.0°
Matches 17; Conservative
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Matches 17; Conservative
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447 AA;
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SEQUENCE 447 AA;
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Banks D.J., Porcella S.F., Barbian K.D., Beres S.B., Philips L.E.,
Voyich J.M., DeLeo F.R., Martin J.M., Somerville G.A., Musser J.M.;
"Progress toward characterization of the group A Streptococcus
metagenome: complete genome sequence of a macrolide-resistant serotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=NEM316 / Serotype III;
MEDLINE=2224508; PubMed=1235421;
Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
Msadek I., Zouine M., Couve B., Lalioui L., Poyart C., Trieu-Cuot P.,
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85.0%; Pred. No. 0.00017;
tive 3; Mismatches 0; Indels
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae;
                                                                                                                                                                                                                                                                                                        Streptococcus agalactiae (serotype III).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                     01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
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J. Infect. Dis. 190:727-738 (2004).

EMBL; CP000003; AAT86152.1; -; Genomic_DNA.
InterPro; IPR001921; CHAP.
InterPro; IPR009148; SibA.
Pfam; PF05257; CHAP; 1.
PRINTS; PR01852; SIBAPROTEIN.
PROSITS; PS01852; SIBAPROTEIN.
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    447 AA
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Mol. Microbiol. 45:1499-1513(2002).
EMBL; AL766843; CAD45661.1; -; Genomic_DNA.
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        PRT;
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InterPro; IPR007921; CHAP.
InterPro; IPR00148; SibA.
Pfam, PP05257; CHAP; 1.
PRINTS; PR01852; SIBAPROTEIN.
Complete proteome.
SEQUENCE 447 AA; 46681 MW;
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QBE7X9_STRA3 PRELIMINARY;
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SEQUENCE

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Hayashi H., Hattori M., Hamada S.;
"Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
large-scale genomic rearrangement in invasive strains and new insights
                                                          FRAIN-MGASBA32 / Serotype M18;

MEDLINE-21927593; PubMed=11917108; DOI=10.1073/pnas.062526099;

MEDLINE-21927593; PubMed=11917108; DOI=10.1073/pnas.062526099;

Smoot J.C., Barbian K.D., Van Gompel J.C., Smoot L.M., Chaussee M.S.,
Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,

Rapur V., Daly J.A., Veasy L.G., Musser J.M.;

Rapur V., Daly J.A., Veasy L.G., Musser J.M.;

Genome sequence and comparative microarray analysis of serotype M18
group A Streptococcus strains associated with acute rheumatic fever
outbreaks.";

Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).

EMBL, AE009955; Aal96849.1; -; Genomic_DNA.

InterPro; IPR007921; CHAP.
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MEDLINE=22133809; PubMed=12122206; DOI=10.1073/pnas.152298499;
MEDLINE=22138009; PubMed=12122206; DOI=10.1073/pnas.152298499;
Mamarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlibevert P.M., Musser J.M.;
Genome sequence of a serotype M3 strain of group A Streptococcus:
phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=SSI-1 / Serotype M3;
MEDLINE=22683278; PubMed=12799345; DOI=10.1101/gr.1096703;
Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 64; DB 2; Length 398;
Pred. No. 0.12;
4; Mismatches 3; Indels
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Streptococcus pyogenes (serotype_M3).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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EMBL; BA000034; BAC63110.1; -; Genomic_DNA.
EMBL; AE014136; AAM78621.1; -; Genomic_DNA.
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Genome Res. 13:1042-1055(2003).
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PROSITE; PS50911; CHAP; 1.
Complete proteome.
SEQUENCE 398 AA; 42028 MW;
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PROSITE; PS50911; CHAP; 1.
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InterPro; IPR009148; SibA.
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MEDLINB=21192684; PubMed=11296296; DOI=10.1073/pnas.071559398;
Perretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
Qian Y., Jia H.G., Najar P.Z., Ren Q., Zhu H., Song L., White J.,
Yuan X., Clifton S.W., Roe B.A., McLaughlin R.E.;
"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
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OrderedLocusNames=spyM18 20020;
Streptococcus pyogens (Serctype M18).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AE006474; AAK33158.1; -; Genomic_DNA.
EMBL; AF319999; AAL73135.1; -; Genomic_DNA.
InterPro; IPR007921; CHAP.
InterPro; IPR009148; SibA.
      42028 MW; 5DCEDA78CB863B60 CRC64;
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09A1Z6; Q7AH59;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Secreted protein SibA precursor.
OrderedLocusNames=SPy0019;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                       DB 2;
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                                                                                              0.12;
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                                                             Query Match
Best Local Similarity 65.0%; Pred. No.
Matches 13; Conservative 4; Mismatc
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                                                                                                                                                                                         1 QQIQTLSSKIVARNESLKQQ 20
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PROSITE, PSS0911; CHAP; 1.
Complete proteome; Signal.
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QTCNQ7 STRP8 PRELIMINARY;
Q7CNQ7;
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398 AA;
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Query Match

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BOTGES F., Layec S., Thibessard A., Fernandez A., Gintz B., Hols P.,
BOTGES F., Layec S., Thibessard A., Fernandez A., Gintz B., Hols P.,
Decaris B., Leblond-Bourget N.;
"cse, a Chimeric and Variable Gene, Encodes an Extracellular Protein
Involved in Cellular Segregation in Streptococcus thermophilus.";
J. Bacteriol. 187:277-2746(1905).
EMBL; CP0000023; AAVS9752.1; -; Genomic_DNA.
EMBL; AY730643; AAW82375.1; -; Genomic_DNA.
InterPro; IPR009121; CHAP.
InterPro; IPR09914; SibA.
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NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

PubMed=15543133; DOI=10.1038/nbt1034;

Bolotin A., Quinquis B., Renault P., Sorokin A., Ehrlich S.D.,

Kulakauskas S., Lapidus A., Goltsman E., Mazur M., Pusch G.D.,

Fonstein M., Overbeek R., Kyprides N., Purnelle B., Prozzi D.,

Ngui K., Masuy D., Hancy F., Burteau S., Boutry M., Delcour J.,

Goffeau A., Hols P.;

"Complete sequence and comparative genome analysis of the dairy
bacterium Streptococcus thermophilus.";

Nat. Biotechnol. 22:1554-1558(2004).
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Glucan binding protein (FCBB)
Wame-pcBs, Order-GLocusNames=stu0022,
Streptococcus thermophilus (strain ATCC BAA-250 / LMG 18311).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 64.1%; Score 59; DB 2; Length 474; Best Local Similarity 68.4%; Pred. No. 0.92; Matches 13; Conservative 3; Mismatches 3; Indels
                                                 Query Match 69.6%; Score 64; DB 2; Length 398; Best Local Similarity 65.0%; Pred. No. 0.12; Matches 13; Conservative 4; Mismatches 3; Indels
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                 42028 MW; 5DCEDA78CB863B60 CRC64;
                                                                                                                                                                                                                                                                474 AA.
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PRINTS; PR01852; SIBAPROTEIN.
PROSITE; PSSO911; CHAP; 1.
Complete proteome.
SEQUENCE 474 AA; 48142 MW;
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Search completed: January 25, 2006, 19:13:42

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SEQ ID NO 67
LENGTH: 210
TYPE: PRT
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6: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-09-583-110-4374

US-09-107-433-3230

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US-10-206-576-484

US-10-206-576-484

US-10-206-576-484

US-09-134-000C-5714

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US-09-2770-767-34326

US-09-2770-767-34326

US-09-2770-767-34326

US-09-2770-767-34326

US-09-270-767-34326

US-09-270-767-34326

US-09-270-767-34016

US-09-270-767-34016

US-09-248-796A-121210

US-09-248-796A-121210

US-09-248-796A-18242

US-09-248-796A-18242

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US-09-489-039A-9573
US-09-252-991A-24600
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                                                                                                                                                                                                                                572060 seqs, 82675679 residues
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Maximum Match 100%
Listing first 45 summaries
                                                OM protein - protein search, using sw model
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1 QQIQTLSSKIVARNESLKQQ 20
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RESULT 2
US-09-583-110-4374
i Sequence 4374, Application US/09583110
i Sequence 4374, Application US/09583110
i Patent No. 6699703
i GENERAL INFORMATION:
i TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
i TITLE OF INVENTION: Neumentiae for Diagnostics and Therapeutics
i TITLE OF INVENTION: Neumentiae for Diagnostics and Therapeutics
i FILE REFERENCE: PATHO0-074
i CURRENT APPLICATION NUMBER: US 09/107,433
i PRIOR PAPLICATION NUMBER: US 69/085,131
i PRIOR PILING DATE: 1998-06-30
i PRIOR PILING DATE: 1998-06-12
i PRIOR PILING DATE: 1998-05-12
i PRIOR PILING DATE: 1998-05-12
i RIOR FILING DATE: 1998-05-12
i RIOR FILING DATE: 1998-05-12
i RUMBER OF SEQ ID NOS: 5322
i ERNGTH: 392
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1071, Ap
9944, Ap
6189, Ap
27959, A
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APPLICANT: Fritz, Christian
APPLICANT: Murphy, Christopher
APPLICANT: Guzman, Luz-Maria
TITLE OF INVENTION: ESSENTIAL BACTERIAL GENES AND THEIR USE
FILE REPERENCE: 07334/060001
CURRENT APPLICATION NUMBER: US/09/222,938A
CURRENT FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 102
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US-09-107-532A-5229
US-09-248-796A-20284
US-08-144-121-4
US-08-735-893-4
US-10-841-139-4
US-09-562-702A-16
US-09-562-702A-16
US-09-562-702A-14
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; Sequence 67, Application US/09222938A
; Patent No. 6437108
; GENERAL INFORMATION:
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Matches 10; Conservat
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Sequence 484, Application US/10206576

Patent No. 6913907

GENERAL INFORMATION:
APPLICANT: Choi et al.
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 497

CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                     Sequence 484, Application US/09071035

Patent No. 6448043

GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITT: ROCKYILLE
COUNTRY: USA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
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PILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: A Anders Brookes
REGISTRATION UNDRER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
TELEFAX: (301) 309-8512
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 484:
SEQUENCE CHARACTERISTICS:
LENGTH: 422 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: Dell Lattitude
OPERATING SYSTEM: Window
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GEITNLNORIEKRNEAIKNO 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QQIQTLSSKIVARNESLKQQ 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 45.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-071-035-484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-206-576-484
                                 US-09-071-035-484
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                                                                                                                                                                                                                                                                                                      Sequence 3230, Application US/09107433

Patent No. 6800747

GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A DOUCEITE ACID AND AMINO ACID
TITLE OF INVENTION: SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                             DB 2; Length 392;
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                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:

MEDIUM TYPE: CD/ROM 1S09660

COMPUTER: CUNKNOWN>
COPERATING SYSTEM: <UNKNOWN>
SOFTWARE: CUNKNOWN>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
FILING DATE: May 12, 1998
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/05153
FILING DATE: May 12, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Atiniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REPERBNCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELERAK: (781)893-5007
INFORMATION FOR SEQ 1D NO: 3230:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 53.3%; Score 49; DB 3
Best Local Similarity 52.6%; Pred. No. 3.1;
Matches 10; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature

LOCATION: (B) LOCATION 1...399

SEQUENCE DESCRIPTION: SEQ ID NO: 3230:
US-09-107-433-3230
                                                                                                                         5; Mismatches
                                                                               53.3%; Score 49; 52.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 100 Beaver Street CITY: Waltham
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 399 amino acids
TYPE: amino acid
                                                                                                                                                                                      :| || ||:||:||:|
89 EITELSKNIVSRNQSLEKQ 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 5206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                             Query Match
Best Local Similarity 52.6
Matches 10; Conservative
                                                                                                                                                                                                                                                                  RESULT 3
US-09-107-433-3230
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Sequence 482, Application US/10206576
Patent No. 6913907
GENERAL INFORMATION:
APPLICANT: Choi et al.
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                              Gaps
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                                                                                                                                         Score 47; DB 2; Length 449;
Pred. No. 7.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER TADBLE FORM:

MEDIUM TYPE: CD-R
COMPUTER: Deal Latitude
OPERATING SYSTEM: Windows 98
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/206,576
FILING DATE: 29-Ual-2002
CLASSIFICATION: «Unknown>
PRIOR APPLICATION NUMBER: US 09/071,035
FILING DATE: 1998-05-04
APPLICATION NUMBER: US 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: US 60/044,031
FILING DATE: 1997-05-16
APPLICATION NUMBER: US 60/044,031
FILING DATE: 1997-05-16
APPLICATION NUMBER: US 60/044,031
FILING DATE: 1997-05-16
APPLICATION NUMBER: US 60/066,009
FILING DATE: 1997-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Hyman, Mark J.
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB369PID1
                                                                                                                                         Query Match 51.1%; Score 47; DB Best Local Similarity 45.0%; Pred. No. 7.8; Matches 9; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Mismatches
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NOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 482:
US-10-206-576-482
                                                                                                                                                                                                                                                                               88 ÓEITNINGRIEKRNEAIKNÓ 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:| |: | ||::| |
88 QEITNLNQRIEKRNEAIKNQ 107
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LENGTH: 449 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 482:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 45.0
Matches 9; Conservative
                                 single
                                                 TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-071-035-482
         TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20850
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US-09-134-000C-5714
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Patent No. 6448043

GENERAL INFORMATION:

APPLICANT: Gil H. Choi

TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides

NUMBER OF EXQUENCES: 496

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM
SOOFWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 51.1%; Score 47; DB 2; Best Local Similarity 45.0%; Pred. No. 7.3; Matches 9; Conservative 5; Mismatches (
                                                                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/071, 035
FILING DATE: 1998-05-04
APPLICATION NUMBER: US 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: US 60/044,031
FILING DATE: 1997-05-16
APPLICATION NUMBER: US 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
NAME: Hyman, Mark J.
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB369PID1
INFORMATION FOR SEQ ID NO: 484:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/206,576
FILING DATE: 29-Jul-2002
CLASSIFICATION: <URLOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 484:
US-10-206-576-484
                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 422 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INPORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB365
TELECOMMUNICATION INFORMATION:
TELEFROM (301) 309-8504
TELEFRAX: (301) 309-8512
INPORMATION POR SEQ ID NO: 482:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |:| |: | ||::| |
61 QEITNLNQRIEKRNEAIKNQ 80
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            449 amino acida
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Patent No. 6703491

GENERAL INFORMATION:

TITUE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;

TITUE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;

TITUE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;

TITUE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;

TITUE OF INVENTION: NUMBER: US/09/270,767

CURRENT FILING DATE: 1995-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 49543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 34326, Application US/09270767

Sequence 34326, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT PALICATION NUMBER: US/09/270,767
CURRENT PILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 34326
LENGTH: 213
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48.9%; Score 45; DB 2; Length 213;
Best Local Similarity 47.1%; Pred. No. 7.2;
Matches 8; Conservative 6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 213;
                                                                                                                                                                                                                                                  Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                     6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 45; DB 2;
Pred. No. 7.2;
                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                      Score 46; DB 2, Pred. No. 9.2; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Mismatches
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ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Drosophila melanogaster
US-09-270-767-34326
                                                                                                                                                                                                                                                                                                                                                                                                                            1:| || | | : |::| | | 265 QLQQLSSAITVKKENIKHQ 283
                                                                                                                                                                                                                                                                                                                                                                                 2 QIQTLSSKIVARNESLKOQ 20
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95 QDLETKULARNQNLAEQ 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | | :|:|||::| :|
95 QDLETKLLARNONLAEQ 111
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                                                                                                                                                                                                                                                      50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vuery Match
Best Local Similarity 47.1%;
Matches 8; Conservative (
                                                                                                                                                                                                                           Query Match
Best Local Similarity 47.**

Best Local Similarity 47.**

Conservative
PRIOR FILING DATE: 1998-08-1
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 20840
LENGTH: 368
                                                                                                                                 ; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-20840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
US-09-489-039A-10276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
US-09-270-767-49543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-270-767-49543
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Sequence 20840, Application US/09248796A

Sequence 20840, Application US/09248796A

Sequence 2084137

GENERAL NO. 6747137

GENERAL INCRMATION:

TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR PLILIG DATE: US 60/096,409
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                                                                                                APPLICANT: Lynn Boucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: BUTENCOCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR PILING DATE: 1998-08-13
PRIOR PILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PATENTIN voices and second 
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Fatent No. 6833447

GENERAL INFORMATION:
FAPPLICANT: Goldman, Barry S.
FAPPLICANT: Slater, Steven C.
FAPPLICANT: Wiegand, Roger C.
FAPPLICANT: Wiegand, Roger C.
FAPPLICANT: Wiegand, Roger C.
FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10
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      Sequence 5714, Application US/09134000C Patent No. 6617156 GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 12334
LENGTH: 352
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113 TMAADVAARNEKLOOO 128
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Matches 9; Conservative
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Best Local Similarity
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Gaps

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Query Match

47.8%; Score 44; DB 2; Length 1780;
Best Local Similarity 31.6%; Pred. No. 1.2e+02;
Matches 6; Conservative 9; Mismatches 4; Indels
                                 PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6899
LENGTH: 1780
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Job time : 16.6 secs
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Sequence 22689, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 22689

LENGTH: 596
Sequence 10276, Application US/09489039A

Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Preton et. al
APPLICANT: Gary Preton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US 60/4001
CURRENT PILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR SEQ ID NOS: 14342
SEQ ID NO 10276
LENGTH: 329
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Patent No. 6812339
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF CURRENT APPLICATION NUMBER: 60/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
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ilarity 40.0%; Pred. No. 35;
Conservative 7; Mismatches 5; Indela
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113 IHTLSABATARMEAVRQQ 130
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ORGANISM: Klebsiella pneumoniae
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Best Local Similarity
Matches 8; Conserv
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US-09-949-016-6899
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JOSEPH PROBLEM 100 Application US/10797821

Sequence 10, Application US/10797821

Sequence 10, Application US/20050031633A1

Sequence 10, Application No. US20050031633A1

APPLICANT: Smith, Daniel J.

APPLICANT: Taubman, Martin A.

TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens

FILE REFERENCE: 25669-020

CURRENT APPLICATION NUMBER: US/10/797,821

CURRENT FILING DATE: 2004-03-09

PRIOR PELING DATE: 2003-03-07

PRIOR PELING DATE: 2002-09-07

PRIOR APPLICATION NUMBER: 60/462,483

PRIOR PLING DATE: 2002-08-08

PRIOR APPLICATION NUMBER: 09/290,049
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Sequence 29, Appl
Sequence 30, Appl
Sequence 33, Appl
Sequence 33, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 32, Appl
Sequence 600, Appl
Sequence 600, Appl
Sequence 600, Appl
Sequence 320, Appl
Sequence 320, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
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Sequence 484, App
Sequence 484, App
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Sequence 1018, Ap
Sequence 51, Appl
                                                                                                                                January 25, 2006, 19:13:51; Search time 60 Seconds (without alignments) 139.276 Million cell updates/sec
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Sequence 10,
Sequence 29,
Sequence 33,
Sequence 29,
Sequence 30,
Sequence 30,
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
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Copyright (c) 1993 - 2006 Compugen Ltd.
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US-10-341-434-51
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Maximum Match 100%
Listing first 45 summaries
                                                                                          OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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US-10-289-647-425
US-10-289-1944-274
US-10-437-963-102819
US-10-437-963-102826
US-10-097-111-328
US-10-282-122A-50448
US-10-425-115-332194
US-10-425-115-332195
US-11-097-143-34887
US-10-425-115-304286
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#### ALIGNMENTS

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US-10-383-930-10

US-10-383-930-10

US-10-383-930-10

Publication No. US20040127400A1

GENERAL INFORMATION:

APPLICANT: Smith, Daniel J

APPLICANT: Taubman, Martin A

TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein

FILE REFERENCE: 25669-018

CURRENT APPLICATION NUMBER: US/10/383,930

CURRENT APPLICATION NUMBER: 06/402,483

PRIOR PILING DATE: 2003-03-07

PRIOR PLING DATE: 2002-08-08

PRIOR APPLICATION NUMBER: 60/363,209

PRIOR APPLICATION NUMBER: 60/363,209

PRIOR APPLICATION NUMBER: 5002-03-07

SOFTWARE: PatentIn version 3.2

SOFTWARE: PatentIn version 3.2

SERVING: 10 NO 10
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100.0%; Score 92; DB 4; I
Best Local Similarity 100.0%; Pred. No. 4.1e-08;
Matches 20; Conservative 0; Mismatches 0;
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Gaps

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Sequence 29, Application US/10797821
; Sequence 29, Application US/10797821
; Sequence 29, Application US/10797821
; GRNERAL INFORMATION:
; APPLICANT: Smith, Daniel J.
; APPLICANT: Staubman, Martin A.
; TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens
; FILE REFERENCE: 25669-020
; CURRENT APPLICATION NUMBER: 10/383,930
; FRICK APPLICATION NUMBER: 10/383,930
; PRIOR FILING DATE: 2002-03-07
; PRIOR FILING DATE: 2002-03-07
; PRIOR FILING DATE: 2002-08-08
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: 60/402,483
; PRIOR FILING DATE: 1999-04-12
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: 60/115,142
; RICK APPLICATION NUMBER: 60/115,142
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; RICK APPLICATION NUMBER: 60/115,142
; RICK FILING DATE: 1998-04-13
; RICK FILING DATE: 1998-04-13
; RICK FILING DATE: 1998-04-13
; RICK FILING DATE: 1998-04-13
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; RICK FILING DATE: 1998-04-13
; SEQ ID NO 29
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Pred. No. 1.4e-06;
Mismatches 0; Indels
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                     LENGTH: 431
TYPE: PRT
ORGANISM: Streptococcus mutans
US-10-383-930-30
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Best Local Similarity 100.0
Matches 20; Conservative
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US-10-797-821-29
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US-10-383-930-33
    SEO ID NO 30
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US-10-383-930-29
i Sequence 29, Application US/10383930
j Publication No. US20040127400A1
j GREERAL INFORMATION:
j APPLICANT: Smith, Daniel J
j APPLICANT: Taubman, Martin A
j TITLE OF INVENTION: Immunogenicity of Glucan Binding Frotein
j CURRENT APPLICATION NUMBER: US/10/383,930
j CURRENT PILING DATE: 2003-03-07
j PRIOR APPLICATION NUMBER: 60/402,483
j PRIOR FILING DATE: 2002-08-08
j PRIOR FILING DATE: 2002-03-07
j NUMBER OF SEQ ID NOS: 41
j SOFTWARE: PatentIn version 3.2
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| Sequence 30, Application US/10383930
| Publication No. US20040127400A1
| GENERAL INPORMATION:
| APPLICANT: Smith, Daniel J
| APPLICANT: Taubman, Martin A
| TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
| FILE REFERENCE: 25669-018
| CURRENT APPLICATION NUMBER: US/10/383,930
| CURRENT APPLICATION NUMBER: 60/402,483
| PRIOR APPLICATION NUMBER: 60/303,209
| PRIOR APPLICATION NUMBER: 60/363,209
| PRIOR APPLICATION NUMBER: 60/363,209
| PRIOR APPLICATION NUMBER: 60/363,209
| NUMBER OF SEQ ID NOS: 41
| SOFTWARE: PatentIn version 3.2
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PRIOR FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: 60/081,550
PRIOR PILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SEQ ID NO 10
LENGTH: 20
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US-10-383-930-29
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Matches 20; Conservative
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US-10-383-930-30
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LENGTH: 431
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US-10-383-30-31
Sequence 31, Application US/10383930
Sequence 31, Application US/10383930
Hublication No. US20040127400A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE NOTE SMITH, Daniel J
APPLICANT: Taubman, Martin A
FILE REFERENCE: 25669-018
CURRENT APPLICATION NUMBER: US/10/383,930
CURRENT FILING DATE: 2003-03-07
FRIOR PILING DATE: 2002-08-08
FRIOR PILING DATE: 2002-08-08
FRIOR PILING DATE: 2002-08-08
FRIOR PILING DATE: 2002-08-08
FRIOR PILING DATE: 2002-08-08
SPRIOR PILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 41
SOFTWARE PARENTIN VETSION 3.2
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| Sequence 32, Application US/10383930
| Publication No. US20040127400A1
| Publication No. US20040127400A1
| GENERAL INFORMATION:
| APPLICANT: Smith, Daniel J
| APPLICANT: Taubman, Martin A
| TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
| FILE REPERENCE: 2566-018
| CURRENT APPLICATION NUMBER: US/10/383,930
| CURRENT APPLICATION NUMBER: 60/402,483
| PRIOR PILING DATE: 2002-08-08
| PRIOR PILING DATE: 2002-08-08
| PRIOR PILING DATE: 2002-03-07
| NUMBER OF SEC ID NOS: 41
| SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 92; DB 5; Length 431; Best Local Similarity 100.0%; Pred. No. 1.4e-06; Matches 20; Conservative 0; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: 60/081,550
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR FILING DATE: 1999-01-08
NUMBER: OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.2
SEQ ID NO 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 QQIQTLSSKIVARNESLKQQ 107
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                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Streptococcus mutans
                                                                                                                                                                                                                                                                         US-10-797-821-33
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LENGTH: 432
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Fublication No. US2005031633A1

GENERAL INFORMATION:

APPLICANT: Smith, Daniel J.

APPLICANT: Smith, Daniel J.

APPLICANT: Taubman, Martin A.

TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens

FILER REFERENCE: 25669-200

CURRENT APPLICATION NUMBER: US/10/797,821

CURRENT PILING DATE: 2004-03-09

FRIOR APPLICATION NUMBER: 60/363,209

FRIOR PILING DATE: 2002-08-08

FRIOR FILING DATE: 2002-08-08

FRIOR FILING DATE: 1999-04-12

FRIOR FILING DATE: 1999-04-12

FRIOR FILING DATE: 1999-04-13

FRIOR FILING DATE: 1999-04-13

FRIOR FILING DATE: 1999-01-08

NUMBER: 60/115,142

FRIOR FILING DATE: 1999-01-08

NUMBER: PATCH OF SEQ ID NOS: 45

SEQ ID NO 30

LEGGTH: 431

FRIOR FILING DATE: 1999-01-08

NUMBER: PATCH OF SEQ ID NOS: 45

SEQ ID NO 30

LEGGTH: 431
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APPLICANT: Smith, Daniel J.
APPLICANT: Taubman, Martin A.
TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens
TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens
FILE REPERENCE: 25669-03-09
CURRENT APPLICATION NUMBER: US/10/797,821
CURRENT FILING DATE: 2004-03-09
PRIOR APPLICATION NUMBER: 60/363,209
PRIOR FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: 60/402,483
PRIOR FILING DATE: 2002-08-08
PRIOR FILING DATE: 1909-04-12
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Publication No. US20050031633A1
GENERAL INFORMATION:
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                            ; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-10-797-821-29
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US-10-797-821-30
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US-10-797-821-33
  LENGTH: 431
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## Sequence 600, Application US/10474792

| Sequence 600, US20040236072A1
| CENERAL INFORMATION:
| APPLICANT: Olmsted, Stephen
| APPLICANT: Application Olmsted, Stephen
| APPLICANT: Winter, Louise
| TILLE OF INVENTION: SURFACE PROTEINS OF STREPTOCOCCUS PYOGENES
| FILE REFERENCE: AM 100399
| CURRENT APPLICATION NUMBER: US/10/474,792
| CURRENT PILING DATE: 2003-10-14
| NUMBER OF SEQ ID NOS: 674
| SOFTWARE: PatentIn version 3.0
| SEQ ID NO 600
                                                                                                                                                                                                                                                                                                                     100.0%; Score 92; DB 5; Length 432; 100.0%; Pred. No. 1.4e-06; tive 0; Mismatches 0; Indel8
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APPLICANT: Youngman, Philip
APPLICANT: Fritz, Christian
APPLICANT: Fritz, Christian
APPLICANT: Guzman, Luz-Maria
APPLICANT: Guzman, Luz-Maria
FITTLE OF INVENTION: ESSENTIAL BACTERIAL GENES AND THEIR USE
FILE REFERENCE: 06286-060002
CURRENT APPLICATION NUMBER: US/10/154,251
CURRENT FILING DATE: 2002-09-16
PRIOR FILING DATE: 2002-05-22
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SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 67
LENGTH: 210
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.2
SEQ ID NO 32
LENGTH: 432
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; ORGANISM: Streptococcus pneumoniae
US-10-154-251-67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88 QQIQTLSSKIVARNESLKQQ 107
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US-10-797-821-32
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Best Local Similarity 100.0
Matches 20; Conservative
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US-10-474-792-600
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US-10-797-821-32

i Sequence 32, Application US/10797821

i Publication No. US20050031633A1

i GENERAL INFORMATION:

APPLICANT: Smith, Daniel J.

i APPLICANT: Taubman, Martin A.

ITILE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens
FILE REFREENCE: 25669-020

CURRENT APPLICATION NUMBER: US/10/797,821

CURRENT FILING DATE: 2004-03-09

PRIOR APPLICATION NUMBER: 60/463,209

PRIOR PLILING DATE: 2002-03-07

PRIOR PLILING DATE: 2002-03-07

PRIOR PLILING DATE: 2002-08-08

PRIOR FILING DATE: 2002-08-08

PRIOR PLILING DATE: 1999-04-12

PRIOR PLILING DATE: 1999-04-12

PRIOR FILING DATE: 1999-04-13

PRIOR FILING DATE: 1999-04-13
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## APPLICANT: Smith, Daniel J.
## APPLICANT: Smith, Daniel J.
## APPLICANT: Taubman, Martin A.
## TITLE OF INVENTION Glucan Binding Protein and Glycosyltransferase Immunogens
## TILE OF INVENTION Glucan Binding Protein and Glycosyltransferase Immunogens
## TILE OF INVENTION Glucan Binding Protein and Glycosyltransferase Immunogens
## TILE OF INVENTION GLATE: 104-03-09
## CURRENT FILING DATE: 2004-03-09
## PRIOR PLILING DATE: 2002-08-08
## PRIOR FILING DATE: 2002-08-08
## PRIOR FILING DATE: 1999-04-12
## PRIOR FILING DATE: 1999-04-13
## PRIOR FILING DATE: 1999-04-13
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## PRIOR FILING DATE: 1999-04-13
## PRIOR FILING DATE: 1999-04-13
## PRIOR FILING DATE: 1999-04-06
## PRIOR FILING DATE: 1999-04-13
## PRIOR FILING DATE: 1999-04-13
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                                                                                                 Query Match 100.0%; Score 92; DB 4; Length 432; Best Local Similarity 100.0%; Pred. No. 1.4e-06; Matches 20; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                      ; Sequence 31, Application US/10797821; Publication No. US20050031633A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QQIQTLSSKIVARNESLKQQ 20
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          ; ORGANISM: Streptococcus mutans US-10-383-930-32
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US-10-472-928-4652

US-10-472-928-4652

Sequence 4652, Application US/10472928

Publication No. US20050020813A1

GENERAL INFORMATION:
APPLICANT: CHIRON SPA

TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
FILE REPRENCE: POSS286W

CURRENT APPLICATION NUMBER: US/10/472,928

PRIOR APPLICATION NUMBER: GB-0107658.7

PRIOR PILING DATE: 2001-03-27

NUMBER OF SEQ ID NOS: 4979

SEQ ID NOS: 4979

LENGTH: 392
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ORGANISM: Streptococcus pneumoniae
FRATURE:
OTHER INFORMATION: secreted 45 kd protein (usp45)
OTHER INFORMATION: Cellular location: outside
OTHER INFORMATION: Similar to strain R6 sequence 15904062 (0.E+01)
US-10-472-928-4652
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                          4; Indels
Best Local Similarity 52.6%; Pred. No. 7.9; Matches 10; Conservative 5; Mismatches
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Result

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Sequence 252, Application US/11052554A
Publication No. US20050288866A1
GENERAL INFORMATION: US20050288866A1
GENERAL INFORMATION: US20050288866A1
APPLICANT: Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC FOTENTIAL
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC FOTENTIAL
FILE REPERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2004-07-20
FRICR APLICATION NUMBER: US 60/589,227
FRICR FILING DATE: 2004-07-20
FRICR FILING DATE: 2004-07-20
FRICR FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Sachdeva, et al.

TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
FILE REPERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT PILING DATE: 2005-02-07
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-06
NUMBER OF SEQ ID NOS: 763
SOFTWARE: PATENTIAL OF SEQ ID NOS: 763
SSEQ ID NOS: 763
LENGTHA: 431
    661, App
662, App
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666, App
23, App
12, App
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US-10-995-561-666
US-10-957-780-23
US-11-052-554A-91
US-11-07-282-12
US-11-007-282-12
US-11-007-282-10
US-11-019-351-8
US-10-613-744-19
US-10-613-744-19
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US-10-878-556A-136
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; ORGANISM: Streptococcus mutans UA159
US-11-052-554A-210
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Matches 20; Conservative
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Sequence 1236, App
Sequence 1032, Ap
Sequence 7, Appli
Sequence 8, Appli
Sequence 23, Appli
Sequence 24, Appli
Sequence 24, Appli
Sequence 24, Appli
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71, Appl
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                                                                                                                                January 25, 2006, 19:15:26; Search time 5.5 Seconds (without alignments) 39.378 Million cell updates/sec
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2: /cgn2_6/prodata/2/pubpaa/USO6 NEW PUB.pep:*

3: /cgn2_6/prodata/2/pubpaa/USO7 NEW PUB.pep:*

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5: /cgn2_6/prodata/2/pubpaa/USO7 NEW PUB.pep:*

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Copyright (c) 1993 - 2006 Compugen Ltd.
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US-11-052-554A-252

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US-10-793-626-420

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US-10-793-626-420

US-10-793-626-760

US-10-796-76A-9

US-11-74-816-18

US-11-174-816-18

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US-11-174-816-18

US-11-152-366-279

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US-11-152-366-38

US-11-173-672-11

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1 QOIOTLSSKTVADNES
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Sequence 8, Application US/10959310

Publication No. US20050287138A1

GENERAL INPORMATION:
TITLE OF INVENTION: CCR4-specific antibody composition
FILE REFERENCE: 249-363

CURRENT APPLICATION NUMBER: US/10/959,310

CURRENT FILING DATE: 2004-10-07

PRIOR APPLICATION NUMBER: US 60572,784

PRIOR PLING DATE: 2003-008

PRIOR PLING DATE: 2004-05-21

NUMBER OF SEQ ID NOS: 46

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 8-
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Sequence 7, Application US/10959310;
Publication No. US20050287138A1;
GENERAL INFORMATION:
TITLE OF INVENTION: CCR4-specific antibody composition;
FILE REFERENCE: 249-363;
CURRENT APPLICATION NUMBER: US/10/959,310
CURRENT FILING DATE: 2004-10-07;
PRIOR APPLICATION NUMBER: US 60/572,784;
PRIOR PLING DATE: 2003-10-08
PRIOR PLING DATE: 2004-08
; PRIOR PLING DATE: 2004-06-21
; NUMBER: DE SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver: 2.1
; SEQ ID NO 7
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Pred. No. 30;
2; Mismatches
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5; Mismatches
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Pred. No.
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; Sequence 23, Application US/11131212
; Publication No. US20050262593A1
                                                                193 QLQRALSKLIERHEILRTQ 211
                                       2 QIQTLSSKIVARNESLKQQ 20
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; ORGANISM: Cricetulus griseus
US-10-959-310-7
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Best Local Similarity 69.4.
Best Local 9; Conservative
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44 SKILAKLERLKQQ 56
  Conservative
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TYPE: PRT
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US-10-959-310-7
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Sequence 1230, Application US/10821234

Publication No. US20050255114A1

GENERAL INFORMATION:

APPLICANT: Labat, Tuan

APPLICANT: Stache-Crain, Birgit

APPLICANT: Andarmani, Susan

TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

FILE REPERENCE: 821A

CURRENT FILING DATE: 2004-04-07

PRIOR APPLICATION NUMBER: US 60/462,047

PRIOR APPLICATION NUMBER: US 60/462,047

NUMBER OF SEQ ID NOS: 1704

SOFTWARE: PL SEQ_genes Version 1.0

SEQ ID NO 1230

LENGTH: 147
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Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCCCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
FILE REFERENCE: PU3480US
CURRENT PAPLICATION NUMBER: US/10/793,626
CURRENT PAPLICATION NUMBER: 60/164,258
PRIOR APPLICATION NUMBER: 60/164,258
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) OTHER INFORMATION: amino acid sequence
US-10-793-626-1032
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                                                                                                                                       Query Match 69.6%; Score 64; DB 7; Length 398; Best Local Similarity 65.0%; Pred. No. 0.0021; Matches 13; Conservative 4; Mismatches 3; Indels
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                                                                                   ORGANISM: Streptococcus pyogenes MGAS8232
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    SOFTWARE: Patentin version 3.3
SEQ ID NO 252
LENGTH: 398
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1032
LENGTH: 252
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Matches 10; Conservative
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Best Local Similarity
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US-10-821-234-1230
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RESULT 9

US-10-793-626-420

Sequence 420, Application US/10793626

Sequence 420, Application Wolloy3626

Publication No. US20050255478A1

GENERAL INFORMATION:

TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

FILE REFERENCE: PU3480US

CURRENT APPLICATION NUMBER: US/10/793,626

CURRENT PILING DATE: 1999-11-09

PRIOR FILING DATE: 1999-11-09

NUMBER OF SEQ ID NOS: 4472

SOFTWARE: Patentin Ver. 2.1

ENGTH: 766
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Publication No. US20050255478A1

GENERAL INFORMATION:
TITLE OF INVENTION: HILLIAM JOHN

TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US

CURRENT APPLICATION NUMBER: US/10/793,626

CURRENT FILING DATE: 1099-11-09

PRIOR FILING DATE: 1999-11-09

NUMBER OF SEQ ID NOS: 4472

SEQ ID NO 760
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US-10-793-626-420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: synthetic; OTHER INFORMATION: amino acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.5%; Score 40; DB 6; Length 766;
42.1%; Pred. No. 42;
tive 5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/10506796A, Publication No. US20660013831A1, GENERAL INFORMATION: APPLICANT: MOR, TSafrix
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167 QLQRALSKLIERHEILRTQ 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
  44 SKILAKLERLKOO 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 42.1
Matches 8; Conservative
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US-10-793-626-760
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                                                        APPLICANT: MILENO SATURAN
APPLICANT: Kazuhasa UGHIDA
APPLICANT: Kazuhasa UGHIDA
APPLICANT: Toyohida SHINKAWA
APPLICANT: Toyohida SHINKAWA
APPLICANT: Notoo YAMASAKI
APPLICANT: Motoo YAMASAKI
TITLE OF INVENTION: ANTIBODY COMPOSITION-PRODUCING CELL
TITLE REFERENCE: 249-202
FILE REFERENCE: 249-202
FILE REFERENCE: 2005-05-18
FRIOR PELICATION NUMBER: US/09/971,773
FRIOR APPLICATION NUMBER: US/09/971,773
FRIOR APPLICATION NUMBER: US 009-306
FRIOR FILING DATE: 2002-08-30
FRIOR FILING DATE: 2002-06-6
FRIOR FILING DATE: 2002-06-6
FRIOR FILING DATE: 2001-06-6
FRIOR FILING DATE: 2001-06-16
NUMBER OF SEQ ID NOS: 73
SEQ ID NO 23
LENGTH: 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: ANTIBODY COMPOSITION-PRODUCING CELL.
FILE REFERENCE: 249-202
CURRENT APPLICATION NUMBER: US/11/131,212
CURRENT APPLICATION NUMBER: US/09/971,773
PRIOR APPLICATION NUMBER: US/09/971,773
PRIOR FILING DATE: 2002-08-30
PRIOR FILING DATE: 2000-10-06
PRIOR PLILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: US 60/268,926
PRIOR PLILING DATE: 2001-0-16
PRIOR PILING DATE: 2001-0-16
PRIOR PILING DATE: 2001-0-16
PRIOR PLILING DATE: 2010-0-16
PRIOR PLILING DATE: 2010-0-16
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Publication No. US20050262593A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kazuyasu NAKAMURA
APPLICANT: Kazuhisa UCHIDA
APPLICANT: Toyohide SHINKAWA
APPLICANT: Nocoo YAMANE
APPLICANT: Notoo YAMASAKI
APPLICANT: Nobuo HANAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Cricetulus griseus
US-11-131-212-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 SKIVARNESLKOO 20
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44 SKILAKLERLKQQ 56
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Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitsuo SATOH
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US-11-131-212-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-11-131-212-24
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US-10-890-188-11B

Phblidation No. US20050255490A1

Sequenc-11B, Application US/10980388

Phblidation No. US20050255490A1

SERVICANT: Vogeli, Gabrie A

PPLICANT: World, Peter

APPLICANT: Bardd, Fals R.

APPLICANT: Hiebsch, Ronald R.

APPLICANT: Hiebsch, Ronald R.

APPLICANT: Hiebsch, Ronald R.

APPLICANT: Hiff, Peter

APPLICANT: Hiff, Peter

APPLICANT: Mayes, Paul S.

APPLICANT: Mayes, Paul S.

APPLICANT: Wiff, Rita M.

APPLICANT: Wiff Rita M.

APPLICANT: Wiff Rita M.

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APPLICANT: Wiff Rita M.

FRIOR PAPLICANT: WINDER: 105/09/731,932

FRIOR PAPLICANT: 2000-02-23

FRIOR PAPLICANT: 2000-02-23

FRIOR PAPLICANT: 2000-02-23

FRIOR PAPLICANT: 2000-02-23

FRIOR PAPLICANT: 2000-02-23

FRIOR PAPLICANT: WINDER: 60/184,397

FRIOR PAPLICANT: WINDER: 60/184,397

FRIOR PAPLICANT: WINDER: 60/184,397

FRIOR PAPLICANT: WINDER: 60/184,397

FRIOR PAPLICANT: WINDER: 60/1184,397

FRIOR FAILING DATE: 2000-07-11

FRIOR FAILING DATE: 2000-07-11

FRIOR FAILING DATE: 2000-07-11

FRIOR FAILING DATE: 2000-07-11

FRIOR FAILING DATE: 2000-07-11

FRIOR FAILING DATE: 2000-07-11

FRIOR FAILING DATE: 2000-07-11

FRIOR FAILING DATE: 2000-07-11

FRIOR FAILING DATE: 2000-07-11

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FRIOR FAILING DATE: 2000-07-11

FRIOR FAILING D
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23;
                                                         42.4%; Score 39; DB 6; Length 181;
47.1%; Pred. No. 11;
iive 5; Mismatches 4; Indels
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Publication No. US20060009441A1
GENERAL INFORMATION
APPLICANT: EBELING, MARTIN
APPLICANT: HOENER, MARIUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :|:| |||: : :|| |
229 KIETTSSKVESSSESYK 245
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163 KIETTSSKVESSSESYK 179
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Best Local Similarity 47.1
Matches 8; Conservative
                                                             Query Match
Best Local Similarity 47.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
JS-10-980-388-118
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US-10-980-388-100
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APPLICANT: Lind, Peter
APPLICANT: Kaytes, Paul S.
APPLICANT: Kaytes, Paul S.
APPLICANT: Kaytes, Paul S.
APPLICANT: Kaytes, Paul S.
APPLICANT: Wiff, Valerie
APPLICANT: Wood, Linda S.
TITLE OF INVENTION: NOVEL G Protein-Coupled Receptors Cross-Reference To Related Appl FILE REPERSING: 00325.US1
FILE REPERSING: 200325.US1
FRIOR PILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/184,305
PRIOR APPLICATION NUMBER: 60/184,305
PRIOR PILING DATE: 2000-02-23
PRIOR PILING DATE: 2000-02-23
PRIOR PILING DATE: 2000-02-23
PRIOR PILING DATE: 2000-02-23
PRIOR PILING DATE: 2000-02-33
PRIOR PILING DATE: 2000-02-33
PRIOR PILING DATE: 2000-02-33
PRIOR PILING DATE: 2000-02-33
PRIOR PILING DATE: 2000-02-33
PRIOR PILING DATE: 2000-03-13
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PRIOR PILING DATE: 2000-03-13
PRIOR PILING DATE: 2000-03-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: Description of Artificial Sequence; note = synthetic construct
US-10-506-796A-9
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                                APPLICANT: ARNTZEN, Charles
TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
FILE REPERRENCE: 01231.006612
CURRENT APPLICATION NUMBER: 105/10/506,796A
CURRENT FILING DATE: 2004-09-03
PRIOR PELLING DATE: 2003-06
PRIOR PELLING DATE: 2003-06
PRIOR PILING DATE: 2002-03-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.2
SEQ ID NO 9
LENGTH: 171
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Publication No. US20050255490A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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APPLICANT: Parodi, Luis A.
APPLICANT: Hiebsch, Ronald R.
APPLICANT: Lind, Peter
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ORGANISM: Homo sapiens
       MATOBA,
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       APPLICANT:
APPLICANT:
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| Belbication No. US2006000880A1
| GENERAL INFORMATION |
| GENERAL INFORMATION |
| APPLICANT: EBELING, MARTIN |
| APPLICANT: LINDEMANN, LOTHAR |
| TITLE OF INVENTION: MOUSE TRACE AMINE ASSOCIATED RECEPTORS AND |
| TITLE OF INVENTION: POLYPEPTIDES |
| FILE REFREENCE: 22646 |
| CURRENT APPLICATION NUMBER: US/11/174,819 |
| CURRENT PILING DATE: 2004-07-08 |
| PRIOR APPLICATION NUMBER: EP 04103262.4 |
| PRIOR FILING DATE: 2004-07-08 |
| NUMBER OF SEQ ID NOS: 136 |
| SEQ ID NO SIA |
| SEQ ID NO SIA |
| LENGTH: 342 |
| TYPE: PRT
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; APPLICANT: LINDEMANN, LOTHAR
; TITLE OF INVENTION: HUMAN TRACE AMINE ASSOCIATED RECEPTORS;
; FILE REPERENCE: 22645;
; CURRENT APPLICATION NUMBER: US/11/174,816
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: EP 04103261.6
; PRIOR PILING DATE: 2004-07-08
; NUMBER OF SEQ ID NOSS: 115
; SEQ ID NOSS: 115
; SQFTWARE: Patentin version 3.3
; SEQ ID NOS: 115
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: huthar 8
US-11-174-816-18
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229 KIETTSSKVESSSESYK 245
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229 KIETTSSKVESSSESYK 245
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US-11-174-819-71
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